

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein, Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein. - protein search, using sw model

Run on: June 20, 2005, 09:35:58 ; Search time 30 Seconds
(without alignments)
624.564 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTVSFSTKGTATYYNF.....AVDQVKPKIALLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 414038

Minimum DB seq length: 0

Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCUTS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	251	1 US-08-425-336-101	Sequence 101, App
2	1277	100.0	251	1 US-08-488-113B-101	Sequence 101, App
3	1277	100.0	251	1 US-08-477-484B-101	Sequence 101, App
4	1277	100.0	251	2 US-08-646-360-101	Sequence 101, App
5	1277	100.0	251	3 US-08-839-765-101	Sequence 101, App
6	1277	100.0	251	3 US-09-136-389-101	Sequence 101, App
7	1277	100.0	251	3 US-09-610-838-101	Sequence 101, App
8	1277	100.0	251	4 US-09-711-485-101	Sequence 101, App
9	1273	99.7	251	1 US-08-425-336-99	Sequence 99, App
10	1273	99.7	251	1 US-08-425-336-100	Sequence 100, App
11	1273	99.7	251	1 US-08-488-113B-99	Sequence 99, App
12	1273	99.7	251	1 US-08-488-113B-100	Sequence 100, App
13	1273	99.7	251	1 US-08-477-484B-99	Sequence 99, App
14	1273	99.7	251	1 US-08-477-484B-100	Sequence 100, App
15	1273	99.7	251	2 US-08-646-360-99	Sequence 99, App
16	1273	99.7	251	2 US-08-646-360-100	Sequence 100, App
17	1273	99.7	251	3 US-08-839-765-99	Sequence 99, App
18	1273	99.7	251	3 US-08-839-765-100	Sequence 100, App
19	1273	99.7	251	3 US-09-136-389-99	Sequence 99, App
20	1273	99.7	251	3 US-09-136-389-100	Sequence 100, App
21	1273	99.7	251	3 US-09-610-838-99	Sequence 99, App
22	1273	99.7	251	3 US-09-610-838-100	Sequence 100, App
23	1273	99.7	251	4 US-09-711-485-99	Sequence 99, App
24	1273	99.7	251	4 US-09-711-485-100	Sequence 100, App
25	1269	99.4	251	1 US-08-425-336-2	Sequence 2, Appli
26	1269	99.4	251	1 US-08-425-336-10	Sequence 10, App
27	1269	99.4	251	1 US-08-488-113B-2	Sequence 2, Appli

28 1269 99.4 251 1 US-08-488-113B-110 Sequence 110, App
29 1269 99.4 251 1 US-08-477-484B-2 Sequence 2, Appli
30 1269 99.4 251 1 US-08-477-484B-110 Sequence 110, App
31 1269 99.4 251 2 US-08-646-360-2 Sequence 2, Appli
32 1269 99.4 251 2 US-08-646-360-110 Sequence 110, App
33 1269 99.4 251 3 US-08-621-803-247 Sequence 247, App
34 1269 99.4 251 3 US-08-839-765-2 Sequence 2, Appli
35 1269 99.4 251 3 US-08-839-765-110 Sequence 110, App
36 1269 99.4 251 3 US-09-136-389-2 Sequence 110, App
37 1269 99.4 251 3 US-09-136-389-110 Sequence 110, App
38 1269 99.4 251 3 US-09-217-352-247 Sequence 247, App
39 1269 99.4 251 3 US-09-610-838-2 Sequence 2, Appli
40 1269 99.4 251 3 US-09-610-838-110 Sequence 110, App
41 1269 99.4 251 4 US-09-711-485-2 Sequence 2, Appli
42 1269 99.4 251 4 US-09-711-485-110 Sequence 110, App
43 1269 99.4 251 4 US-09-645-603B-2 Sequence 2, Appli
44 1266 99.1 251 1 US-07-901-707-2 Sequence 2, Appli
45 1266 99.1 251 1 US-07-988-430-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-425-336-101
; Sequence 101, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGTATYTYVNFNLRLVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGTATYTYVNFNLRLVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
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QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
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DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2

US-08-488-113B-101
; Sequence 101, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION NUMBER: US 08/425,336
; APPLICATION DATA:
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION NUMBER: US 08/064,691
; APPLICATION DATA:
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION NUMBER: US 07/988,430
; APPLICATION DATA:
; FILING DATE: 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNITKRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNITKRLHFGGSYPSLEGEK 120
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DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
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DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3

US-08-477-484B-101
; Sequence 101, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
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DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVMSAARFTFIENQIRNN 180
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DB 181 FQORIRPANNITSLNKGKLSFQIRTSANGMFSEAVLERANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-101
Sequence 101, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
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DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNITKRLHFGSGVPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVMSAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVMSAARFTFIENQIRNN 180
QY 181 FQORIRPANNITSLNKGKLSFQIRTSANGMFSEAVLERANGKYYVTVADQVKPKI 240
DB 181 FQORIRPANNITSLNKGKLSFQIRTSANGMFSEAVLERANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5
US-08-839-765-101
Sequence 101, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA

/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 15-APR-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 101:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-839-765-101

Query Match 100.0%; Score 1277; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFLELRVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60

QY 61 GOLAEIADVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
DB 61 GOLAEIADVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 6
US-09-136-389-101
/ Sequence 101, Application US/09136389
/ Patent No. 6146850
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.

/
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 101:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-136-389-101

Query Match 100.0%; Score 1277; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFLELRVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60

QY 61 GOLAEIADVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
DB 61 GOLAEIADVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

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DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

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DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKPK 251
DB 241 ALLKFVDKPK 251

RESULT 7

US-09-610-838-101
; Sequence 101, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-101

Query Match 100.0%; Score 1277; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYITYVNFLELRLVRLKLPBGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

DB 1 GLDTVSFSTKGATYITYVNFLELRLVRLKLPBGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDGIPLRIGIKKLDENADNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDGIPLRIGIKKLDENADNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKKYVYTTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKKYVYTTAVDQVKPKI 240
QY 241 ALLKFVDKPK 251
DB 241 ALLKFVDKPK 251

RESULT 8
US-09-711-485-101
; Sequence 101, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-711-485-101

Query Match 100.0%; Score 1277; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDVSFSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLABIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 120
Db 61 GOLABIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 9
US-08-425-336-99
; Sequence 99, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDVSFSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLABIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 120
Db 61 GOLABIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 10
US-08-425-336-100
; Sequence 100, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYTYVNFNLKVPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYYTYVNFNLKVPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFTENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFTENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
US-08-488-113B-99
Sequence 99, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYTYVNFNLKVPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYYTYVNFNLKVPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFTENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFTENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12
US-08-488-113B-100
Sequence 100, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 100:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-488-113B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
US-08-477-484B-99
/ Sequence 99, Application US/08477484B
/ Patent No. 5756699
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,484B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 99:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-477-484B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
US-08-477-484B-100
/ Sequence 100, Application US/08477484B
/ Patent No. 5756699
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
```

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;;
;; NUMBER OF INVENTIONS: Proteins
;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;;
;; ZIP: 60661

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEFAX: 312/707-9155
;;
;; INFORMATION FOR SEQ ID NO: 100:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-477-484B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYNFLNELRVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYNFLNELRVKLPKPGNSHGIPLLRKADDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDPADPAAYEGFLFKNTIKTLRHFGGSYPSPLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDPADPAAYEGFLFKNTIKTLRHFGGSYPSPLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTFIASLLVVIQVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTFIASLLVVIQVSEAAFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLELRANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLELRANGKYYVTAVDQVKPKI 240

QY 241 ALLKFDKDPK 251
DB 241 ALLKFDKDPK 251

RESULT 15

US-08-646-360-99
; Sequence 99, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;;
;; INFORMATION FOR SEQ ID NO: 99:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-646-360-99

Query Match 99.7%; Score 1273; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYNFLNELRVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYNFLNELRVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDPADPAAYEGFLFKNTIKTLRHFGGSYPSPLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDPADPAAYEGFLFKNTIKTLRHFGGSYPSPLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTFIASLLVVIQVSEAAFTFIENQIRNN 180

Db 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
Qy 181 FQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:49:13
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:34:33 ; Search time 25 Seconds
(without alignments)
966.016 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDTSFSTKGATYTYNF.....AVDQVKPKIALLKFDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 130334

Minimum DB seq length: 0
Maximum DB seq length: 251
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:***
1: pir1:***
2: pir2:***
3: pir3:***
4: pir4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	353.5	27.7	245	JC4840	rRNA N-glycosidase
2	330	25.8	251	C39761	abrin (clone 7.2)
3	317	24.8	247	JU0393	karasurin - Mongol
4	312	24.4	247	CJ5032	karasurin-B - Tric
5	274	21.5	250	JN0108	luffin-B - smooth
6	195	15.3	40	S17574	rRNA N-glycosidase
7	149	11.7	236	S17932	rRNA N-glycosidase
8	121	9.5	106	B39761	abrin (clone 3.7)
9	82	6.4	220	D96702	unknown protein, 6
10	79.5	6.2	249	B95186	rRNA pseudouridine
11	78.5	6.1	249	B98053	pseudouridyate sy
12	75.5	5.9	244	A28053	carboxyl reductase
13	74	5.8	245	B70247	conserved hypothet
14	73.5	5.8	246	F72769	hypothetical prote
15	73	5.7	202	S26074	hypothetical prote
16	73	5.7	249	T47996	hypothetical prote
17	72.5	5.7	220	B82472	hypothetical prote
18	71.5	5.6	169	F82403	hypothetical prote
19	71.5	5.6	204	AB3024	transcription regu
20	71.5	5.6	222	AE1826	hypothetical prote
21	71.5	5.6	234	E96957	HAD superfamily by
22	71	5.6	139	D86753	hypothetical prote
23	71	5.6	139	G86681	hypothetical prote
24	71	5.6	221	AE1143	hypothetical prote
25	71	5.6	242	C90415	uroporphyrinogen I
26	71	5.6	245	J01607	polyhedrin - Antic
27	70.5	5.5	246	G70452	hypothetical prote
28	69.5	5.4	211	A64490	precorrin-6f methy
29	69.5	5.4	223	A90523	hypothetical prote

30	69	5.4	112	2	AG2275	hypothetical prote
31	69	5.4	145	2	AE1714	flavodoxin homolog
32	69	5.4	211	2	A84006	GTP pyrophosphokin
33	69	5.4	232	2	S47846	rfaY protein - Esc
34	69	5.4	234	2	A82814	thiamin-phosphate
35	68.5	5.4	194	2	T33345	hypothetical prote
36	68.5	5.4	238	1	CYCHB1	beta-crystallin BI
37	68.5	5.4	239	2	C84994	hypothetical prote
38	68	5.3	122	1	MNIV23	nonstructural prot
39	68	5.3	185	2	D97187	DTDP-4-dehydrotram
40	68	5.3	205	2	T16560	hypothetical prote
41	68	5.3	211	2	C90330	partial transposas
42	67.5	5.3	181	2	A11682	conserved hypothet
43	67.5	5.3	191	2	C75011	hypothetical prote
44	67.5	5.3	231	2	S77879	glucose-inhibited
45	67.5	5.3	241	2	AH3543	gtp-binding protei

ALIGNMENTS

RESULT 1

JC4840
rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd
C:Species: Trichosanthes anguina (snake gourd)
C>Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C:Accession: JC4840; JT0701; JT0677
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Biomed. Sci. 3, 178-186, 1996
A>Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from 7
A:Reference number: JC4840
A:Accession: JC4840
A:Molecule type: protein
A:Residues: 1-132, 'S', 134-245 <CHO1>
A:Experimental source: seed
A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
Submitted to JIPID, August 1995
A:Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from
A:Reference number: JT0677
A:Accession: JT0701
A:Molecule type: protein
A:Residues: 1-50, 'L', 52-245 <CHO2>
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F:4-242/Domain: rRNA N-glycosidase homology <RNG>
F:51.201/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:70.158.161/Active site: Tyr, Glu, Arg #status predicted
F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match		27.7%	Score	353.5	DB 2	Length	245
Best Local Similarity		36.3%	Pred. No.	1.1e-21			
Matches		91	Conservative	44	Mismatches	95	Indels
						21	Gaps
7;							
QY	5	VSFSTKGATYTYN	NFLNELRVKL	PEGNHSHGIP	LLRKADDP	KGAFVLV	ALSDNMGQLA 64
Db	2	VSFDSLSTATKKS	YSFFITQLRD	ALPTQGTGYG	IPLLPSTAG	-SQRFRFNL	TNYNDET 60
QY	65	ETAI	DVTSVYVGVQ	VRNRSYFFK	ADAPAAV	RGELFKNT	IKRLHFGGSYPSLE---GEKA 121
Db	61	TVAVD	VTVNVIYV	ADAVSYFF	EDTPAEAF	KLIIFAGT	KTVKLPYSNGTDKLQSVVGRQ- 119
QY	122	YRETTDLG	IEPLRIGIK	LDENAI	DN---YK	PEIASSLL	VVIQWSEARFTFIENQIR 178
Db	120	-RDMIEL	GIPAL-----	SSAITN	MVYDYQ	STAAALL	VLIQSTAEAAKYKIEQQVS 170
QY	179	NNFQOR	IRPANN	TISLEN	KWGLSFQ	ITSG--	ANGMFSEAVELERANKKYV---TAVD 234
Db	171	SHISSN	FYFNQAV	ISLEN	KWGLSK	QIQIAN	RTGHGFENPVELYNPDGTRFSVTHTSAG 230
QY	235	QVKPK	IALLK	245			
Db	231	VVKG	NIKLLY	241			


```
C;Species: Saponaria officinalis (common soapwort)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: SI7932; SI5458
R;Fortham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Croy, R.R.D.
Mol. Gen. Genet. 229, 460-466, 1991
A;Title: Characterisation of saporin genes: in vitro expression and ribosome inactivation
A;Reference number: SI7932; MUID:92049247; PMID:1719367
A;Accession: SI7932
A;Molecule type: DNA
A;Residues: 1-236 <FOR>
A;Cross-references: UNIPROT:P27560; EMBL:X59256; NID:G21322; PIDN:CAA41949.1; PID:G21323
A;Note: The authors translated the codon CTC for residue 75 as Phe and GCA for residue 1
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: Glycosidase; hydrolase; monomer; toxin
F;1-221/Domain: rRNA N-glycosidase homology (fragment) <RNG>
```

Query Match	11.7%; Score 149; DB 2; Length 236;
Best Local Similarity	25.2%; Pred. No. 6.6e-05;
Matches	58; Conservative 39; Mismatches 77; Indels 56; Gaps 11;

```
QY      51 FVLVALSNDNGQLAEIAIDVTSVVYGVQVR-----NRSYFFKD-----APDAA- 94
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
Db      22 FLRLNFQSSRGTVS-LGLKRENLVYVAYLAMDNANVNRAYYFGTETTSABLTLLPEATV 80
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
QY      95 -----YEGLFKNITIKTRLHFGSGSYPSLEGEKAYRETLDIGIEPIRIGIKKL DEN 143
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
Db      81 ANOKALEYTEDYQSIERNAKIT-----EGDKT-RKEILGLGINLSTLMDAVNKK 128
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
QY     144 A-IDNKYPTEIASLLVVIQMVSEAAFTFIENQIRNNFOQIRPANNTISLENKGKGL 201
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
Db     129 ARVKNE-----ARELLAIQTAEARPRYIQLNVTKPNPKFNSEDKVIQOVNWSKI 183
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
QY     202 SFQIRTSGANGMFSEAVELERANGKKYYVTAVDVQKP-KIALLKFDVKDP 250
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
Db     184 SKALYGDAKNGVFNK--DYDFGFK-----VRQVKDLQMGLLMYLGTTP 225
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
```

RESULT 8
B39761
abrin (clone 3.7) precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 05-Jun-1998
C;Accession: B39761
R;Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
A;Accession: B39761
A;Molecule type: DNA
A;Residues: 1-106 <EVE>
A;Cross-references: GB:X54873
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F;1-106/Product: abrin chain A (fragment) #status predicted <ACH>
F;1-101/Domain: rRNA N-glycosidase homology (fragment) <RNG>
F;19,22/Active site: Glu, Arg #status predicted

Query Match	9.5%; Score 121; DB 2; Length 106;
Best Local Similarity	35.3%; Pred. No. 0.0044;
Matches	36; Conservative 16; Mismatches 46; Indels 4; Gaps 3;

```
QY     152 EIASSLVVIQMVSEAAFTFIENQIRNNFO-QRIIRPANNTISLENKGKLSFQIRTSG 209
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
Db      5 EKARTLIIVIQMVSEAAFRYSINRVGSIRGTAFQPDPMISLENNWNLSCGVQQS- 63
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
QY     210 ANGFMFSEAVELERANGKKYYVTAVDQ-VKPKIALLKFDVKDP 250
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
Db      64 VQGTFPHPTVLNRNICNEPVIDSLSHPTVAVLALMLFVCNPP 105
       |: : : : : : : : : : | : | : | : | : | : | : | : | : | : |
```

RESULT 9
D96702

RESULT 11
B98053
pseudouridylylate synthase [EC 4.2.1.70] [imported] - Streptococcus pneumoniae (B
C; Species: Streptococcus pneumoniae
C; Date: 22-Oct-2001 #sequence revision 22-Oct-2001 #text change 09-Jul-2004

C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Accession: B98053
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.O.; Lu, J.; Matsushima, P.; McAnir
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskun
A; Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: B98053
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-249 <KUR>
A; Cross-references: UNIPROT:Q8CWL1; GB:A007317; PIDN:AAL00255.1; PID:g15459107
C; Genetics:
A; Gene: trxA
C; Superfamily: tRNA-pseudouridine synthase I
C; Keywords: carbon-oxygen lyase; hydro-lyase

[illegible]

A:Title: A growth factor-repressible gene associated with protein kinase C-mediated inhibition
A:Reference number: S03382; MUID:98273310; PMID:2455724
A:Accession: S03382
A:Molecule type: mRNA
A:Residues: 1-244 <NAV>
A:Cross-references: UNIPROT:P08074; EMBL:X07411; MID:g50003; PIDN:CAA30309.1; PID:g50004
A:Experimental source: strain C3H
R:Nakanishi, M.; Deyashiki, Y.; Ohshima, K.; Hara, A.
Eur. J. Biochem. 228, 381-387, 1995
A:Title: Cloning, expression and tissue distribution of mouse tetrameric carbonyl reductase
A:Reference number: S69141; MUID:95220366; PMID:7705352
A:Accession: S69141
A:Molecule type: mRNA
A:Residues: 1-244 <NAV>
A:Cross-references: EMBL:D26123; MID:g440371; PIDN:BAA05120.1; PID:g699608
A:Experimental source: lung; strain CD-1
A:Accession: S69142
A:Molecule type: protein
A:Residues: 1-29; 40-80; 84-96; 110-198; 209-223; 227-244 <NAW>
A:Experimental source: lung; strain CD-1
C:Genetics:
A:Genome: nuclear
C:Complex: homotetramer
C:Function:
A:Description: catalyzes the reduction of various carbonyl compounds to corresponding alcohols
A:Pathway: involved in pulmonary metabolism of endogenous carbonyl compounds and xenobiotics
A:Note: member of short-chain alcohol dehydrogenase family
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: mitochondrial; NADP; oxidoreductase
F:1-244/Product: carbonyl reductase (NADPH) [status experimental <MAT>
F:8-180/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 5.9%; Score 75.5; DB 1; Length 244;
Best Local Similarity 24.2%; Pred. No. 74;
Matches 46; Conservative 32; Mismatches 71; Indels 41; Gaps 10;

QY 94 AVEGLFKNTIKTRLHFGSGVPSLEGEKAYRETTDL-----GIEPLRIGIKKLD--EN 143
DB 15 AGKIGRDITVKA--LHASGA----KVAVTRTNSDLVSLAKECPGIEPVCVDLGDWDATBK 69

QY 144 AIDNYKPTSE--IASSLLVVIQVSEAAARFTFEN---QIRNNPQQRIRPANNTI----- 192
DB 70 ALGGIGPDLVNNALVIMQPLEVTKEAFDSFVNLRSVQVSQWARMINGVPG 129

QY 193 SLEN-----KWGKLSFQIRTSANGMFSEAVELERANGKYKYVTAVDVQPKIALI-- 243
DB 130 SIWVSSVMAHVTFPNLITYSTSTKGAMTMTLTKAMAMELGPHK----IRVNSVNPVTVLTD 185

QY 244 --KFVDKDPK 251
DB 186 MGKVSADPE 195

RESULT 13
B70247
conserved hypothetical protein BB17 - Lyme disease spirochete plasmid J/lp38
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: B70247
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <KLE>
A:Cross-references: UNIPROT:O50772; GB:AE000787; MID:g2690175; PIDN:AAC66087.1; PID:g269
A:Experimental source: strain B31
C:Genetics:

A:Genome: plasmid
C:Superfamily: Lyme disease spirochete plasmid probable stage 0 sporulation protein J

Query Match 5.8%; Score 74; DB 2; Length 245;
Best Local Similarity 26.4%; Pred. No. 99;
Matches 37; Conservative 23; Mismatches 38; Indels 42; Gaps 10;

QY 2 LDT---VSFSTKGATYITVNFELNRLVKLKEGNS-HGIPILRKADDPGKAFVLVALS 57
DB 128 LTPPSFSFILKNA-----LNTNHHIIPVQPTWSIESLEILMKKITD--RSY----- 174

QY 58 NDGQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYVEGLFKNTIKTRLHFGGSY---- 113
DB 175 -----NISI-----VVNQFIKARN-ILKEVEDALYK-RYSNYIKGKIHYNSIKVTI 219

QY 114 -----PSLEGEKAYRETTDL 128
DB 220 INRLPEPIK-SKYVKEANDV 238

RESULT 14
F72769
hypothetical protein APE0145 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: F72769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <KAW>
A:Cross-references: UNIPROT:O9YFV5; DBJ:AP000058; NID:g5103388; PIDN:BAA79056.1; PID:dl
A:Experimental source: strain K1
C:Genetics:
A:Genes: APE0145
C:Superfamily: Aeropyrum pernix hypothetical protein APE0145

Query Match 5.8%; Score 73.5; DB 2; Length 246;
Best Local Similarity 21.0%; Pred. No. 11e+02;
Matches 43; Conservative 39; Mismatches 64; Indels 59; Gaps 10;

QY 66 IADIVTSVY-VVGVQVRNRSYFFKADPAAYVEGLFKNTIKTRLHFGGSYPSLEGEKAYRE 124
DB 1 MAIKVDTFYGVIGSEVRDE-----YERVVGTIVSFSSNVDGEIQSIE-----LK 44

QY 125 TTDLGIEPLRIG-IXKLD-----ENAIQNY-KPTFIASS 156
DB 45 IVDRGIERIPGGRVKIVDGKIVVPEWKYEATRVIEALERAYKRRRAVENIAKQSSIPSS 104

QY 157 LL--VVIQMVSEAAARFTFIENQIRNFFQIRP-----ANNITSLNKW--GKLSFQ 204
DB 105 IVENMKRQTEIEIKLKIKAEBAKTRIKERIAIDDEMLHIAGATLANQLWYFSGEISDR 164

QY 205 IRTSGANGM--FSEAVELERANGKK 227
DB 165 SYTSGNNHLKLNDSLEREKSDAKR 189

RESULT 15
S26074
hypothetical protein R - Methanobacterium thermoformicum plasmid pf21
C:Species: Methanobacterium thermoformicum
C:Date: 22-Nov-1993 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S26074; S30322; S23894; S26456
R:Noelling, J.; de Vos, W.M.
Nucleic Acids Res. 20, 5047-5052, 1992
A:Title: Identification of the CTAG-recognizing restriction-modification systems MthZI ar
A:Reference number: S26073; MUID:93027239; PMID:1408820
A:Accession: S26074

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:22:52 ; Search time 111.5 Seconds
(without alignments)
1152.752 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GEDTVSFSTKGATITYYVNF.....AVDQVKPKIALLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 827211

Minimum DB seq length: 0
Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	321	25.1	Q7DM12	Q7dm12 abrus preca
2	317	24.8	Q6BBQ4	Q6bbq4 trichosanthe
3	317	24.8	Q9LRE3	Q9lre3 trichosanthe
4	315	24.7	Q96236	Q96236 abrus preca
5	314.5	24.6	Q8XKH7	Q8xkh7 viscum albu
6	314	24.6	Q96237	Q96237 abrus preca
7	312.5	24.5	Q8LQK5	Q8lkq5 viscum albu
8	309.5	24.2	Q8LQK4	Q8lkq4 viscum albu
9	308	24.1	Q96235	Q96235 abrus preca
10	300	23.5	Q8RY69	Q8ry69 gynoSTEMMA
11	290	22.7	Q7YIU7	Q7yiu7 gynoSTEMMA
12	286	22.4	Q7YIU5	Q7yiu5 gynoSTEMMA
13	282	22.1	Q6J3N3	Q6j3n3 phytolacca
14	278	21.8	Q6J3N4	Q6j3n4 phytolacca
15	278	21.8	Q9ATB3	Q9atb3 phytolacca
16	274	21.5	R1PB LUFCY	P22851 luffa cylin
17	268	21.0	Q6J3N2	Q6j3n2 phytolacca
18	260	19.6	Q7SIF0	Q7sif0 trichosanthe
19	243	19.0	R1P3 GELMU	P24475 gelonium mu
20	238	18.6	Q7YIU6	Q7yiu6 gynoSTEMMA
21	197.5	15.5	Q8SAD7	Q8sad7 cucurbita m
22	187.5	14.7	Q84LI9	Q84li9 cucurbita m
23	187.5	14.7	Q84LI7	Q84li7 cucurbita m
24	186.5	14.6	Q8S2R5	Q8s2r5 cucurbita m
25	186.5	14.6	Q84LI8	Q84li8 cucurbita m
26	185.5	14.5	Q8SAGO	Q8sago benincasa h
27	168.5	13.2	Q84859	Q4859 amarantus
28	149	11.7	R1P3 SAPOF	P27560 saponaria o
29	131	10.3	Q9S8P3	Q9s8p3 gelonium mu
30	91.5	7.2	Q6Z425	Q6z425 oryza sativ
31	90	7.0	Q6Z4E3	Q6z4e3 oryza sativ

32	89.5	7.0	213	2	Q9K3E8	Q9k3e8 staphylococ
33	87.5	6.9	204	2	Q8IFY4	Q8ify4 bacillus ce
34	85	6.7	191	2	Q99XL9	Q99xl9 streptococc
35	84.5	6.6	187	2	Q7P521	Q7p521 fusbacteri
36	84	6.6	228	2	Q6MRV4	Q6mrv4 mycoplasma
37	82.5	6.5	101	2	Q7YIU4	Q7yiu4 gynoSTEMMA
38	82.5	6.5	195	1	RS4 FUSNN	Q8r43 fusbacteri
39	82	6.4	205	2	Q63DV2	Q63dv2 bacillus ce
40	82	6.4	205	2	Q8IY42	Q8ily42 bacillus an
41	82	6.4	205	2	Q6HLC7	Q6hlc7 bacillus th
42	82	6.4	220	2	Q9C9W1	Q9c9w1 arabidopsis
43	82	6.4	249	2	Q8RMD6	Q8rmd6 mycoplasma
44	81	6.3	189	1	SSB MYCPE	Q8est6 mycoplasma
45	81	6.3	198	2	Q7R5S9	Q7r5s9 plasmodium

ALIGNMENTS

RESULT 1

Q7DM12 PRELIMINARY; PRT; 251 AA.
AC Q7DM12;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Abrin A-chain (Fragment).
OS Abrin precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abrease; Abrus.
OX NCBI_TaxID=3816;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94139756; PubMed=8307038;
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
RT "Cloning and expression of three abrin A-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.";
RL Eur. J. Biochem. 219:83-87(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; X76720; CA54138.1; -.
DR HSSP; F11140; 1ABR.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGA_RICIN; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28098 MW; 817B8B5C2A4AECCE CRC64;

Query Match 25.1%; Score 321; DB 2; Length 251;

Best Local Similarity 35.7%; Pred. No. 5.4e-18;

Matches 91; Conservative 39; Mismatches 107; Indels 18; Gaps 8;

QY	5	VSFSTKGATITYYVNFNLRLVKLPKPNHSHGIPLLRKKADDP-----CKAFVLVSLND	59
Db	5	IKFSTEGATSQYKQFIEALRRLR-GGLIHDPVL-----PDPTLQERNRITVELSNS	59
QY	60	NGQLAEIADTVTSVYVVGQVNRNRYFFKADPAAYEGFLKNTIKTRLHFGSGYPSLE-G	118
Db	60	DFRESIEVGIDVTNAVYVYRAGTQSYFLRDPASSADYLFCTGDQSLSPFYGYGLERW	119
QY	119	EKAYRETTDLGLEPIRIGIKKLDAENAINDKETETASSLLVVIQWVSEAAARTFTENQIR	178

Db 120 AHQSRQIQPLGLQALHGISFFRSGNDN---EKKARTLIVIIQWVAEARFRYISNRVR 178

Qy 179 NNFC--QRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYVYVAVDQ- 235

Db 177 VSIQTGTAQFDAAWISLENNWDLNLSRGVQES-VQDTFPNQVTLTNRNEPVIWLSLSP 233

Qy 236 VKPKIALLKQFVDKDP 250

Db 236 TVAVLALMLFVCNPP 250

RESULT 2

Q6BBQ4 PRELIMINARY; PRT; 247 AA.

AC Q6BBQ4;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Trichosanthin (Fragment).

GN Name=TCS;

OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

OX NCBI_TaxID=3677;

RP [1]

RN SEQUENCE FROM N.A.

RA Mi S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;

RA "Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL; AY669811; AAT91090.1; --

DR GO; GO:0030539; F:RNA N-glycosylase activity; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN

DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.

FT NON_TER 1

FT CHAIN <1> >247 trichosanthin.

FT NON_TER 247

FT SEQUENCE 247 AA; 27172 MW; BCBA762884F89CCE CRC64;

Query Match 24.8%; Score 317; DB 2; Length 247;

Best Local Similarity 37.1%; Pred. No. 1.1e-17;

Matches 91; Conservative 35; Mismatches 107; Indels 12; Gaps 7

Qy 5 VSFSTKGTATITYNFNELRVLKPEGNHSGIPLLRKKADDPGKAFVLVALSNDNGQLA 64

Db 2 VSFRLSGATSSYGVFISNLRRALPNERLYDIPLLRSTLQG-SORYALIHITNYADETI 60

Qy 65 EIAIDVTSVYVGVGVNRKRSYFFKDA-PDAAVEGLFKNTI-KTRLHFGGSYPSE-GEKA 121

Db 61 SVALDVTNVIYMGYPAGTSTFFNEASATEAAKYVKDMRWKTLFPGSYNVELQTAAG 120

Qy 122 YRETTDLGIEPLRIGIKKLDENADINYKPTETASSLLVVIQWVSAARPTFTFENIRNF 181

Db 121 IRENIPLGLPALSAI-----TTLFYNANSAASALMVLIIQSTSEARYKFTIEQIQKRA 175

Qy 182 QQRIRPANNTISLENKWKGLSFQIR-TSGANGMFSEAVELERANGKYVYVAVDQ--VKP 238

Db 176 DKTELPSSAIIISLENSWALSQIQIASTNNQGFETFPVVLINAQNORVAITNVDAGVWTS 235

Qy 239 KIALL 243

Db 236 NIALL 240

RESULT 3

.09LRE3


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FT NON TER 251
SQ SEQUENCE 251 AA; 28090 MW; A1177489012E989 CRC64;

Query Match
Best Local Similarity 24.2%; Score 309.5; DB 2; Length 251;
Matches 87; Conservative 40; Mismatches 111; Indels 13; Gaps 6;

QY 5 VSFSTKGATYIYVNFNLRLVRLKPEGNHSGHPIPLRKKAD-DPGKAFVLVALSNDNGQL 63
DB 8 VTHQTGDSEYF---RFIKLLRDSVSGSFDIPLPPSIPVSSAQRFVLVELTNQLGKM 64

64 AE---IAIDVTSVYVGVQVRNRSYFFKADPAAYEGLEFKNTIKTRLHFGGSYPSLE 120
DB 65 EDSITAADVTNLYVYVYAGQOSVFLRDAPGAEHLFTGTRSLPENGSLADLERYA 124

121 AYRETTDLGIEPLRIGIKKLDENADINYPKTRIASLLVVIQMVSEAAARFTFIENQ 180
DB 125 CHRDRIPGLRPLRSVSALD---YPGSSTRAQAGSSIIIVIQMISEAARFNPILWEARQY 181

181 FQORIR--PANNTISLENKWKGLSFQIRTSANGMSEAVELEERANKKKYVYTAVDQVP 238
DB 182 INSGVSYLFDVYVYMLEASWGQOSTQVOQS--TDGFNNPRLGISTGNFVWLSNRDVIA 240

239 KIALKLFVDKD 249
DB 241 SLGIWVFCRD 251

RESULT 9
QY 096235 PRELIMINARY; PRT; 251 AA.
AC Q96235;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Abrin A chain E164A/R167L (Fragment).
CN Name=pcDNAC-1-E164A/R167L;
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucoside I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID=3816;
[1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94139756; PubMed=8307038;
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
RT "Cloning and expression of three abrin A-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.";
RL Eur. J. Biochem. 219:83-87(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; X76644; CAAS4092.1; -
DR HSSP; P11140; IABR.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005098; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON TER 1 251
FT NON TER 1 251
SQ SEQUENCE 251 AA; 27997 MW; 3B60351839AEPB7E CRC64;

Query Match
Best Local Similarity 24.1%; Score 308; DB 2; Length 251;
Matches 89; Conservative 39; Mismatches 109; Indels 18; Gaps 8;

QY 5 VSFSTKGATYIYVNFNLRLVRLKPEGNHSGHPIPLRKKADDP-----GKAFVLVALSND 59

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DB 5 IKFSTEGATSGSYKQFIEALRERLR--GGLIHDIPLV-----PDPTLQERNRITVELSNS 59
QY 60 NQQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLEFKNTIKTRLHFGGSYPSLE-G 118
DB 60 DTESIEVGIDVTNAVYVYVYAGQOSVFLRDAPSSASDYLFTGTDQHSLEPFYGTGDLRW 119

119 EKAYRETTDLGIEPLRIGIKKLDENADINYPKTRIASLLVVIQMVSEAAARFTFIENQ 178
DB 120 AHQSRQQIPLGQALTHGISFERSGNDN---EEKARTLIVIIQMVAAALFRYISNRVR 176

179 NNFO--QRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELEERANKKKYVYTAVDQ- 235
DB 177 VSIQGTAFQPDPAAMISLENNDNLRSVQES--VQDTPNQVTLNIRNEPVIDSLSRP 235

236 VKPKIALLKFVDKOP 250
DB 236 TVAVLALMLFVCNPP 250

RESULT 10
QY 08RY69 PRELIMINARY; PRT; 203 AA.
AC Q8RY69;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type I ribosome-inactivating protein (fragment).
OS Gynostemma pentaphyllum (Jiaogulan).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucoside I; Cucurbitales; Cucurbitaceae; Gynostemma.
OX NCBI_TaxID=182084;
[1]
RN
RP SEQUENCE FROM N.A.
RA Lin Y., Wu Z.J., Lin Q.Y., Xie L.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY075115; AAL82822.2; -
DR HSSP; P24817; 1CES.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005098; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON TER 1 203
FT NON TER 1 203
SQ SEQUENCE 203 AA; 22692 MW; 8CCA3228286E09EF CRC64;

Query Match
Best Local Similarity 23.5%; Score 300; DB 2; Length 203;
Matches 80; Conservative 22; Mismatches 89; Indels 18; Gaps 4;

QY 5 VSFSTKGATYIYVNFNLRLVRLKPEGNHSGH-----IPLRKKADDPGKAFVLVALSN 58
DB 2 INFLAGADGGTYNTFIARQLQEL-----SIGTKQVANITVLKHHVSSNTQFLSINLNF 56

59 DNGQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEG---LFPKNTIKTRLHFGGSYPSL 116
DB 57 YNNAKITIGIDVDFVVGFLTGTSYIFKEAPDILAYNQSLFPGSRNLSYTGYYDDL 116

117 EGKAYRETTDLGIEPLRIGIKKLDENADINYPKTRIASLLVVIQMVSEAAARFTFIENQ 176
DB 117 ERGGARREDIPLGLPLNTAINTLPHR-----DSTSFRESFVLIQMVSEAAARFKIEAQ 171

177 IRNNFQORIRPANNTISLENKWKGLSFQI 205

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DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: GO:0009405; P:apoptosis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
SQ SEQUENCE 237 AA; A274F9BA402031DA CRC64;

Query Match 22.1%; Score 282; DB 2; Length 237;
Best Local Similarity 30.6%; Pred. No. 7.4e-15;
Matches 76; Conservative 44; Mismatches 96; Indels 32; Gaps 8;

QY 2 LDTVSFSTKGATVITYVNFNLRLVKLK-PEGNSHGIPILRRKADDPGKAFVLVALSNDN 60
DB 1 MNTIIVGVSTTSKYATFLNLRNEAKDPSLKCYGIPMLPNTNTP--KYVLVELQGSN 58
QY 61 GOLAEIAIDVTSVYVVGQ-----VNRNSYFFKD-----APDAAYEGLFKNT 102
DB 59 KKTITLMLRNLNLYVMGYSDPFETNRCRYHIFNDISGTERQDVETTLCPNA-----NSR 112
QY 103 IKTRLHFGSGYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENADINYPTEIASLLV 160
DB 113 VSRNINFDSDRYPTLESKAGVRSQVQLGIQILDSNIGKI--SGVMSFTEKTEAEFLVA 170
QY 161 IQWSEARFTEIQRNFOQIRPANNITSLNKGKLSFQIRTSANGMSEAVEL 220
DB 171 IQWSEARFTEIQRNFOQIRPANNITSLNKGKLSFQIRTSANGMSEAVEL 220
QY 221 ERANGKKY 228
DB 230 VDASGAKW 237

RESULT 14
Q6J3N4 PRELIMINARY; PRT; 237 AA.
AC Q6J3N4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Antiviral protein PAP (Fragment).
GN Name=pap;
OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen G., Lei J., Cao B., Zeng G.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY603352; AAT12447.1; -.
DR HSSP; Q03464; IAPA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: GO:0009405; P:apoptosis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1

SQ SEQUENCE 237 AA; 26622 MW; FE576A3C96A1F6C6 CRC64;

Query Match 21.8%; Score 278; DB 2; Length 237;
Best Local Similarity 30.2%; Pred. No. 1.6e-14;
Matches 75; Conservative 45; Mismatches 96; Indels 32; Gaps 8;

QY 2 LDTVSFSTKGATVITYVNFNLRLVKLK-PEGNSHGIPILRRKADDPGKAFVLVALSNDN 60
DB 1 MNTIIVGVSTTSKYATFLNLRNEAKDPSLKCYGIPMLPNTNTP--KYVLVELQGSN 58
QY 61 GOLAEIAIDVTSVYVVGQ-----VNRNSYFFKD-----APDAAYEGLFKNT 102
DB 59 KKTITLMLRNLNLYVMGYSDPFETNRCRYHIFNDISGTERQDVETTLCPNA-----NSR 112
QY 103 IKTRLHFGSGYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENADINYPTEIASLLV 160
DB 113 VSKNINFDSDRYPTLESKAGVRSQVQLGIQILDSNIGKI--SGVMSFTEKTEAEFLVA 170
QY 161 IQWSEARFTEIQRNFOQIRPANNITSLNKGKLSFQIRTSANGMSEAVEL 220
DB 171 IQWSEARFTEIQRNFOQIRPANNITSLNKGKLSFQIRTSANGMSEAVEL 220
QY 221 ERANGKKY 228
DB 230 VDASGAKW 237

RESULT 15
Q9ATB3 PRELIMINARY; PRT; 237 AA.
AC Q9ATB3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Antiviral protein (Fragment).
GN Name=mpap;
OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen D., Wang X., Zhou G.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF338910; AAK21951.1; -.
DR HSSP; P10297; IDGA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: GO:0009405; P:apoptosis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
SQ SEQUENCE 237 AA; FE4ADCBE03464783 CRC64;

Query Match 21.8%; Score 278; DB 2; Length 237;
Best Local Similarity 30.2%; Pred. No. 1.6e-14;
Matches 75; Conservative 45; Mismatches 96; Indels 32; Gaps 8;

QY 2 LDTVSFSTKGATVITYVNFNLRLVKLK-PEGNSHGIPILRRKADDPGKAFVLVALSNDN 60
DB 1 MNTIIVGVSTTSKYATFLNLRNEAKDPSLKCYGIPMLPNTNTP--KYVLVELQGSN 58
QY 61 GOLAEIAIDVTSVYVVGQ-----VNRNSYFFKD-----APDAAYEGLFKNT 102

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:21:47 ; Search time 113.5 Seconds
(without alignments)
855.303 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDVSFSTKGTATYYVNF.....AVDQVKPKIALLKFDKDKP 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1545266

Minimum DB seq length: 0
Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003Bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	251	2 AAR63914	Type I RI
2	1273	99.7	251	2 AAR63912	Type I RI
3	1269	99.4	251	2 AAR63903	Type I RI
4	1269	99.4	251	2 AAR63915	Type I RI
5	1269	99.4	251	8 ADG63044	Gelonium
6	1264	99.0	251	2 AAR63923	Type I RI
7	1261	98.7	251	2 AAR63921	Type I RI
8	1261	98.7	251	2 AAR63918	Type I RI
9	1261	98.7	251	2 AAR63920	Type I RI
10	1261	98.7	251	2 AAR63919	Type I RI
11	1261	98.7	251	2 AAR63924	Type I RI
12	1260	98.7	251	2 AAR63922	Type I RI
13	1260	98.7	251	2 AAR63916	Type I RI
14	1260	98.7	251	2 AAR63917	Type I RI
15	1257	98.4	251	2 AAR74177	Type I RI
16	1251	98.0	251	2 AAR37291	Plant typ
17	1171	91.7	235	2 AAR63913	Type I RI
18	323	25.3	247	3 AAY69048	Amino aci
19	323	25.3	248	2 AAR07518	Synthetic
20	323	25.3	248	2 AAR25573	Mature al
21	322	25.2	247	2 AAR67359	Trichosan
22	317	24.8	247	2 AAR21605	Antitumou
23	317	24.8	251	2 AAW14228	Mature po
24	316	24.7	247	2 AAW14232	Mature po
25	316	24.7	248	2 AAW14231	Mature po

26	316	24.7	249	2 AAW14230	Mature po
27	316	24.7	250	2 AAW14229	Mature po
28	315	24.7	251	3 AAB19267	Amino aci
29	315	24.7	251	7 ADC24290	A. precat
30	309	24.2	244	2 AAW14235	Mature po
31	309	24.2	245	2 AAW14234	Mature po
32	309	24.2	246	2 AAW14233	Mature po
33	308.5	24.2	250	2 AAW21700	hbrin-A A
34	308.5	24.2	250	2 AAW25137	Abrin A A
35	307	24.0	247	3 AAY69043	Amino aci
36	307	24.0	248	4 AAB36824	Residues
37	303	23.7	243	2 AAW14236	Mature po
38	302	23.6	246	2 AAR52636	Bioactive
39	299	23.4	242	2 AAW14237	Mature po
40	299	22.9	241	2 AAW14238	Mature po
41	291	22.8	240	2 AAW14239	Mature po
42	290.5	22.7	233	2 AAW14246	Mature po
43	290.5	22.7	234	2 AAW14245	Mature po
44	290.5	22.7	235	2 AAW14244	Mature po
45	290.5	22.7	236	2 AAW14243	Mature po

ALIGNMENTS

RESULT 1

AAR63914

ID AAR63914 standard; protein; 251 AA.

XX AAR63914;

AC AAR63914;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX

DE Type I RIP gelonin analog Gel(A44/A50).

XX

KW Type I ribosome-inactivating proteins; RIPS; gelonin;

KW cytotoxic therapeutic agents; autoimmune disease; cancer;

KW graft-versus-host disease.

XX

OS Gelonium multiflorum.

XX

PN WO9426910-A1.

XX

PD 24-NOV-1994.

XX

PF 12-MAY-1994; 94WO-US005348.

XX

PR 12-MAY-1993; 93US-00064691.

XX

PA (XOMA) XOMA CORP.

PI Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

DR

XX

PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which

are suitable for use as components of cytotoxic therapeutic agents.

XX

PS Example 3; Page 181-182; 221pp; English.

XX

CC AAR63912-RG3924 are analogs of AAR63903 type I ribosome-inactivating

protein (RIP) gelonin, one of the nine RIPS described in AAR63903-RG3911.

CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which

include gene fusion products and immunoconjugates. CTAs may be used to

selectively eliminate any cell type to which a RIP component is

targeted, by the specific binding capacity of the second component of

the agent. They can be used in the treatment of diseases where the

elimination of a particular cell type is desired, such as autoimmune

disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

correct PN field.)

XX

SQ Sequence 251 AA;


```
XX Sequence 251 AA;
SQ
Query Match 99.4%; Score 1269; DB 2; Length 251;
Best Local Similarity 99.2%; Pred. No. 2.7e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTSFSFGKATYTYVNFNLRLVKLPKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSFGKATYTYVNFNLRLVKLPKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLRHFGSGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLRHFGSGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 4
AAR63915
ID AAR63915 standard; protein; 251 AA.
XX
AC AAR63915;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C10/A44/A50).
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691..
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Carroll SP, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 189-190; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIFs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
```

```
CC correct PN field.)
XX Sequence 251 AA;
SQ
Query Match 99.4%; Score 1269; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-119;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSFGKATYTYVNFNLRLVKLPKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSFGKATYTYVNFNLRLVKLPKPEGNHSHGIPILRRKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLRHFGSGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLRHFGSGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 5
ADG63044
ID ADG63044 standard; protein; 251 AA.
XX
AC ADG63044;
XX
DT 11-MAR-2004 (first entry)
XX
DE Gelonium anti-HIV protein 31kDa (GAP31).
XX
KW anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
XX
OS Gelonium multiflorum.
XX
PN US6652861-B1.
XX
PD 25-NOV-2003.
XX
PF 25-AUG-2000; 2000US-00645603.
XX
PR 26-AUG-1999; 99US-0150885P.
XX
PA (UNYNY ) UNIV NEW YORK STATE.
XX
PI Lee-Huang S;
XX
DR WPI; 2004-050519/05.
XX
PT New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
PT antiviral activity, useful for treating human immunodeficiency virus
PT infection or tumor.
XX
PS Example 1; SEQ ID NO 2; 22pp; English.
XX
CC The invention describes an isolated peptide or polypeptide having an anti-
CC tumour and antiviral activity. Also described is a composition
CC comprising the isolated peptide or polypeptide, and a carrier, excipient
CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
CC polypeptides. The peptide or polypeptide is useful for treating HIV
CC infection, and tumour. This is the amino acid sequence of Gelonium anti-
CC HIV protein 30kDa (MAP30).
XX
SQ Sequence 251 AA;
```

Query Match 99.4%; Score 1269; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 2.7e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATITTYNFLNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATITTYNFLNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 6
AAR63923
ID AAR63923 standard; protein; 251 AA.
AC AAR63923;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX Type I RIP gelonin analog Gel(C103).
XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX WO9426910-A1.
XX 24-NOV-1994.
XX 12-MAY-1994; 94WO-US005348.
XX 12-MAY-1993; 93US-00064691.
XX (XOMA) XOMA CORP.
XX Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX Example 3; Page 187-188; 221pp; English.
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

SQ Sequence 251 AA;
Query Match 99.0%; Score 1264; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 8.7e-119;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATITTYNFLNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATITTYNFLNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 7
AAR63921
ID AAR63921 standard; protein; 251 AA.
AC AAR63921;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX Type I RIP gelonin analog Gel(C10).
XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX WO9426910-A1.
XX 24-NOV-1994.
XX 12-MAY-1994; 94WO-US005348.
XX 12-MAY-1993; 93US-00064691.
XX (XOMA) XOMA CORP.
XX Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX Example 3; Page 186; 221pp; English.
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

XX Sequence 251 AA;
SQ
Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 8
AAR63918
ID AAR63918 standard; protein; 251 AA.
XX
AC AAR63918;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C248).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 183-184; 22ipp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

CC correct PN field.)
XX Sequence 251 AA;
SQ
Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 9
AAR63920
ID AAR63920 standard; protein; 251 AA.
XX
AC AAR63920;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C244).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 185; 22ipp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLCFVDKDPK 251

RESULT 10
AAR63919
ID AAR63919 standard; protein; 251 AA.
XX
AC AAR63919;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I RIP gelonin analog Gel (C239).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
FN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 184; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the

CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
AAR63924
ID AAR63924 standard; protein; 251 AA.
XX
AC AAR63924;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I RIP gelonin analog Gel (C184).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
FN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 188-189; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of

CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
 Best Local Similarity 98.8%; Pred. No. 1.7e-118;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSFSFKGATYTYVNFNLNLRVKKLPEGNHSGIPLLRKKADDPGKAFVLVALSNDN 60
 DB 1 GLDTSFSFKGATYTYVNFNLNLRVKKLPEGNHSGIPLLRKKADDPGKAFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKADPAAAYEGLPKNTIKTRLHFGGSSPSLEGEK 120
 DB 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKADPAAAYEGLPKNTIKTRLHFGGSSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180
 QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 12

AAR63922
 ID AAR63922 standard; protein; 251 AA.

XX AAR63922;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

DE Type I RIP gelonin analog Gel (C60).

KW Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX Gelonium multiflorum.

PN WO9426910-A1.

PD 24-NOV-1994.

PF 12-MAY-1994; 94WO-US005348.

PR 12-MAY-1993; 93US-00064691.

PA (XOMA) XOMA CORP.

PI Better MD, Carroll SF, Studnicka GM;

DR WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

PS Example 3; Page 187; 221pp; English.

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is

CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 98.7%; Score 1260; DB 2; Length 251;
 Best Local Similarity 98.8%; Pred. No. 2.2e-118;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSFSFKGATYTYVNFNLNLRVKKLPEGNHSGIPLLRKKADDPGKAFVLVALSNDN 60
 DB 1 GLDTSFSFKGATYTYVNFNLNLRVKKLPEGNHSGIPLLRKKADDPGKAFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKADPAAAYEGLPKNTIKTRLHFGGSSPSLEGEK 120
 DB 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKADPAAAYEGLPKNTIKTRLHFGGSSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180
 QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 13

AAR63916

ID AAR63916 standard; protein; 251 AA.

XX AAR63916;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

DE Type I RIP gelonin analog Gel (C247/A44/A50).

KW Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX Gelonium multiflorum.

PN WO9426910-A1.

PD 24-NOV-1994.

PF 12-MAY-1994; 94WO-US005348.

PR 12-MAY-1993; 93US-00064691.

PA (XOMA) XOMA CORP.

PI Better MD, Carroll SF, Studnicka GM;

DR WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

PS Example 3; Page 190-191; 221pp; English.

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to

CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1260; DB 2; Length 251;
Best Local Similarity 99.2%; Pred. No. 2.2e-118;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTSFSTKATYITYVNFNLRLKLPKGNHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKATYITYVNFNLRLKLPKGNHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYPTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYPTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKEFVKD PK 251
DB 241 ALLKEFVKD PK 251

RESULT 14
AAR63917
ID AAR63917 standard; protein; 251 AA.
XX
AC AAR63917;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I RIP gelonin analog Gel (C247).
XX
XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
XX (XOMA) XOMA CORP.
PA Better MD, Carroll SF, Studnicka GM;
PI WPI; 1995-006804/01.
DR
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
PT
PS Example 3; Page 182-183; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which

CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1260; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 2.2e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSTKATYITYVNFNLRLKLPKGNHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKATYITYVNFNLRLKLPKGNHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYPTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYPTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKEFVKD PK 251
DB 241 ALLKEFVKD PK 251

RESULT 15
AAR74177
ID AAR74177 standard; protein; 251 AA.
XX
AC AAR74177;
XX
DT 25-MAR-2003 (revised)
DT 04-JAN-1980 (first entry)
DE Type I ribosome-inactivating protein gelonin.
XX
XX Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin.
OS Gelonium multiflorum.
FH Key Location/Qualifiers
FT Misc-difference 10 /label= Cys in claimed analogue
FT Misc-difference 17 /label= invariant residue
FT /note= "in ricin A-chain and the Type I RIPs"
FT Misc-difference 25 /label= see above
FT Misc-difference 44 /label= non-Cys residue in claimed analogue
FT Misc-difference 44 /label= Ala in claimed analogue
FT Misc-difference 50 /label= Non-Cys residue in claimed analogue
FT Misc-difference 50 /label= see above
FT Misc-difference 60 /label= Cys in claimed analogue
FT Misc-difference 74 /label= see above
FT Misc-difference 113 /label= see above
FT Misc-difference 133

FT Misc-difference 166..167 /label= see above
 FT Misc-difference 169 /label= see above
 FT Misc-difference 198 /label= see above
 FT Misc-difference 239..251 /label= see above
 FT Misc-difference 239 /label= location of Cys in claimed analogue
 FT Misc-difference 239 /label= Cys in claimed analogue
 FT Misc-difference 244 /label= see above
 FT Misc-difference 247..248 /label= see above
 FT Misc-difference 247..248 /label= see above
 XX US5416202-A.
 PN 16-MAY-1995.
 PD 09-DEC-1992.; 92US-00988430.
 XX 04-NOV-1991.; 91US-00787567.
 PR 19-JUN-1992.; 92US-00901707.
 XX (XOMA) XOMA CORP.
 PA Lei S, Carroll SF, Lane JA, Bernhard SL, Better MD;
 XX WPI; 1995-193480/25.
 DR Polynucleotide(s) encoding gelonin analogues - having a cysteine residue
 PT for intermolecular bonding for the prodn. of immuno-toxin(s).
 XX
 PS Claim 1; Fig 1; 66pp; English.
 XX
 CC Analogues of Type I RIP are defined as non-naturally occurring
 CC polypeptides that share the ribosome-inactivating activity of the natural
 CC protein but differ in AA sequence. Preferred analogues have a Cys
 CC available for disulfide bonding located at a posn. it its AA sequence
 CC from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy
 CC terminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA,
 CC which is a Type II RIP). The primary AA sequence of the Type I RIPs
 CC gelonin, BRIP, momordin II, luffin [see Islam et al. Agricultural
 CC Biological Chem., 54(5) 1343-45 1991], alphatriconanthin [see Chow et
 CC al., J. Biol. Chem., 265, 8670-74 1990], momordin I [see Ho et al., BBA,
 CC 1088, 311-14 1991], Mirabilis antiviral protein [see Habuka et al., J.
 CC Biol. Chem., 264(12) 6629-37 1989], pokeweed antiviral protein isolated
 CC from seeds [see Kung et al., Agric. Biol. Chem., 54(12), 3301-18 1990]
 CC and saporin [see Banatti et al., Eur. J. Biochem., 183, 465-70 1989] are
 CC individually aligned with the primary sequence of the ricin A-chain [see
 CC Halling et al., Nucleic Acids Res., 13, 8019-8033 1985] respectively in
 CC Figures 1-9. The AAs invariant among the ricin A-chain and the Type I
 CC RIPs are indicated in Ft. Also indicated are the preferred sites of Cys
 CC substitution. It is also preferred that the gelonin cysteine residues at
 CC positions 44 and 50 be replaced with alanine residues. (Updated on 25-MAR
 CC -2003 to correct PR field.)
 XX Sequence 251 AA;
 SQ

Query Match 98.4%; Score 1257; DB 2; Length 251;
 Best Local Similarity 98.4%; Pred. No. 4.4e-118;
 Matches 247; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITVNFNLRLKLPKGNHSGIPLLRKADDPGKAFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYITVNFNLRLKLPKGNHSGIPLLRKADDPGKAFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGFLFKNTIKRLHFGGYSPLSEGEK 120
 DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGFLFKNTIKRLHFGGYSPLSEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAI DNYKPTETIASLLVVIQMVSEARFTFIENQIRNN 180

Db 121 AYRETTDLGIEPLRIGIKKLDENAI DNYKPTETIASLLVVIQMVSEARFTFIENQIRNN 180
 QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELANGKYYVTVAVDQVKPKI 240
 Db 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 Db 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:43:21
 Job time : 114.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:47:23 ; Search time 104.5 Seconds

(without alignments)

922.286 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTSFSPKGTATITYNF.....AVDQVKPIALLKFVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1177303

Minimum DB seq length: 0

Maximum DB seq length: 251

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	251	14	US-10-127-890-101
2	1277	100.0	251	17	US-10-717-243-101
3	1273	99.7	251	14	US-10-127-890-99
4	1273	99.7	251	14	US-10-127-890-100
5	1273	99.7	251	17	US-10-717-243-99
6	1273	99.7	251	17	US-10-717-243-100
7	1269	99.4	251	9	US-09-765-527-247
8	1269	99.4	251	14	US-10-127-890-2
9	1269	99.4	251	14	US-10-127-890-110
10	1269	99.4	251	17	US-10-717-243-2
11	1269	99.4	251	17	US-10-717-243-110

12	1264	99.0	251	14	US-10-127-890-108	Sequence 108, App
13	1264	99.0	251	17	US-10-717-243-108	Sequence 108, App
14	1261	98.7	251	14	US-10-127-890-103	Sequence 103, App
15	1261	98.7	251	14	US-10-127-890-104	Sequence 104, App
16	1261	98.7	251	14	US-10-127-890-105	Sequence 105, App
17	1261	98.7	251	14	US-10-127-890-106	Sequence 106, App
18	1261	98.7	251	14	US-10-127-890-109	Sequence 109, App
19	1261	98.7	251	17	US-10-717-243-103	Sequence 103, App
20	1261	98.7	251	17	US-10-717-243-104	Sequence 104, App
21	1261	98.7	251	17	US-10-717-243-105	Sequence 105, App
22	1261	98.7	251	17	US-10-717-243-106	Sequence 106, App
23	1261	98.7	251	17	US-10-717-243-109	Sequence 109, App
24	1260	98.7	251	14	US-10-127-890-102	Sequence 102, App
25	1260	98.7	251	14	US-10-127-890-107	Sequence 107, App
26	1260	98.7	251	14	US-10-127-890-111	Sequence 111, App
27	1260	98.7	251	17	US-10-717-243-102	Sequence 102, App
28	1260	98.7	251	17	US-10-717-243-107	Sequence 107, App
29	1260	98.7	251	17	US-10-717-243-111	Sequence 111, App
30	323	25.3	247	9	US-09-792-793A-39	Sequence 39, Appli
31	323	25.3	247	15	US-10-375-209A-39	Sequence 39, Appli
32	318	24.9	247	14	US-10-127-890-6	Sequence 6, Appli
33	318	24.9	247	17	US-10-717-243-6	Sequence 6, Appli
34	315	24.7	251	14	US-10-282-935-3	Sequence 3, Appli
35	315	24.7	251	15	US-10-440-796-3	Sequence 3, Appli
36	307	24.0	247	9	US-09-792-793A-34	Sequence 34, Appli
37	307	24.0	247	15	US-10-375-209A-34	Sequence 34, Appli
38	277	21.7	248	14	US-10-127-890-5	Sequence 5, Appli
39	277	21.7	248	17	US-10-717-243-5	Sequence 5, Appli
40	248.5	19.5	200	14	US-10-083-336A-10	Sequence 10, Appli
41	246.5	19.3	190	14	US-10-083-336A-11	Sequence 11, Appli
42	245.5	19.2	198	14	US-10-083-336A-3	Sequence 3, Appli
43	245.5	19.2	198	14	US-10-083-336A-7	Sequence 7, Appli
44	245.5	19.2	199	14	US-10-083-336A-5	Sequence 5, Appli
45	243.5	19.1	188	14	US-10-083-336A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-127-890-101
; Sequence 101, Application US/10127890
; Publication No. US20030166196A1

GENERAL INFORMATION:
APPLICANT: Better, Marc D.

Carroll, Stephen F.
Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

PROTEINS

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

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/
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70-P4
/ TELEPHONE: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 101:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-127-890-101

Query Match      100.0%; Score 1277; DB 14; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYTYVNFNLRLVRLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGATYTYVNFNLRLVRLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2
US-10-717-243-101
/ Sequence 101, Application US/10717243
/ Publication No. US20050054835A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Studnika, Gary M.
/ Carroll, Stephen F.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/717,243
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/
/ FILING DATE: 18-NOV-2003
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 101:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-717-243-101

Query Match      100.0%; Score 1277; DB 17; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYTYVNFNLRLVRLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGATYTYVNFNLRLVRLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3
US-10-127-890-99
/ Sequence 99, Application US/10127890
/ Publication No. US20030166196A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Carroll, Stephen F.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
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; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99

; Query Match 99.7%; Score 1273; DB 14; Length 251;
; Best Local Similarity 99.6%; Pred. No. 2.7e-115;
; Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GLDTSFSTKGATYITYVNFNLELVKLPKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
; DB 1 GLDTSFSTKGATYITYVNFNLELVKLPKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
;
; QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSPSLEGEK 120
; DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSPSLEGEK 120
;
; QY 121 AYRETTDLGIEPLRIGIKLDENADINYPKPTETASLLVVIQMVSEAAFTFIENQIRNN 180
; DB 121 AYRETTDLGIEPLRIGIKLDENADINYPKPTETASLLVVIQMVSEAAFTFIENQIRNN 180
;
; QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELELANGKKYYVTVADVQVKPKI 240
; DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELELANGKKYYVTVADVQVKPKI 240
;
; QY 241 ALLKFVDKDPK 251
; DB 241 ALLKFVDKDPK 251
;
; RESULT 4
; US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
;
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100

; Query Match 99.7%; Score 1273; DB 14; Length 251;
; Best Local Similarity 99.6%; Pred. No. 2.7e-115;
; Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GLDTSFSTKGATYITYVNFNLELVKLPKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
; DB 1 GLDTSFSTKGATYITYVNFNLELVKLPKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
;
; QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSPSLEGEK 120
; DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSPSLEGEK 120
;
; QY 121 AYRETTDLGIEPLRIGIKLDENADINYPKPTETASLLVVIQMVSEAAFTFIENQIRNN 180
; DB 121 AYRETTDLGIEPLRIGIKLDENADINYPKPTETASLLVVIQMVSEAAFTFIENQIRNN 180
;
; QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELELANGKKYYVTVADVQVKPKI 240
; DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELELANGKKYYVTVADVQVKPKI 240
;
; QY 241 ALLKFVDKDPK 251
; DB 241 ALLKFVDKDPK 251
;

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RESULT 5
US-10-717-243-99
; Sequence 99, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-NOV-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-717-243-99
Query Match 99.7%; Score 1273; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGATYITYYNFLNELRVKLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYYNFLNELRVKLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYGVQVRNRSYFFKDPAAAYEGLFKNTIKTLRHFGSGYPSLGEK 120
DB 61 GOLAEIAIDVTSVYGVQVRNRSYFFKDPAAAYEGLFKNTIKTLRHFGSGYPSLGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFOIRTSYGANGMFSEAVELEBRANGKYYVTVADQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFOIRTSYGANGMFSEAVELEBRANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
RESULT 6
US-10-717-243-100
; Sequence 100, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-NOV-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100
Query Match 99.7%; Score 1273; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGATYITYYNFLNELRVKLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60

Db 1 GLDTSFSTKGATYYVNFLELRVLPKPEGNHSHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 7

US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match 99.4%; Score 1269; DB 9; Length 251;
Best Local Similarity 99.2%; Pred. No. 6.7e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYYVNFLELRVLPKPEGNHSHGIPLLRKADDPGKAFVLVALSNDN 60
Db 1 GLDTSFSTKGATYYVNFLELRVLPKPEGNHSHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 8

US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2


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/
/
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match          99.4%; Score 1269; DB 17; Length 251;
Best Local Similarity 99.2%; Pred. No. 6.7e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYTYVNFLELRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYYTYVNFLELRVKKLPEGNHSHGIPLLRKKADDPGKCFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240
DB 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
US-10-717-243-110
/ Sequence 110, Application US/10717243
/ Publication No. US20050054835A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Carroll, Stephen F.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/717,243
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
```

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/
/
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 110:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-717-243-110

Query Match          99.4%; Score 1269; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 6.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYTYVNFLELRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYYTYVNFLELRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240
DB 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12
US-10-127-890-108
/ Sequence 108, Application US/10127890
/ Publication No. US20030166196A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Carroll, Stephen F.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
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/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/10/127,890
/ APPLICATION NUMBER: US/10/127,890
/ FILING DATE: 23-Apr-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-9155
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108

Query Match          99.0%; Score 1264; DB 14; Length 251;
Best Local Similarity 98.8%; Pred. No. 2e-114;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
```

```
/
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/717,243
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-9155
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108

Query Match          99.0%; Score 1264; DB 17; Length 251;
Best Local Similarity 98.8%; Pred. No. 2e-114;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
US-10-127-890-103
; Sequence 103, Application US/10127890
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Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103
Query Match 98.7%; Score 1261; DB 14; Length 251;
Best Local Similarity 98.8%; Pred. No. 4e-114; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 3;
QY 1 GLDTSVSTKGTATYYTNFLNELRVKLPKPNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYTNFLNELRVKLPKPNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIADIVTSYVVGQVRNRSYFFKADPAAVEGLFKNTIKTLRHFGSGYPSLEGEK 120
DB 61 GQLAEIADIVTSYVVGQVRNRSYFFKADPAAVEGLFKNTIKTLRHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAINDKYPTETIASLLVVIQWVSAARFTTIEQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAINDKYPTETIASLLVVIQWVSAARFTTIEQIRNN 180
QY 181 FQORIRPANNITSLNENKWKLSFQIRTSANGWFSFAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNITSLNENKWKLSFQIRTSANGWFSFAVELERANGKYYVTAVDQVKPKI 240
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QY 241 ALLKFVDDPK 251
DB 241 ALLKFVDDPK 251
RESULT 15
US-10-127-890-104
Sequence 104, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-890-104
Query Match 98.7%; Score 1261; DB 14; Length 251;
Best Local Similarity 98.8%; Pred. No. 4e-114; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 3;
QY 1 GLDTSVSTKGTATYYTNFLNELRVKLPKPNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYTNFLNELRVKLPKPNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIADIVTSYVVGQVRNRSYFFKADPAAVEGLFKNTIKTLRHFGSGYPSLEGEK 120
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Db	61	GQAEIAIDVTSYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	120
Qy	121	AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN	180
Db	121	AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN	180
Qy	181	FQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAELEERANGKYYVTVAVDQVKPKI	240
Db	181	FQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAELEERANGKYYVTVAVDQVKPKI	240
Qy	241	ALLKFVDKDPK	251
Db	241	ALLKFVDKDPK	251

Search completed: June 20, 2005, 10:05:45
Job time : 104.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:10:06.; Search time 30 Seconds
(without alignments)
624.564 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDVSFSTKGNATITVNF.....AVDQVKPKIALKFVDKDKP 251

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*

5: /cgn2_6/prodata/1/iaa/PCUTS COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	251	1	US-08-425-336-101
2	1277	100.0	251	1	US-08-488-113B-101
3	1277	100.0	251	1	US-08-477-484B-101
4	1277	100.0	251	2	US-08-646-360-101
5	1277	100.0	251	3	US-08-839-765-101
6	1277	100.0	251	3	US-09-136-389-101
7	1277	100.0	251	3	US-09-610-838-101
8	1277	100.0	251	4	US-09-711-485-101
9	1273	99.7	251	1	US-08-425-336-99
10	1273	99.7	251	1	US-08-425-336-100
11	1273	99.7	251	1	US-08-488-113B-99
12	1273	99.7	251	1	US-08-488-113B-100
13	1273	99.7	251	1	US-08-477-484B-99
14	1273	99.7	251	1	US-08-477-484B-100
15	1273	99.7	251	2	US-08-646-360-99
16	1273	99.7	251	2	US-08-646-360-100
17	1273	99.7	251	3	US-08-839-765-99
18	1273	99.7	251	3	US-08-839-765-100
19	1273	99.7	251	3	US-09-136-389-99
20	1273	99.7	251	3	US-09-136-389-100
21	1273	99.7	251	3	US-09-610-838-99
22	1273	99.7	251	3	US-09-610-838-100
23	1273	99.7	251	4	US-09-711-485-99
24	1273	99.7	251	4	US-09-711-485-100
25	1269	99.4	251	1	US-08-425-336-2
26	1269	99.4	251	1	US-08-425-336-110
27	1269	99.4	251	1	US-08-488-113B-2

28 1269 99.4 251 1 US-08-488-113B-110 Sequence 110, App

29 1269 99.4 251 1 US-08-477-484B-2 Sequence 2, Appli

30 1269 99.4 251 1 US-08-477-484B-110 Sequence 110, App

31 1269 99.4 251 2 US-08-646-360-2 Sequence 2, Appli

32 1269 99.4 251 2 US-08-646-360-110 Sequence 110, App

33 1269 99.4 251 2 US-08-621-803-247 Sequence 247, App

34 1269 99.4 251 3 US-08-839-765-2 Sequence 2, Appli

35 1269 99.4 251 3 US-08-839-765-110 Sequence 110, App

36 1269 99.4 251 3 US-09-136-389-2 Sequence 2, Appli

37 1269 99.4 251 3 US-09-136-389-110 Sequence 110, App

38 1269 99.4 251 3 US-09-217-352-247 Sequence 247, App

39 1269 99.4 251 3 US-09-610-838-2 Sequence 2, Appli

40 1269 99.4 251 3 US-09-610-838-110 Sequence 110, App

41 1269 99.4 251 4 US-09-711-485-2 Sequence 2, Appli

42 1269 99.4 251 4 US-09-711-485-110 Sequence 110, App

43 1269 99.4 251 4 US-09-645-603B-2 Sequence 2, Appli

44 1266 99.1 251 1 US-07-901-707-2 Sequence 2, Appli

45 1266 99.1 251 1 US-07-988-430-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-425-336-101
; Sequence 101, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2

US-08-488-113B-101
; Sequence 101, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70-P3.C2A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3

US-08-477-484B-101
; Sequence 101, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein.
US-08-477-484B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-101
Sequence 101, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5
US-08-839-765-101
Sequence 101, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-101

Query Match 100.0%; Score 1277; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
QY 61 GOLAEIADVTSVVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIADVTSVVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFDKDPK 251
DB 241 ALLKFDKDPK 251

RESULT 6

US-09-136-389-101
Sequence 101, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-101

Query Match 100.0%; Score 1277; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
QY 61 GOLAEIADVTSVVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIADVTSVVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 7
US-09-610-838-101
; Sequence 101, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-101

Query Match 100.0%; Score 1277; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYNFFLNELRVKLPKPGNHSCHGIPILRRKADDPGKAFVLVALSDN 60
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLPKNTIKTRLHFGGSPSLEGEK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLPKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYPKPTIASLLVVIQMVSEAAARFTFIENIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYPKPTIASLLVVIQMVSEAAARFTFIENIRNN 180
QY 181 FQORIRPANNTISLENKMGKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 240
Db 181 FQORIRPANNTISLENKMGKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 8
US-09-711-485-101
; Sequence 101, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-711-485-101

Query Match      100.0%; Score 1277; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIADVTSVVVGQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVVVGQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
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RESULT 9
US-08-425-336-99
; Sequence 99, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-99

Query Match      99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIADVTSVVVGQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVVVGQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
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RESULT 10
US-08-425-336-100
; Sequence 100, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
;
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; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-100

Query Match          99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYYVNFLELVKLPKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTVSFSTKGATYYVNFLELVKLPKPEGNHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFHGGSSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFHGGSSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGWFSEAVLERANGKKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGWFSEAVLERANGKKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
US-08-488-113B-99
; Sequence 99, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-99

Query Match          99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYYVNFLELVKLPKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTVSFSTKGATYYVNFLELVKLPKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFHGGSSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLHFHGGSSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGWFSEAVLERANGKKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGWFSEAVLERANGKKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12
US-08-488-113B-100
; Sequence 100, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
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/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,484B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ INFORMATION FOR SEQ ID NO: 100:
/ LENGTH: 251 amino acids
/ SEQUENCE CHARACTERISTICS:
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-488-113B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 GLDTSFSTKGATYTYVNFNLELRVCLKPEGNHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
US-08-477-484B-99
/ Sequence 99, Application US/08477484B
/ Patent No. 5756699
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,484B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ INFORMATION FOR SEQ ID NO: 99:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-477-484B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
US-08-477-484B-100
/ Sequence 100, Application US/08477484B
/ Patent No. 5756699
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
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;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

;; TITLE OF INVENTION: Proteins

;; NUMBER OF SEQUENCES: 169

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

;; STREET: 500 West Madison Street, 34th floor

;; CITY: Chicago

;; STATE: Illinois

;; COUNTRY: USA

;; ZIP: 60661

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/477,484B

;; FILING DATE: 07-JUN-1995

;; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/425,336

;; FILING DATE: 18-APR-1995

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/064,691

;; FILING DATE: 12-MAY-1993

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/988,430

;; FILING DATE: 09-DEC-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/901,707

;; FILING DATE: 19-JUN-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/787,567

;; FILING DATE: 04-NOV-1991

;; ATTORNEY/AGENT INFORMATION:

;; NAME: McNicholas, Janet M.

;; REGISTRATION NUMBER: 32,918

;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 312/707-8889

;; TELEFAX: 312/707-9155

;; TELEX: 650 388-1248

;; INFORMATION FOR SEQ ID NO: 100:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 251 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-477-484B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	1	GLDTVSFSTKGATYYTYVNFNLRLVKLPKPEGNHSHGIPLLRKADDPGKCFVLVALSNDN	60
QY	61	GQLAEIAIDVTSVYVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	120
DB	61	GQLAEIAIDVTSVYVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	120
QY	121	AYRETTDLGIEPLRIGIKKLDENAIQVSEAAARFTFIENQIRNN	180
DB	121	AYRETTDLGIEPLRIGIKKLDENAIQVSEAAARFTFIENQIRNN	180
QY	181	FOQIRPANNITSLNWKGLSPQIRTSANGMFSEAVELERANGKKYVTVADQVKPKI	240
DB	181	FOQIRPANNITSLNWKGLSPQIRTSANGMFSEAVELERANGKKYVTVADQVKPKI	240
QY	241	ALLKFKVDKDKP	251
DB	241	ALLKFKVDKDKP	251

RESULT 15

US-08-646-360-99

;; Sequence 99, Application US/08646360

;; Patent No. 5837491

;; GENERAL INFORMATION:

;; APPLICANT: Better, Marc D.

;; APPLICANT: Carroll, Stephen F.

;; APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

;; TITLE OF INVENTION: Proteins

;; NUMBER OF SEQUENCES: 173

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

;; STREET: 500 West Madison Street, 34th floor

;; CITY: Chicago

;; STATE: Illinois

;; COUNTRY: USA

;; ZIP: 60661

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/646,360

;; FILING DATE: 13-MAY-1996

;; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US94/05348

;; FILING DATE: 12-MAY-1994

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/064,691

;; FILING DATE: 12-MAY-1993

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/988,430

;; FILING DATE: 09-DEC-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/901,707

;; FILING DATE: 19-JUN-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/787,567

;; FILING DATE: 04-NOV-1991

;; ATTORNEY/AGENT INFORMATION:

;; NAME: McNicholas, Janet M.

;; REGISTRATION NUMBER: 32,918

;; REFERENCE/DOCKET NUMBER: 200-70.P4

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 312/707-8889

;; TELEFAX: 312/707-9155

;; TELEX: 650 388-1248

;; INFORMATION FOR SEQ ID NO: 99:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 251 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-646-360-99

Query Match 99.7%; Score 1273; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GLDTVSFSTKGATYYTYVNFNLRLVKLPKPEGNHSHGIPLLRKADDPGKAFVLVALSNDN	60
DB	1	GLDTVSFSTKGATYYTYVNFNLRLVKLPKPEGNHSHGIPLLRKADDPGKAFVLVALSNDN	60
QY	61	GQLAEIAIDVTSVYVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	120
DB	61	GQLAEIAIDVTSVYVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	120
QY	121	AYRETTDLGIEPLRIGIKKLDENAIQVSEAAARFTFIENQIRNN	180

Db	121	AYRETTDLGIEPLRIGIKKLDENAI	DNYPTEIASLLVVIQWSEAAARFT	ENQIRNN	180
Qy	181	FOORIRPANNTISLENKWKLSFO	IRTSGANGMFSEAVELEERANGK	YVVTAVDQVKPKI	240
Db	181	FOORIRPANNTISLENKWKLSFO	IRTSGANGMFSEAVELEERANGK	YVVTAVDQVKPKI	240
Qy	241	ALLKFVDKDPK	251		
Db	241	ALLKFVDKDPK	251		

Search completed: June 20, 2005, 09:22:44
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 09:09:06 ; Search time 25.5 Seconds
(without alignments)
947.075 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTSFSTKGATYTYNFF.....AVDQVKPKIALKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	353.5	27.7	245	JC4840	rRNA N-glycosidase
3	348	27.3	286	JC25560	rRNA N-glycosidase
4	346	27.1	576	RLCSD	ricin D precursor
5	343	26.9	286	JC4235	rRNA N-glycosidase
6	337.5	26.4	564	RLCSAG	agglutinin precursor
7	334.5	26.2	527	S32430	abrin-b precursor
8	332.5	26.0	294	S28421	rRNA N-glycosidase
9	330	25.8	251	C39761	abrin (Clone 7.2)
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11	323	25.3	289	RLT72T	rRNA N-glycosidase
12	321	25.1	528	TZLSA	abrin-a precursor
13	317	24.8	247	JU0393	karasurin - Mongol
14	317	24.8	289	JC5066	karasurin C - Tric
15	313.5	24.5	261	JE0401	antiviral protein
16	312	24.4	247	JC5032	karasurin-B - Tric
17	310.5	24.3	277	S22494	rRNA N-glycosidase
18	304.5	23.8	254	PD0018	mistletoe lectin I
19	299	23.4	528	S32431	abrin-c precursor
20	299	23.4	562	SLP022	rRNA N-glycosidase
21	292	22.9	286	RLPUGG	agglutinin I precu
22	290.5	22.7	570	S62627	beta-luffin - smoo
23	287.5	22.5	278	S23519	luffin-b - smooth
24	274	21.5	250	JN0108	rRNA N-glycosidase
25	215.5	16.9	272	JC49817	betavulgin - beet
26	210	16.4	272	JC4811	ribosome-inactivat
27	204	16.0	310	S46239	rRNA N-glycosidase
28	195	15.3	40	S17574	
29	184.5	15.4	253	S28542	

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35	179.5	14.1	253	2	S28539	rRNA N-glycosidase
36	179.5	14.1	253	2	S29931	rRNA N-glycosidase
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38	149	11.7	236	2	S17932	rRNA N-glycosidase
39	122.5	9.6	1948	2	B69511	N conserved hypoth
40	121	9.5	106	2	B39761	abrin (clone 3.7)
41	115.5	9.0	275	2	S33631	tritin - wheat
42	115.5	9.0	280	1	RLBH	rRNA N-glycosidase
43	108.5	8.5	456	2	T05612	hypothetical prote
44	106.5	8.3	281	2	B38664	30K ribosome inact
45	104	8.1	280	2	JC5848	protein synthesis

ALIGNMENTS

RESULT 1

JT0753

rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum

N;Alternate names: gelonin; type I ribosome-inactivating protein

C;Species: Gelonium multiflorum

C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C;Accession: JT0753; S16489

R;Nolan, P.A.; Garrison, D.A.; Better, M.

Gene 134, 223-227, 1993

A;Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating prote

A;Reference number: JT0753; MUID:94085781; PMID:7916721

A;Accession: JT0753

A;Molecule type: mRNA

A;Residues: 1-316 <NOL>

A;Cross-references: UNIPROT:P33186; GB:L12243; NID:G388633; PIDN:AAA16312.1; PID:G388634

R;Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Soria, M.; Lappi, D.

Int. J. Pept. Protein Res. 33, 263-267, 1989

A;Title: N-terminal sequence of some ribosome-inactivating proteins.

A;Reference number: S16331; MUID:89326691; PMID:2753596

A;Accession: S16489

A;Molecule type: protein

A;Residues: 47-89, 'K', '91-92, 'D' <MON>

C;Function:

A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA there

C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C;Keywords: glycosidase; hydrolase

F;1-46/Domain: signal sequence #status predicted <SIG>

F;47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>

F;53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 99.4%; Score 1269; DB 2; Length 316;
Best Local Similarity 99.2%; Pred. No. 1.1e-96;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATYTYNFFLNELRVKLPEGNHGIPLLRKADDPGKAFVLVALSNDN 60

Db 47 GLDTSFSTKGATYTYNFFLNELRVKLPEGNHGIPLLRKADDPGKAFVLVALSNDN 106

Qy 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 120

Db 107 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 166

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQWVSEAAAFRTFFENQIRNN 180

Db 167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQWVSEAAAFRTFFENQIRNN 226

Qy 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 240

Db 227 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 286

Qy 241 ALLKFDVKDPK 251

Db 287 ALLKFVDKPK 297

RESULT 2

rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd
C:Species: Trichosanthes anguina (snake gourd)
C:Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C:Accession: J06701; J06701; J06701
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Blomed. Sci. 3, 178-186, 1996
A:Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from
A:Reference number: J06701
A:Accession: J06701
A:Molecule type: protein
A:Residues: 1-132, 'S', 134-245 <CHO1>
A:Experimental source: seed
A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
submitted to JIPID, August 1995
A:Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from
A:Reference number: J06701
A:Accession: J06701
A:Molecule type: protein
A:Residues: 1-50, 'L', 52-245 <CHO2>
C:Superfamily: rRNA N-glycosidase
C:Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F:4-242/Domain: rRNA N-glycosidase homology <RNG>
F:51,201/Binding site: carboxylate (Asn) (covalent) #status experimental
F:70,158,161/Active site: Tyr, Glu, Arg #status predicted
F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 27.7%; Score 353.5; DB 2; Length 245;
Best Local Similarity 36.3%; Pred. No. 1.1e-21;
Matches 91; Conservative 44; Mismatches 95; Indels 21; Gaps 7;

QY 5 VSFSTKGTATYTYVNFNLRLVKLKEGNSHGIPILRRKADDPGKAFVLVALSDNGQLA 64
DB 2 VSFDLSTATKYSFITTQRLALPTQGVYGLPLPSTAG-SQRFNFNTNNDENV 60
QY 65 EIAIDVTSYVYGVQVNRNRSYFFKADPADAAVEGLFKNTIKRLHFGSGYPSLE---GEKA 121
DB 61 TVAVDVTNVTYVAYRADAVSYFFEDTPAEAFKLIPAGTKTVKLPYSGNYDKLQSVVGKQ- 119
QY 122 YETDGLGIEPLRIGIKKLDEAIDN---YKTEIASSLLVVIQWSEAAARFTFENQIR 178
DB 120 -RDMIELGLPAL-----SSAITNMVYDYQSTAAALLVLIQSTAAEARYKYIEQQVS 170
QY 179 NNFOQRIIPANNTISLENKWKLSFOIRTSG--ANGMFSEAELEERANGKYYV--TAVD 234
DB 171 SHISSNFYQNAVISLENKWKLSKQIQIANRTGHCQFENPVELYNDPQDTRFSVHTSAG 230
QY 235 QVKKPIALKLF 245
DB 231 VVKGNIKLLLY 241

RESULT 3

rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple
C:Species: Momordica balsamina (balsam apple)
C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S25560
R:Ortigao, M.; Better, M.
Nucleic Acids Res. 20, 4662, 1992
A:Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homologous to the B-chain of ricin
A:Reference number: S25560; MUID:93027170; PMID:1408771
A:Accession: S25560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-286 <ORT>
A:Cross-references: UNIPROT:P29339; EMBL:Z12175; NID:g19525; PID:CAA78166.1; PID:g19526
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase
F:27-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match 27.3%; Score 348; DB 2; Length 286;
Best Local Similarity 37.4%; Pred. No. 4e-21;
Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

QY 5 VSFSTKGTATYTYVNFNLRLVKLKEGNSHGIPILRRKADDPGKAFVLVALSDNGQLA 64
DB 25 VNFDLSTATKYSFITTQRLALPTQGVYGLPLPSTAG-SQRFNFNTNNDENV 60
QY 65 EIAIDVTSYVYGVQVNRNRSYFFKADPADAAVEGLFKNTIKRLHFGSGYPSLE-GEKAYR 123
DB 84 SVAIDVTNVTYVAYRADAVSYFFEDTPAEAFKLIPAGTKTVKLPYSGNYDKLQSVVGKQ- 143
QY 124 ETTDGLGIEPLRIGIKKLDEAIDNKTPTETIASSLLVVIQWSEAAARFTFENQIRNFQ 183
DB 144 ENIDIGLPLALSAI-----TTLFYNAQSAPSAALLVLIQTAAEAFKYIERHVAKYVAT 198
QY 184 RIRPANNTISLENKWKLSFOI-RTSGANGMFSEAELEERANGKYYVTVAVDQ--VKPKI 240
DB 199 NFKPNLAISLENKWKLSKQIFLAQNGGKFRNPVDLIKPTGERFQVTVNVDSDVVKGNI 258
QY 241 ALL 243
DB 259 KLL 261

RESULT 4

RICSD
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2999712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <HAL>
A:Cross-references: UNIPROT:P02879; GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083
R:Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <TRE>
A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>
A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of ile ch
A:Reference number: A03372
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-37, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>
A:Note: this paper cites the others in the series providing experimental details for the
R:Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein

A;Residues: 315-383, 'PS', 386-576 <ARA>
R;Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A;Title: Primary structure of Ala chain of ricin D.
A;Reference number: A03374
A;Accession: A03374
A;Molecule type: protein
A;Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405, 'G', 407, 'H', 409, 'I', 411, 'L', 413, 'M', 415, 'P', 417, 'Q', 419, 'R', 421, 'S', 423, 'V', 425, 'W', 427, 'X', 429, 'Y', 431, 'Z', 433, 'aa' <FUN>
A;Note: this paper, one of a series, summarizes the experimental details for the determination of the primary structure of ricin D.
R;Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of ricin toxicity.
A;Reference number: A48237; MUID:91352006; PMID:1881883
A;Contents: annotation; active site
R;Rutenber, E.; Robertus, J.D.
Proteins 10, 260-269, 1991
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Reference number: A48238; MUID:91352005; PMID:1881882
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Reference number: A48239; MUID:91352004; PMID:1881881
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). This protein is cytotoxic and very poisonous to animals.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-302/Product: ricin D chain A #status experimental <ACH>
F;46-293/Domain: rRNA N-glycosidase homology <RNG>
F;315-576/Product: ricin D chain B #status experimental <BCH>
F;331-373, 374-414, 417-455, 462-497, 501-540, 543-576/Region: 40-residue repeats
F;45, 409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;115, 158, 243, 244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;212/Active site: Glu #status experimental
F;215/Active site: Arg #status predicted
F;294-318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental
F;336, 349, 360/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status experimental
F;548, 569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental

Query Match 27.1%; Score 346; DB 1; Length 576;
Best Local Similarity 36.8%; Pred. No. 1.5e-20;
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;

QY 5 VFSSTKGATYITVNFNLRLVKLKEGNSHGIPILRKADDP-GKAFVLVSLNDNGQ 62
DB 44 INFTTAGATVQSYTNFIRAVRGELTTGADVRHEIPVLPNRVGLPINQRFILVELSHAE 103
QY 63 LABAIDVTSVVVGVQVRNRSYFFKADPD-----AAVEGLFKNTIKTR--LHFGGSYPS 115
DB 104 SVTLALDVTNVAVVGVFRAGNSAIFFH--PDNQDEAIAITLFTD--VQNRVTFAGNGYDR 160
QY 116 LEEKA-YRETTDLGIEPLRIGIKLDENAINDKYKPTETIASLLVVIQVSEARFTFIE 174
DB 161 LEQAGNLRENIEGLNGPLEEAISALVYVYTGQTLPILARSFIIQIMSEARFQYIE 220
QY 175 NQIRN--NFQQRIRPANNITSLNKKGKLSFQIRTSGANGMFSEAVELEERANGKYYVTA 232
DB 221 GEMRTIRYNNRSAPDSVITLNSWGRSLTAQESN-QGAFASPIQLORNGSKFSVYD 279
QY 233 VDOVKPKIALKF 245
DB 280 VSLIPILALMVY 292

RESULT 5
JC4235
rRNA N-glycosidase (EC 3.2.2.22) map30 precursor - balsam pear
N;Alternate names: anti-HIV 30K protein

C;Species: Momordica charantia (balsam pear, bitter melon)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4235; S12869
R;Lee-Huang, S.; Huang, P.L.; Chen, H.C.; Huang, P.L.; Bourinbaiar, A.; Huang, H.I.; Kung, Gene 161, 151-156, 1995
A;Title: Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter melon.
A;Reference number: JC4235; MUID:95394347; PMID:7665070
A;Accession: JC4235
A;Molecule type: DNA
A;Residues: 1-286 <LEE>
A;Cross-references: UNIPROT:P24817
A;Experimental source: mature seeds
A;Note: The authors translated the codon TAC for residue 37 as Thr and ACT for residue 18 as Lys. The authors also translated the codon TAC for residue 37 as Thr and ACT for residue 18 as Lys. The authors also translated the codon TAC for residue 37 as Thr and ACT for residue 18 as Lys. The authors also translated the codon TAC for residue 37 as Thr and ACT for residue 18 as Lys.
R;Lee-Huang, S.; Huang, P.L.; Nara, P.L.; Chen, H.C.; Kung, H.; Huang, H.I.; Kung, F.E.S. Lett. 272, 12-18, 1990
A;Title: MAP 30: a new inhibitor of HIV-1 infection and replication.
A;Reference number: S12869; MUID:91032105; PMID:1699801
A;Accession: S12869
A;Molecule type: protein
A;Residues: 24-36, 'T', 38-66, 'P' <LEW>
C;Comment: This plant protein has anti-HIV activity. It possesses antiviral action, anti-activation activities. It is capable of acting against multiple stages of the viral life cycle. This protein has conserved unique residues Trp-213 and Met-277.
C;Genetics:
A;Gene: map30
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: antiviral; glycoprotein; glycosidase; hydrolase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-286/Product: rRNA N-glycosidase (EC 3.2.2.22) map30 #status predicted <MAT>
F;27-264/Domain: rRNA N-glycosidase homology <RNG>
F;74/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;93, 181, 184/Active site: Tyr, Glu, Arg #status predicted

Query Match 26.9%; Score 343; DB 2; Length 286;
Best Local Similarity 37.0%; Pred. No. 1e-20;
Matches 90; Conservative 34; Mismatches 109; Indels 10; Gaps 5;

QY 5 VFSSTKGATYITVNFNLRLVKLKEGNSHGIPILRKADDPGKAFVLVSLNDNGQLA 64
DB 25 VNFDLSTATAKTYTTFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSAVETI 83
QY 65 ETADIVTSVVVGVQVRNRSYFFKADPDAAVEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
DB 84 SVAIDVTVNVAVVAVTRDVSYFFKESPPPEAYNLFKGTTRKITLPYTGNYENLQTAHKIR 143
QY 124 ETTDLGIEPLRIGIKLDENAINDKYKPTETIASLLVVIQVSEARFTFIEQIRNFFQ 183
DB 144 ENIDGLPALSAI-----TTLFYNAQSPASALLVLIQTAAEARFKYTERHVAKYVAT 198
QY 184 RIRPANNITSLNKKGKLSFQI-RTSGANGMFSEAVELEERANGKYYVTAVDQ--VKPKI 240
DB 199 NFKPNLAIIISLENQWSALSQIFLAQNGGKFRNPVDLIKPTGERFQVTVNDSVDVVGNI 258
QY 241 ALL 243
DB 259 KLL 261

RESULT 6
RLCSAG
agglutinin precursor - castor bean
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A24261; A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A;Reference number: A24261; MUID:86059449; PMID:2999130
A;Accession: A24261
A;Molecule type: mRNA
A;Residues: 1-564 <ROB>
A;Cross-references: UNIPROT:P06750; GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701

A:Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHE>
R:Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A:Title: Probing the domain structure of abrin-a by tryptic digestion.
A:Reference number: S74110; MUID:97008945; PMID:8856055
A:Accession: S74110
A:Molecule type: protein
A:Residues: 89-108;154-172 <LIN>
A:Experimental source: seed
A:Accession: S74111
A:Molecule type: protein
A:Residues: 262-276, 'X', 278-280;329-348;369-388;399-418 <LIW>
A:Experimental source: seed
C:Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits protein synthesis, and a B chain, which binds to cell surface receptors on the cell surface. The A and B chains are linked by a single disulfide bond.
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
F:1-251/Product: abrin-a chain A #status experimental <ACH>
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
F:261-528/Product: abrin-a chain B #status experimental <BCH>
F:283-325,326-366,369-407,414-449,453-482,495-528/Region: 40-residue repeats
F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status experimental
F:164,167/Active site: Glu, Arg #status predicted
F:247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F:288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F:361,401/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 25.1%; Score 321; DB 1; Length 528;
Best Local Similarity 35.7%; Pred. No. 1.5e-18;
Matches 91; Conservative 39; Mismatches 107; Indels 18; Gaps 8;
QY 5 VFSFKGATYITVYVNFNLRLVKLPKPGNSHGIPILRKKADDP-----GKAFVLVALSND 59
DB 5 IKFSTEGATSQSKQFIALRRLR-GGLIHDPVL---PDPITLQERNRYITVELNS 59
QY 60 NQLAEIADVTSVYVGVQVNRNSYFFKDA-PDAAYEGFLFKNT-IKTRLHFGGSYPSLE-G 118
DB 60 DTESIEVGIDVTNAVYVAYRAGTQSYFLRDAPSSASDYLFTGDQHSPLFYGTGDLERW 119
QY 119 EKAYRETTDLGIEPLRIGIKKLDENADINVKPTEIASLLVVIQVMSAAFTFIENQIRN 178
DB 120 AHQSROQIPLGLQALTHGISFRSGNDN---EKARTLIVIQVMAEARFYISNRVR 176
QY 179 NNFQ--QRIRPANNTISLENKMGKLSFQIR-TSGANGMFSEAVELEFRANKKYVTVAVDQ- 235
DB 177 VSIQTGTAFQPDAAAMISLENNWNLRSRGVQES-VQDTFNPQVTLTNRNEPVIDSLSH 235
QY 236 VKPKTALLKFDKDP 250
DB 236 TVAVLALMLFVCNPP 250

RESULT 13
JU0393
Karasurin - Mongolian snake-gourd
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JU0393; PS0163
R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A:Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A:Reference number: JU0393; MUID:92005921; PMID:1914000
A:Accession: JU0393
A:Molecule type: protein
A:Residues: 1-247 <TOY>
A:Cross-references: UNIPROT:P24478
A:Note: a sequence which lacks Ala-247 is also shown in this publication
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient
F:4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 24.8%; Score 317; DB 2; Length 289;
Best Local Similarity 38.2%; Pred. No. 1.4e-18;
Matches 94; Conservative 33; Mismatches 105; Indels 14; Gaps 8;
QY 5 VFSFKGATYITVYVNFNLRLVKLPKPGNSHGIPILRKKADDPG-KAFVLVALSNDNGQL 63
DB 25 VSFRLSGATSSYGVFISNLRKALPYERKLYDIPLLRSTL--PGSQRYALIHLYTNYDET 82
QY 64 ASIAIDVTSVYVGVQVNRNSYFFKDA-PDAAYEGFLFKNT-IKTRLHFGGSYPSLE-GEK 120
DB 83 ISVAIDVTNVYVNGYRAGDTSYFFNEASATEAAKYVFKDAKRVTLFPGSGYERLQIAAG 142
QY 121 AVRETTDLGIEPLRIGIKKLDENADINVKPTEIASLLVVIQVMSAAFTFIENQIRN 180
DB 143 KIRENIPGLPALDSAI-----TTLFYVANGAASALMWLIQSTSEARAYKFTIEQQIGKR 197
QY 181 FQORIRPANNTISLENKMGKLSFQIR-TSGANGMFSEAVELEFRANKKYVTVAVDQ--VK 237

Query Match 24.8%; Score 317; DB 2; Length 247;
Best Local Similarity 38.2%; Pred. No. 1.1e-18;
Matches 94; Conservative 33; Mismatches 105; Indels 14; Gaps 8;
QY 5 VFSFKGATYITVYVNFNLRLVKLPKPGNSHGIPILRKKADDPG-KAFVLVALSNDNGQL 63
DB 2 VSFRLSGATSSYGVFISNLRKALPYERKLYDIPLLRSTL--PGSQRYALIHLYTNYDET 59
QY 64 ASIAIDVTSVYVGVQVNRNSYFFKDA-PDAAYEGFLFKNT-IKTRLHFGGSYPSLE-GEK 120
DB 60 ISVAIDVTNVYVNGYRAGDTSYFFNEASATEAAKYVFKDAKRVTLFPGSGYERLQIAAG 119
QY 121 AVRETTDLGIEPLRIGIKKLDENADINVKPTEIASLLVVIQVMSAAFTFIENQIRN 180
DB 120 KIRENIPGLPALDSAI-----TTLFYVANGAASALMWLIQSTSEARAYKFTIEQQIGKR 174
QY 181 FQORIRPANNTISLENKMGKLSFQIR-TSGANGMFSEAVELEFRANKKYVTVAVDQ--VK 237
DB 175 VDKTFLPSLAITISLENSWSALSQIQAISTNNGQPTPVLINAQNRVTIINVDAGVVT 234
QY 238 PKIALL 243
DB 235 SNIAALL 240

RESULT 14
JC5606
Karasurin C - Trichosanthes kirilowii var. japonica
N:Contains: Karasurin A
C:Species: Trichosanthes kirilowii var. japonica
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C:Accession: JC5606; JC5033
R:Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A:Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein
A:Reference number: JC5606; MUID:97356562; PMID:9212998
A:Accession: JC5606
A:Molecule type: DNA
A:Residues: 1-289 <MIZ>
A:Cross-references: UNIPROT:P24478; DBJ:AB000666; NID:92329830; PIDN:BAA21786.1; PID:92;
R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and karasurin-C
A:Reference number: JC5033; MUID:97108848; PMID:8951169
A:Accession: JC5033
A>Status: preliminary
A:Molecule type: protein
A:Residues: 22-270 <KON>
C:Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortifacient activity.
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:22-270/Product: Karasurin C #status predicted <MAC>
F:224-270/Product: Karasurin A #status predicted <MAC>
F:27-266/Domain: rRNA N-glycosidase homology <RNG>

Db	198	VDKTFPLSLATISLENSWSALSKQIQIASTNNGQFETPVLINAQNRVTITNDAGVVT	257
Qy	238	PKIAL	243
Db	258	SNIAL	263

RESULT 15

JE0401
antiviral protein - Virginian pokeweed
C:Species: *Phytolacca americana* (Virginian pokeweed)
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: JE0401
R:Kung, S.S.; Kimura, M.; Funatsu, G.
Agric. Biol. Chem. 54, 3301-3318, 1990
A:Title: The complete amino acid sequence of antiviral protein from the seeds of pokeweed
A:Reference number: JE0401; MUID:91242096; PMID:1368643
A:Accession: JE0401
A:Molecule type: protein
A:Residues: 1-261 <KUN>
A:Cross-references: UNIPROT:P23339
A:Experimental source: seed
C:Comment: This protein prevents the replication of a number of plant viruses, and inhibits the replication of tobacco etch virus.
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: disulfide bond; glycoprotein
F:6-254/Domain: rRNA N-glycosidase homology <RNG>
F:10,44,255/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:34-258,84-105/disulfide bonds: #status experimental

Query Match	24.5%;	Score 313.5;	DB 2;	Length 261;
Best Local Similarity	32.4%;	Pred. No. 2.4e-18;		
Matches 85;	Conservative 49;	Mismatches 105;	Indels 23;	Gaps 9;
Qy	2	LDTVSFSTKATYTYVNFNLNKLK-PCGNHGIPLLRKAKDPPKAFVLVALSNDN	60	
Db	1	INTITFDAGNATINKYATFMSLENEAKPSLKCVGIPMLPN--TNSTIKYLLVKLGAS	58	
Qy	61	QLAEIAIDVTSVVVG-----YQVRNSRYFKDAPDAAYEGLFKPT-----IKTRLH	108	
Db	59	LKTTTLMRLRNLYVMGSDPYDNKCRHYHFNDIKGTEYSDV-ENTTLCPSNPRVAKPIN	117	
Qy	109	FGGSYPLEGEKA---YRETTDLGIEPLRIGIKKLDENAINDYKPTBIASLLVVIQMV	165	
Db	118	YNGLYPTL-KKAGVTSRNEVQLGIQLSSDIGKISQG--SFTEKTEAKFLLVAIQMV	174	
Qy	166	EAAFTTIEQIRNFOORIPANNYTISLENKWKLSFOJRTSCANGMFSEAVLEANG	225	
Db	175	EAAFKYIENQVTFNRDPSFNQDKVLDEENWGKISTAHNS--KNGALPKPLSLKNADG	233	
Qy	226	KYYVTVAVDQVKPKIALLKFPD	247	
Db	234	TKMIVLRVDEIKPDVGLIYNV	255	

Search completed: June 20, 2005, 09:21:38
Job time : 26.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:00:50 ; Search time 114.5 Seconds

(without alignments)
1122.549 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTVSFSFKGATYYVNF.....AVDQVKPITALLKFKVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1269	99.4	316	1 RIPG_GELMU	P33186 gelonium mu
2	1235.5	96.8	258	2 Q9S9E4	Q98964 gelonium mu
3	398.5	31.2	581	2 Q94BW5	Q94bw5 cinnamomum
4	397.5	31.1	580	2 Q94BW3	Q94bw3 cinnamomum
5	396.5	31.0	549	2 Q9FV22	Q9fv22 cinnamomum
6	391	30.6	299	2 Q8GZN9	Q8gz9 euphorbia s
7	390.5	30.6	580	2 Q94BW4	Q94bw4 cinnamomum
8	365.5	28.6	583	2 Q8GT32	Q8gt32 sambucus ni
9	359.5	28.2	297	2 Q8GZP0	Q8gzp0 euphorbia s
10	356	27.9	563	1 NIGB_SAMNI	P33183 sambucus ni
11	356	27.9	563	2 Q94S52	Q94s52 sambucus ni
12	352.5	27.6	563	2 Q04367	Q04367 sambucus ni
13	348	27.3	264	2 Q684J5	Q684j5 momordica c
14	348	27.3	286	1 RIP2_MONBA	P29339 momordica b
15	348	27.3	286	1 RIP3_MONCH	P24817 momordica c
16	347	27.2	541	2 Q41174	Q41174 ricinus com
17	346	27.1	576	1 RIC1_RICCO	P02879 ricinus com
18	343.5	26.9	265	1 RIP2_PHYDI	P34967 phytolacca
19	341.5	26.7	294	1 RIP1_TRIAN	P56626 trichosanthe
20	341.5	26.7	564	2 Q9AVR2	Q9avr2 sambucus eb
21	337.5	26.4	564	1 AGGL_RICCO	P06750 ricinus com
22	337	26.4	282	1 RIP2_BRYDI	P98184 bryonia dio
23	334.5	26.2	527	1 ABRB_ABRPR	Q06077 abrus preca
24	332.5	26.0	294	1 RIPA_PHYAM	Q03464 phytolacca
25	330.5	25.9	293	2 Q8VU00	Q8vuo0 jatrophia cu
26	330	25.8	252	2 Q38760	Q38760 abrus preca
27	329.5	25.8	294	2 Q8HIW1	Q8hiw1 phytolacca
28	328.5	25.7	275	2 Q84LJ1	Q84lj1 gynostemma
29	327.5	25.6	277	2 Q84JR1	Q84jr1 gynostemma
30	327	25.6	313	1 R1P1_PHYAM	P10297 phytolacca
31	327	25.6	313	2 Q6PWU4	Q6pwu4 phytolacca

32	326.5	25.6	277	2 Q8GV09	Q8gv09 gynostemma
33	326	25.5	289	2 Q41216	Q41216 trichosanthe
34	325.5	25.5	275	2 Q8HIY4	Q8hiy4 gynostemma
35	325.5	25.5	293	2 Q8S452	Q8s452 jatrophia cu
36	325	25.5	567	2 Q6H267	Q6h267 viscum albu
37	323.5	25.3	277	2 Q8GV11	Q8gv11 gynostemma
38	323	25.3	289	1 R1PT_TRIKI	P09989 trichosanthe
39	323	25.3	289	2 Q94KE4	Q94ke4 trichosanthe
40	322	25.2	289	2 Q84SV8	Q84sv8 trichosanthe
41	321.5	25.2	565	2 Q04071	Q04071 sambucus ni
42	321	25.1	251	2 Q7DM12	Q7dm12 abrus preca
43	321	25.1	252	2 Q38761	Q38761 abrus preca
44	321	25.1	528	1 ABR4_ABRPR	P11140 abrus preca
45	318.5	24.9	277	2 Q8HIY5	Q8hiy5 gynostemma

ALIGNMENTS

RESULT 1
RIPG_GELMU STANDARD; PRT; 316 AA.
AC P33186;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
DE Name=GEL;
OS Gelonium multiflorum (Euphorbiaceae himalayal).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Malpighiales; Euphorbiaceae; Crotonoideae; Geloniaceae;
OC Gelonium.
OX NCBI_TaxID=3979;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;
RA Nolan P.A., Garrison D.A., Better M.;
RT "Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein from Gelonium multiflorum,"
RL Gene 134:223-227(1993).
RN [2]
RP SEQUENCE OF 47-93.
RC TISSUE=Seed;
RX MEDLINE=89326691; PubMed=2753596;
RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.;
RT "N-terminal sequence of some ribosome-inactivating proteins.";
RL Int. J. Pept. Protein Res. 33:263-267(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=95333189; PubMed=7608981;
RA Hosur M.V., Nair B., Satyamurthy P., Misquith S., Suroolia A., Kannan K.K.;
RT "X-ray structure of gelonin at 1.8-A resolution.";
RL J. Mol. Biol. 250:368-380(1995).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -I- SUBUNIT: Homodimer.
CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.
Type 1 RIP subfamily.

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EMBL: L12243; AAA16312.1; --
PIR: JT0753; JT0753.

```

DR HSP; P09989; 1MRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; FALSE NEG.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
KW Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 26
FT PROPEP 27 46
FT CHAIN 47 297
FT PROPEP 298 316
FT DISULFID 90 96
FT CARBOHYD 235 235
FT ACT SITE 212 212
FT CONFLICT 90 90
FT CONFLICT 93 93
SQ SEQUENCE 316 AA; 35418 MW; 1252F3E710901B85 CRC64;

Query Match          99.4%; Score 1269; DB 1; Length 316;
Best Local Similarity 99.2%; Pred. No. 5.8e-95;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYNFLNELRVKLPENSHGIPLLRKADDPGKAFVLVALSNDN 60
Db 47 GLDTSFSTKGATYITYNFLNELRVKLPENSHGIPLLRKCDPGKCFVLVALSNDN 106
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGFLPKNTIKTRLHFGGSYP 120
Db 107 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGFLPKNTIKTRLHFGGSYP 166
QY 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAFTFIENQIRNN 180
Db 167 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAFTFIENQIRNN 226
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 227 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 286
QY 241 ALLKFVDKDPK 251
Db 287 ALLKFVDKDPK 297

RESULT 2
Q9S9E4 PRELIMINARY; PRT; 258 AA.
AC Q9S9E4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE rRNA - glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
OS Gelonium multiflorum (Euphorbiaceae himalaya).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids I; Malpighiales; Euphorbiaceae; Crotonoideae; Geloniace;
OC Gelonium.
OX NCBI_TaxID=3979;
RN [1]_TaxID=3979;
RP SEQUENCE.
RA Rosenthal M.G., Kohn W.A., Beattie K.L., Beattie W.G., Marks W.,
RA Toman P.D., Cheung L.;
RT "Amino acid sequence analysis, gene construction, cloning, and
RT expression of gelonin, a toxin derived from Gelonium multiflorum.";
RL J. Interferon Cytokine Res. 15:547-555(1995).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR HSP; P09989; 1MRJ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

```

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DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
SQ SEQUENCE 258 AA; 28826 MW; 13D68B673F4D6B06 CRC64;

Query Match          96.8%; Score 1235.5; DB 2; Length 258;
Best Local Similarity 95.4%; Pred. No. 2.4e-92;
Matches 247; Conservative 1; Mismatches 2; Indels 9; Gaps 2;

QY 1 GLDTSFSTKGATYITYNFLNELRVKLPENSHGIPLLRKADDPGKAFVLVALSNDN 60
Db 1 GLDTSFSTKGATYITYNFLNELRVKLPENSHGIPLLR-KGDDPGKCFVLVALSNDN 59
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGFLPKNTI-----KTRLHFGGS 112
Db 60 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGFLPKNTIKNPLLFGGKTRLHFGGS 119
QY 113 YPSLEGEKAYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAFTFI 172
Db 120 YPSLEGEKAYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAFTFI 179
QY 173 IENQIRNNFOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTV 232
Db 180 IENQIRNNFOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTV 239
QY 233 VDQVKPKIALLKFDVKDPK 251
Db 240 VDQVKPKIALLKFDVKDPK 258

RESULT 3
Q94BW5 PRELIMINARY; PRT; 581 AA.
AC Q94BW5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]_TaxID=13429;
RP SEQUENCE FROM N.A.
RX MEDLINE=2188636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
RT from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY039801; AAK82458.1; -.
DR HSP; P02879; 2AAL.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008997; RicinB like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; RIP.
DR Pfam; PF001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 581

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FT Q44B3 SEQUENCE 581 AA; 64215 MW; 6E8F5F8FBA3D196 CRC64; cinnaomnin I

Query Match 31.2%; Score 398.5; DB 2; Length 581;
Best Local Similarity 39.7%; Pred. No. 7.8e-24;
Matches 100; Conservative 46; Mismatches 93; Indels 13; Gaps 8;

QY 4 TVSFSTKATYITYVNFNLKRLKPEGNHGIPILRRKADDP-GKAFVLVALSN---D 59
DB 35 TVTFTTKATKTSYTOFIEALRAQLASGEPHGIPVWRERSTVPDSKRFLVLSNWAAD 94

QY 60 NQGLAEIAIDVTSVYVGVQVNRNRSYFFK-DAPDAAYEGFLFKNTIKTRHLHFGSGYSLE- 117
DB 95 SP-VTLADVNTAVYVYRTGQSFFLRDNDPAIENLLPDKRYTTPFSGSYDLE 152

QY 118 --GEKAYRETTDLGIEPIRIGIKLDENAINDKPTEIASLLIVTIQMVSEARFTFIEN 175
DB 153 VAGER--REILLGMDPLENALSALWISLNQOR--ALARSLIVIQMVAEAVRFFIEY 208

QY 176 QIRNFP--QORIRPANNTISLENKWKLSFQIRTSANGMPSEAVELEERANGKYYVTAV 233
DB 209 RVRESITRAEMFRPDPAIENLWISLNQOR--ALARSLIVIQMVAEAVRFFIEY 268

QY 234 -DQVKPKIALLKVF 246
DB 269 SDRVISGLAIMLFI 282

RESULT 5
Q9FV22 PRELIMINARY; PRT; 549 AA.

AC Q9FV22; (1)
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type II ribosome-inactivating protein cinnaomnin (Fragment).
OS Cinnaomnin camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnaomnin.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF259548; AAF68978.2; -;
DR HSSP; P02879; 2AAL.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0008952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008997; RicinB like.
DR InterPro; IPR000772; RicinB_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; RicinB_lectin; 5.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
SQ SEQUENCE 549 AA; 60648 MW; 02607FE607CA44B0 CRC64;

Query Match 31.0%; Score 396.5; DB 2; Length 549;
Best Local Similarity 39.7%; Pred. No. 1.1e-23;
Matches 100; Conservative 46; Mismatches 93; Indels 13; Gaps 8;

QY 4 TVSFSTKATYITYVNFNLKRLKPEGNHGIPILRRKADDP-GKAFVLVALSN---D 59
DB 35 TVTFTTKATKTSYTOFIEALRAQLASGEPHGIPVWRERSTVPDSKRFLVLSNWAAD 62

QY 60 NQGLAEIAIDVTSVYVGVQVNRNRSYFFK-DAPDAAYEGFLFKNTIKTRHLHFGSGYSLE 118
DB 95 SP-VTLADVNTAVYVYRTGQSFFLRDNDPAIENLLPDKRYTTPFSGSYDLE 152

QY 118 --GEKAYRETTDLGIEPIRIGIKLDENAINDKPTEIASLLIVTIQMVSEARFTFIEN 175
DB 153 VAGER--REILLGMDPLENALSALWISLNQOR--ALARSLIVIQMVAEAVRFFIEY 208

QY 176 QIRNFP--QORIRPANNTISLENKWKLSFQIRTSANGMPSEAVELEERANGKYYVTAV 233
DB 209 RVRESITRAEMFRPDPAIENLWISLNQOR--ALARSLIVIQMVAEAVRFFIEY 268

QY 234 -DQVKPKIALLKVF 246
DB 269 SDRVISGLAIMLFI 282

RESULT 4
Q94BW3 PRELIMINARY; PRT; 580 AA.

AC Q94BW3; (1)
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnaomnin III precursor.
OS Cinnaomnin camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnaomnin.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RL "Studies of three genes encoding Cinnaomnin (a type II RIP) isolated from the seeds of camphor tree and their expression patterns."
RL Gene 284:215-223(2002).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY039803; AAK82460.1; -;
DR HSSP; P02879; 2AAL.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0008952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008997; RicinB like.
DR InterPro; IPR000772; RicinB_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; RicinB_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1
FT CHAIN 33 580 type 2 ribosome-inactivating protein cinnaomnin III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match 31.1%; Score 397.5; DB 2; Length 580;

Db 63 SP--VTLAVDTNAYVAYRTGSQFFLEDPDPAIENLLPDKRTYTFPFGSYTDLEG 120
 QY 119 EKA-VRETTDLGIEPLRIGIKKLDENAIQNYKPTRIASSLLVVIQWSEAAARFTFENQI 177
 Db 121 VAGERRELLGWDPLENAISALWISNLNQQR--ALARSLVVIQWVAEAVRFRFIEYRV 178
 QY 178 RNNFQ--QRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYAV-D 234
 Db 179 RGSISRAEMFRDPAPMLSLLENKWSALSNAVQSQNGGVFSSPVELRSISNKPVYVGSVD 238
 QY 235 QVKPKIALKLFV 246
 Db 239 RVISGLAIMLFI 250

RESULT 6

Q8GZN9 PRELIMINARY; PRT; 299 AA.
 AC Q8GZN9;
 DT 01-MAR-2003 (TremBLrel. 23, Created)
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Ribosome inactivating protein Euseratin 2 precursor (EC 3.2.2.22).
 GN Name=Eus2;
 OS Euphorbia serrata.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbiae;
 OC Euphorbia.
 OC NCBI_TaxID=196589;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Girbes T., Arias F.J., Benvenuto E.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -! SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AF457875; AA015531.1; --
 DR HSSP; Q9AVR2; 1HNW.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 299 ribosome inactivating protein Euseratin 2.
 FT
 SQ SEQUENCE 299 AA; 33115 MW; DE791872B9CE2A7D CRC64;

Query Match 30.6%; Score 391; DB 2; Length 299;
 Best Local Similarity 41.3%; Pred. No. 1.4e-23;
 Matches 102; Conservative 36; Mismatches 97; Indels 12; Gaps 5;
 QY 4 TVSFSTKCATYITYNVLNLRVKKLPEGNHGIPLLRKKAD-DPCKAFVLVSLNDNGQ 62
 Db 30 SVKFTHLASVGSQSFMSLSRLKLEDGSGESHDIPLLRKPTEITNNKLLVNLINYSQ 89
 QY 63 LA-EIAIDVTSYVVGQVVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEKA 121
 Db 90 LSITLAVTVVYVIGYKSAGNSFFLKADPSAKTLFFQTNKITL---SSVDSNNYNNIG 146
 QY 122 YRETTDLGIEPLRIGI---KKLDENAIQNYKPTETASSLLVVIQWSEAAARFTFENQIR 178
 Db 147 DRSKVGLGIGPLRSIDTLNKFNGSVNNV----FKESLLVVIQWVAEAAARFKFIQLKIE 202

QY 179 NNFOQIRIPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYAVDQVKP 238
 Db 203 NLLDDEYKPKNDTISYENNWKLSEQLSGTDGKFKKPVLLLYANGTKIVSTVAQVKP 262
 QY 239 KIALKLF 245
 Db 263 DISILLY 269
 RESULT 7
 Q94BW4 PRELIMINARY; PRT; 580 AA.
 ID Q94BW4;
 AC Q94BW4;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin II precursor.
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OC NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
 RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
 RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated from the seeds of camphor tree and their expression patterns."
 RL Gene 284:215-223(2002).
 CC -! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -! SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AY039802; AAK82459.1; --
 DR HSSP; P02879; 2AAI.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008997; RicinB-like.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 580 type 2 ribosome-inactivating protein cinnamomin II.
 FT
 SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECC0CBFF CRC64;
 Query Match 30.6%; Score 390.5; DB 2; Length 580;
 Best Local Similarity 39.8%; Pred. No. 3.5e-23;
 Matches 101; Conservative 44; Mismatches 92; Indels 17; Gaps 9;
 QY 4 TVSFSTKCATYITYNVLNLRVKKLPEGNHGIPLLRKKADDP-GKAFVLVALSN---D 59
 Db 35 TVTFTTKNATKTSYQTFEALRAQLASGEHPHGFVMDGSGTVPDSKRFILVELSNWAAD 94
 QY 60 NGQLAEIAIDVTSYVVGQVVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 117
 Db 95 SP--VALAVDTNAYVAYRTGSQFFLEDPDPAIENLLPDKRTYTFPFGSYTDLER 152
 QY 118 --GEKAYRETTDLGIEPLRIGIKKLDENAIQNYKPTETASSLLVVIQWSEAAARFTFEN 175
 Db 153 VAGE--LREEILLGMDPLENAISALWISNLNQQR--ALARSLVVIQWVAEAVRFRFIEY 208
 QY 176 QIRNFP--QQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYAV 233
 Db 209 RVRESITRAEMFRDPAPMLSLLENKWSALSNAVQSQNGGVFSSPVELRSISNKPVYVGSV 268

QY 234 -DQVRPKIALKLV 246
DB 269 SDRVSGLAIMLF 282

RESULT 8
Q8GT32 PRELIMINARY; PRT; 563 AA.
AC Q8GT32;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein Nigrin 1 (BC 3.2.2.22).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Girbes T., Arias P.J., Antolin P.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF249280; AAN86130.1; -;
DR HSP; Q9AVR2; 1HW.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008997; RicinB_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
KW Toxin.
SQ SEQUENCE 563 AA; 62173 MW; 0EB236421FC5E04F CRC64;
Query Match 28.6%; Score 365.5; DB 2; Length 563;
Best Local Similarity 41.0%; Pred. No. 3.6e-21;
Matches 94; Conservative 38; Mismatches 80; Indels 17; Gaps 8;
QY 1 GLD--TVSFSTKGATITYVNFNLRLVRLKPEG--NSHGIPLLRKADDPCKA-FVLVA 55
DB 25 GDYFSVSNLDGAKSATYRDFLSNL-RKTVATGYEVNGLFVLRESVQKSFVLVP 83
QY 56 LSNDRGLAIAIDVTSVYVVGQVVRNRSYFFKADPAAYEGFLKNTIKRLHFGSGYPS 115
DB 84 LTVNGTNTVTLAVDTNLVYVAFSGNANSYFFKDATEVQKSNLFVGTQNTLSFTGNDN 143
QY 116 LE-GEKAVRETTDLGIEPLRIGIKKLDENAINDKY-PTEIASLLVVIQMVSEAAARFTFIE 174
DB 144 LETANTRRESIELGSPLDGATSL-----YHGDSVARSLLVVIQMVSEAAARFYIE 196
QY 175 NOIRNFFQ--RIRPANNITISLENKWLKLSFOIRTSKAN-GMFSEAVEL 220
DB 197 QEVRRSLQQAFTFTNASMLSENWSSMSLEIQAGNNVSPSGTVQL 245

RESULT 9
Q8GZP0 PRELIMINARY; PRT; 297 AA.
AC Q8GZP0;
DT 01-MAR-2003 (Tremblrel. 23, Created)

QY 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Ribosome inactivating protein Euseratin 1 precursor (EC 3.2.2.22).
GN Name=Eus1;
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Malpighiales; Euphorbiaceae; Euphorbiaceae; Euphorbiae;
OX NCBI_TaxID=196589;
RN [1]
RP SEQUENCE FROM N.A.
RA Girbes T., Arias P.J., Benvenuto E.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF457874; AAO15530.1; -;
DR HSP; P33185; 1BRY.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
KW Signal; Toxin.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 297 ribosome inactivating protein Euseratin 1.
SQ SEQUENCE 297 AA; 33146 MW; A5269E1DD891287A CRC64;
Query Match 28.2%; Score 359.5; DB 2; Length 297;
Best Local Similarity 39.8%; Pred. No. 4.9e-21;
Matches 98; Conservative 40; Mismatches 97; Indels 11; Gaps 7;
QY 4 TVSFSTKGATITYVNFNLRLVRLKPEGNSHGIPLLRKAD--DPGKAFVLVALSN-DN 60
DB 29 TVKFTHLASGVSYQTLMSALRVNLSKLESNIPLLRRPSDITDQNK-YLLVLTNYDT 87
QY 61 GOLAEIAIDVTSVYVVGQVVRNRSYFFKADPAAYEGFLKNTIKRLHFGSGYPSLEGEK 120
DB 88 KETVTLATLVNLVYVIGYKSGTSKFLKADPSDAKTLFTDTTPKLTVDVTNNL-GD- 145
QY 121 AYRETTDLGIEPLRIGIKKLDENAINDKY-PTEIASLLVVIQMVSEAAARFTFIENQIRN 179
DB 146 --RSKVGGLGIPALKNAINL--NQFDGVSTDDQFKHSLLLVVIQMVSEAAARFKIOLKIEG 201
QY 180 NFQQRIRPANNITISLENKWLKLSFOIRTSKANMSEAVELEANGKYYVTAVDOVKPK 239
DB 202 GLLTQYLPKPTDISYQNNSALSLSIQLADANGRLSESVTLKYEDGKDRVWFVMEQVORD 261
QY 240 IALLKF 245
DB 262 ISLLLY 267

RESULT 10
NIGB SAMNI
ID NIGB SAMNI STANDARD; PRT; 563 AA.
AC P33183; P33184; P93542;
DT 01-OCT-1993 (Rel. 27, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nigrin b precursor (Agglutinin V) (SNAV) (Contains: Nigrin b A chain (EC 3.2.2.22) (rRNA N-glycosidase); Nigrin b B chain).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Dipsacales; Adoxaceae; Sambucus.
 OC NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Barb;
 RX MEDLINE=96215449; PubMed=8647092;
 RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
 from the bark of elderberry (Sambucus nigra).";
 RL Eur. J. Biochem. 237:505-513(1996).
 RN [2]
 RP SEQUENCE OF 26-49 AND 298-321.
 RC TISSUE=Barb;
 RX MEDLINE=94003077; PubMed=8400135;
 RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
 RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
 RT "Isolation and partial characterization of nigrin b, a non-toxic novel
 type 2 ribosome-inactivating protein from the bark of Sambucus nigra
 L";
 RL Plant Mol. Biol. 22:1181-1186(1993).
 CC -!- FUNCTION: Non-toxic type 2 RIP which strongly inhibits mammalian
 protein synthesis but does not affect plant nor bacterial protein
 synthesis. The A chain is responsible for inhibiting protein
 synthesis through the catalytic inactivation of 60S ribosomal
 subunits by removing adenine from position 4,324 of 28S rRNA.
 CC -!- FUNCTION: The B chain is a galactose-specific lectin that
 facilitates the binding of nigrin b to the cell membrane that
 precedes endocytosis.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -!- SIMILARITY: In the N-terminal section; belongs to the ribosome-
 inactivating protein family. Type 2 RIP subfamily.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U41299; AAB39475.1; -.
 DR PIR; S37382; S37382.
 DR PIR; S37383; S37383.
 DR HSP; Q9AVR2; 1HWM.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR008997; RicinB_Like.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR Direct protein sequencing; Glycoprotein; Hydrolase; Lectin;
 KW Plant defense; Protein synthesis inhibitor; Repeat; Signal; Toxin.
 FT SIGNAL 1 25
 FT CHAIN 26 297 Nigrin b A chain.
 FT CHAIN 298 533 Nigrin b B chain.
 FT DOMAIN 305 431 Ricin B-type lectin 1.
 FT DOMAIN 434 559 Ricin B-type lectin 2.
 FT REPEAT 316 356 1-alpha.
 FT REPEAT 357 397 1-beta.
 FT REPEAT 400 432 1-gamma.
 FT REPEAT 445 482 2-alpha.
 FT REPEAT 486 524 2-beta.
 FT REPEAT 527 554 2-gamma.
 FT ACT SITE 188 198 By similarity.
 FT DISULFID 274 302 Interchain (By similarity).
 FT DISULFID 319 338 By similarity.

FT DISULFID 360 377 By similarity.
 FT DISULFID 448 463 By similarity.
 FT DISULFID 489 506 By similarity.
 FT CARBOHYD 221 221 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 483 483 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 537 537 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 39 K -> V (in Ref. 2).
 SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRC64;
 Query Match 27.9%; Score 356; DB 1; Length 563;
 Best Local Similarity 41.1%; Pred. No. 2.1e-20;
 Matches 90; Conservative 36; Mismatches 77; Indels 16; Gaps 7;
 QY 1 GLD--TVSFTKGYTYTYVNFNLRLVRLKLPKPEG--NSHGIPLLRKKADDPCKA-FVLVA 55
 DB 25 GIDYPSVSNLDGAKSATYRDLFSLNLR-KTVATGTVEYVNGLVFLRRESEVQVKSRLVLP 83
 QY 56 LSNONGQLAEIAIDVTSVVVGVGVNRNRSYFFKQADAPDAAYEGLFKNVTKIKRLHFGGSYPS 115
 DB 84 LTVNGNTVTLVADVTVNLVYVAFSGNANSYFFKQATEVQKSNLFVGTQNTLSFTGNVDN 143
 QY 116 LE-GEKAYRETTDLGIEPLRIGIKLDENAIKNYKPTETIASLLVVIQVWSEAAFTFIE 174
 DB 144 LETAANTRRRESIELGPSLDCATISL-----YHGDSVARSLLVVIQVWSEAAFRFYIE 196
 QY 175 NQIRNNFQ--RIRPANTTISLENKWKGLSFQIRTSKAN 211
 DB 197 QEVRRSQQATSFPTNALMLSMENNWSMSLEIQOAGNN 235
 RESULT 11
 Q945S2 PRELIMINARY; PRT; 563 AA.
 AC Q945S2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ribosome-inactivating protein.
 GN Name=AVI;
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Dipsacales; Adoxaceae; Sambucus.
 OC NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Van Damme E.J.M.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AF409135; AAL04123.1; -.
 DR HSP; Q9AVR2; 1HWM.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008997; RicinB_Like.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 27.9%; Score 356; DB 2; Length 563;
 Best Local Similarity 41.1%; Pred. No. 2.1e-20;
 Matches 90; Conservative 36; Mismatches 77; Indels 16; Gaps 7;

QY 1 GLD--TVSFSTKGATYITVNFELNLR--NSHGIPLLRKKADDPGKA-FVLVA 55
 DB 25 GIDYPSVFNLDGAKSATYRDFLSNLR-KTVATGTVEVNGLPVLRSESEVQVKSRLVLP 83

QY 56 LNDNGQLAIAIDVTSVTVVGVQVNRNRSYFFPKDAPDAAYEGFLFKNTIKTRLHFHFGSYPSS 115
 DB 84 LTYNGNTVTLAVDVTNLVYVAFSGNANSYFFPKDATEVQKSNLFGVTKQNTLSFTGNDN 143

QY 116 LE-GEKAYRETTDLGIEPRIGIKKL DENAIDNYKPTETAIASSLLVVIQMVSEAAARFTTE 174
 DB 144 LETAANTRESIELGSPDLGATSL-----YHGDVSARSLVLLVVIQMVSEAAARFTTE 196

QY 175 NOIRNNFQQ--RIRPANNTISLENKWKLSFOIRTSKAN 211
 DB 197 QEVRSLSQATSTFPNALMSMENNWSMSLEIQAGNN 235

RESULT 12
 ID 004367 PRELIMINARY; PRT; 563 AA.
 AC 004367;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ribosome inactivating protein precursor.
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98112023; PubMed=9450339;
 RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
 RA Peumans W.J.;
 RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
 RT derived from a truncated type 2 ribosome-inactivating protein.";
 RL Plant J. 12:1251-1260(1997)
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; J765324; AAC15885.1; -;
 DR HSSP; Q9AVR2; 1HW.
 DR GO; GO:0030125; C:clathrin vesicle coat; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001473; Clathrin prop_N.
 DR InterPro; IPR008997; RicinB-like.
 DR InterPro; IPR000772; RicinB lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; RicinB lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN B LECTIN; 2.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 25
 FT CHAIN 26 297 ribosome inactivating protein, A chain.
 FT CHAIN 298 563 ribosome inactivating protein, B chain.
 SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

Query Match 27.6%; Score 352.5; DB 2; Length 563;
 Best Local Similarity 39.7%; Pred. No. 4.1e-20;
 Matches 91; Conservative 37; Mismatches 86; Indels 15; Gaps 7;

QY 1 GLD--TVSFSTKGATYITVNFELNLR--VCLKPEGNHSHGIPLLRKKADDPGK-AFVLVAL 56
 DB 25 GIDYPSVFNLDGAKSATYRDFLKNLRTIVATGTVEVNGLPVLRSESEVQVKNRFLVLL 84

QY 57 SNDNGQLAIAIDVTSVTVVGVQVNRNRSYFFKADAPDAAYEGFLFKNTIKTRLHFHFGSYPSS 116
 DB 85 TNYNGNTVTLAVDVTNLVYVAFSANANSYFFKDATQLOKSNLFGVTRQHTLPTGTGYDNL 144

QY 117 E-GEKAYRETTDLGIEPRIGIKKL DENAIDNYKPTETAIASSLLVVIQMVSEAAARFTTE 175
 DB 145 ETAAGTRRESIELGSPDLGATSL-----YDESVARSLVLLVVIQMVSEAAARFTTE 197

QY 176 QIRNNFQQ--RIRPANNTISLENKWKLSFOIRTSKAN-GMFESEAVELE 221
 DB 198 EVRSLSQATSTFPNALMSMENNWSMSLEVQQSGDNVSPFTGTVOLQ 246

RESULT 13
 ID 0684J5 PRELIMINARY; PRT; 264 AA.
 AC 0684J5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Type I ribosome inactivating protein precursor (Fragment).
 GN Name-rip;
 OS Momordica charantia (Bitter melon) (Balsam pear).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,
 RA Tran Thi Phuong L., Nong Van H.;
 RT "Expression of a gene encoding ribosome inactivating protein from
 RT bitter melon (Momordica charantia).";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nong V.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AJ748278; CAH19208.1; -;
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT NON TER 1 1
 FT SIGNAL <1 1 Potential.
 FT CHAIN 2 264 type I ribosome inactivating protein.
 SQ SEQUENCE 264 AA; 29775 MW; AD9E1175B70521AD CRC64;

Query Match 27.3%; Score 348; DB 2; Length 264;
 Best Local Similarity 37.4%; Pred. No. 3.7e-20;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

QY 5 VSFSTKGATYITVNFELNLRVCLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDNGQLA 64
 DB 3 VNFDLSTAKTYTKPIEDFRATLPFSHKVYDIPLYSTISD-SRFFILLNTLSYAYETI 61

QY 65 ETAIDVTSVTVVGVQVNRNRSYFFKADAPDAAYEGFLFKNTIKTRLHFHFGSYPSSLE-GEKAYR 123
 DB 62 SVALDVNVTVVAYTRDVSYFFKSPPEAYNLFKGTIKTILPTGTGVNLTAAHKIR 121

QY 124 ETTDLGIEPRIGIKKL DENAIDNYKPTETAIASSLLVVIQMVSEAAARFTTEIENRNNFQQ 183
 DB 122 ENIDLGLPALSSAI-----TTLFYNAQAPSALLVIQTAAEARFKYIERHAKYVAT 176

QY 184 RIRPANNTISLENKWKLSFOI-RTSGANGMFSEAVELERANGKYYVTAVDQ--VKPKI 240

```
Db 177 NFKPNLAITISLENSALSQKIFLAQNGGKFRNPFVDLIKPTGERFQVNTVDSVVVKGNI 236
QY 241 ALL 243
Db 237 KLL 239

RESULT 14
RIP2_MOMBA
ID RIP2_MOMBA STANDARD; PRT; 286 AA.
AC P29339;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ribosome-inactivating protein momordin II precursor (EC 3.2.2.22)
DE (tRNA N-glycosidase).
OS Momordica balsamina (Bitter gourd) (Balsam apple).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3672;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=93027170; PubMed=1408771;
RA Ortigao M., Better M.;
RT "Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologous to other plant proteins.";
RL Nucleic Acids Res. 20:4662-4662(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC Type 1 RIP subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z12175; CAA78166.1; -
DR PIR; S25560; S25560.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 23
FT CHAIN 24 286 Ribosome-inactivating protein momordin
II.
FT ACT_SITE 181 181 By similarity.
FT SEQUENCE 286 AA; 32031 MW; 3B89FF1AE6B25986 CRC64;
Query Match 27.3%; Score 348; DB 1; Length 286;
Best Local Similarity 37.4%; Pred. No. 4.1e-20;
Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;
QY 5 VSFSTKGTATYIVYVNFPLNELRVKLKPEGNHSHGTLPLLRKKADDPGRKAFVLVALSDNGQLA 64
Db 25 VNFLLSTAKYTKYTFIEDFRATLPESHVKVYDIPLLYSTISD-SRRFILLDLTSTVAYETI 83
QY 65 ETADIVTSVYGVYQVNRNSYFKDAPDAAYSGLFKNTIKTRLHFGSGSYPSLE-GEKAYR 123
Db 84 SVAIDVTNYYVAYRTRDVSFFKSPPEAYNLLFKGTRKITLPYTGNYENLQTAHKIR 143
QY 124 ETTDLGIEPLRIGIKKLDENADINVKPTETIASLVLVQWSEARFTFENQIRNFFQ 183
Db 144 ENIDGLPALSSAI-----TTLFYNAQAPSALLVLIQTAEARFKYIERHVKVAT 198
QY 184 RIRPANNTISLENKMGKLSFQI-RTSGANGMFSEAVELERANGKKYVTVADQ--VKPKI 240
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Db 199 NFKPNLAITISLENSALSQKIFLAQNGGKFRNPFVDLIKPTGERFQVNTVDSVVVKGNI 258
QY 241 ALL 243
Db 259 KLL 261

RESULT 15
RIP3_MOMCH
ID RIP3_MOMCH STANDARD; PRT; 286 AA.
AC P24817; Q41257; Q9FSH2; Q9FUV7;
DT 01-MAR-1992 (Rel. 21, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)
DE (tRNA N-glycosidase) (MAP 30) (B-MMC).
GN Name=MAP30; Synonyms=RIP;
OS Momordica charantia (Bitter melon) (Balsam pear).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3673;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=Leaf;
RX MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A;
RA Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbaier A.,
Huang H.-I., Kung H.-F.;
RT "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
melon.";
RL Gene 161:151-156(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Quanhong Y., Rihe P., Aisheng X.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 23-286 FROM N.A.
RA Wei Y.-P., Cai L.-B., Zhuang W.;
RT "Cloning rip gene and identification of its resistance to Aspergillus
flavus.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 23-286 FROM N.A.
RA Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;
RT "Expression of a RIP gene from Momordica charantia in E. coli.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 24-67.
RC TISSUE=Seed;
RX MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-O;
RA Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-P., Huang P.,
Huang H.-I., Huang P.L.;
RT "MAP 30: a new inhibitor of HIV-1 infection and replication.";
RL FEBS Lett. 272:12-18(1990).
RN [6]
RP STRUCTURE BY NMR OF 24-286. AND DNA BINDING.
RX PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;
RA Wang Y.-X., Neamaty N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,
Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T.,
Lee-Huang S., Bax A., Torchia D.A.;
RT "Solution structure of anti-HIV-1 and anti-tumor protein MAP30:
structural insights into its multiple functions.";
RL Cell 99:433-442(1999).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.
RX PubMed=10329776; DOI=10.1107/S0907444999003297;
RA Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;
RT "Three-dimensional structure of beta-momorcharin at 2.55 A
resolution.";
RL Acta Crystallogr. D 55:1144-1151(1999).
CC -!- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inhibits
HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes
```

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Qy      241 ALL 243
      ||
Db      259 KLL 261

Search completed: June 20, 2005, 09:20:41
Job time : 114.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:00:05 ; Search time 117 Seconds
(without alignments)
829.717 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDVSFSTKGATYYVNF.....AVDQVKPKIALKLFVDKPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Match	Length	DB ID	Description
	Score	Match				
1	1277	100.0	251	2	AAR63914	Type I RI
2	1273	99.7	251	2	AAR63912	Type I RI
3	1269	99.4	251	2	AAR63903	Type I ri
4	1269	99.4	251	2	AAR63915	Type I RI
5	1269	99.4	251	8	ADG63044	Gelonium
6	1269	99.4	316	5	ABG71551	G. multif
7	1269	99.4	507	5	ABG71552	Marine sc
8	1266	99.1	293	2	AAR29300	BPI pepti
9	1266	99.1	309	2	AAR29303	BPI pepti
10	1266	99.1	332	2	AAR29294	BPI pepti
11	1264	99.0	251	2	AAR63923	Type I RI
12	1261	98.7	251	2	AAR63921	Type I RI
13	1261	98.7	251	2	AAR63918	Type I RI
14	1261	98.7	251	2	AAR63920	Type I RI
15	1261	98.7	251	2	AAR63919	Type I RI
16	1261	98.7	251	2	AAR63924	Type I RI
17	1260	98.7	251	2	AAR63922	Type I RI
18	1260	98.7	251	2	AAR63916	Type I RI
19	1260	98.7	251	2	AAR63917	Type I RI
20	1257	98.4	251	2	AAR741177	Type I ri
21	1251	98.0	251	2	AAR37291	Plant typ
22	1235.5	96.8	258	2	AAR22227	Geloniin t
23	1171	91.7	235	2	AAR63913	Type I RI
24	348	27.3	263	2	AAR63905	Type I ri
25	348	27.3	263	2	AAR741179	Type I ri

26	348	27.3	263	8	ADG63043	Adg63043 Momordica
27	347	27.2	565	1	AAP50166	Sequence
28	347	27.2	565	4	AAG78300	Castor be
29	347	27.2	574	1	AAP70325	Sequence
30	346	27.1	267	2	AAR30722	Ricin A f
31	346	27.1	267	2	AAR37290	Ricin A c
32	346	27.1	267	2	AAR63902	Ricin A c
33	346	27.1	267	3	AAB19265	Amino aci
34	346	27.1	267	7	ADC24288	Ricin tox
35	346	27.1	268	2	AAR39570	Sequence
36	346	27.1	290	2	AAR21699	Ricin A-C
37	346	27.1	290	2	AAR25136	Ricin A-C
38	346	27.1	332	1	AAP70097	Ricin A.
39	346	27.1	332	1	AAP70838	Sequence
40	346	27.1	332	1	AAP95639	Ricin A e
41	346	27.1	554	2	AAR70827	Anti-cata
42	346	27.1	562	1	AAP90079	Ricin D.
43	346	27.1	565	4	AAG78304	Modified
44	346	27.1	576	1	AAP70326	Sequence
45	346	27.1	576	2	AAW25787	Castorbea

ALIGNMENTS

RESULT 1
AAR63914
ID AAR63914 standard; protein; 251 AA.
XX
AC AAR63914;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel(A44/A50).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX (XOMA) XOMA CORP.
PI Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 181-182; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match	100.0%;	Score 1277;	DB 2;	Length 251;
Best Local Similarity	100.0%;	Pred. No. 4.2e-120;		
Matches 251;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GLDTSVSTKGTATYTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVLSNDN	60	
DB	1	GLDTSVSTKGTATYTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVLSNDN	60	
QY	61	GOLAEIAIDVTSVVVGVQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGSYPSEGEK	120	
DB	61	GOLAEIAIDVTSVVVGVQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGSYPSEGEK	120	
QY	121	AYRETTDLGIEPLRIGIKKLDENADINVKPTEIASSLLVVIQMVSEAAARTFFIENQIRNN	180	
DB	121	AYRETTDLGIEPLRIGIKKLDENADINVKPTEIASSLLVVIQMVSEAAARTFFIENQIRNN	180	
QY	181	FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI	240	
DB	181	FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI	240	
QY	241	ALLKFVDKDPK 251		
DB	241	ALLKFVDKDPK 251		
RESULT 2				
AA063912				
ID	AA063912	standard; protein; 251 AA.		
XX	AA063912;			
XX	AC			
XX	XX			
DT	25-MAR-2003	(revised)		
DT	27-JUL-1995	(first entry)		
XX	XX			
DE	XX	Type I RIP gelonin analog Gel (A50/C44).		
XX	XX			
KW	XX	Type I ribosome-inactivating proteins; RIPs; gelonin;		
KW	XX	cytotoxic therapeutic agents; autoimmune disease; cancer;		
KW	XX	graft-versus-host disease.		
XX	XX			
OS	XX	Gelonium multiflorum.		
XX	XX			
PN	XX	WO9426910-A1.		
XX	XX			
PD	XX	24-NOV-1994.		
XX	XX			
PF	XX	12-MAY-1994; 94WO-US005348.		
XX	XX			
PR	XX	12-MAY-1993; 93US-00064691.		
XX	XX			
PA	XX	(XOMA) XOMA CORP.		
XX	XX			
PI	XX	Better MD, Carroll SF, Studnicka GM;		
XX	XX			
WPI	XX	WPI; 1995-006804/01.		
XX	XX			
PT	XX	Polynucleotide(s) encoding type I ribosome-inactivating proteins - which		
PT	XX	are suitable for use as components of cytotoxic therapeutic agents.		
XX	XX			
XX	XX	Example 3; Page 179-180; 221pp; English.		
XX	XX			
CC	XX	AA063912-R63924 are analogs of AA063903 type I ribosome-inactivating		
CC	XX	protein (RIP) gelonin, one of the nine RIPs described in AA063903-R63911.		
CC	XX	RIPs are key components of cytotoxic therapeutic agents (CTAs), which		
CC	XX	include gene fusion products and immunoconjugates. CTAs may be used to		
CC	XX	selectively eliminate any cell type to which a RIP component is		
CC	XX	targetted, by the specific binding capacity of the second component of		
CC	XX	the agent. They can be used in the treatment of diseases where the		
CC	XX	elimination of a particular cell type is desired, such as autoimmune		
CC	XX	disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to		
CC	XX	correct PN field.)		


```
XX SQ Sequence 251 AA;
Query Match 99.4%; Score 1269; DB 2; Length 251;
Best Local Similarity 99.2%; Pred. No. 2.7e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 4
AAR63915
ID AAR63915 standard; protein; 251 AA.
AC AAR63915;
XX
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
XX
DE Type I RIP gelonin analog Gel(C10/A44/A50).
XX
XX Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
XX Gelonium multiflorum.
XX
XX WO9426910-A1.
PN
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US005348.
PF
XX 12-MAY-1993; 93US-00064691.
PR
XX (XOMA ) XOMA CORP.
XX
XX PA
XX
XX PI Better MD, Carroll SF, Studnicka GM;
XX
XX WPI; 1995-006804/01.
DR
XX
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
PT
XX
XX Example 3; Page 189-190; 221pp; English.
XX
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

XX SQ Sequence 251 AA;
Query Match 99.4%; Score 1269; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-119;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 5
ADG63044
ID ADG63044 standard; protein; 251 AA.
AC ADG63044;
XX
XX
DT 11-MAR-2004 (first entry)
XX
XX Gelonium anti-HIV protein 31kDa (GAP31).
DE
XX
XX anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
XX
XX Gelonium multiflorum.
OS
XX
XX US6652861-B1.
PN
XX
XX 25-NOV-2003.
XX
XX 25-AUG-2000; 2000US-00645603.
PF
XX 26-AUG-1999; 99US-0150885P.
PR
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX PA
XX
XX PI Lee-Huang S;
XX
XX WPI; 2004-050519/05.
DR
XX
XX New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
PT antiviral activity, useful for treating human immunodeficiency virus
PT infection or tumor.
XX
XX Example 1; SEQ ID NO 2; 22pp; English.
XX
XX The invention describes an isolated peptide or polypeptide having an anti-
CC -tumour and antiviral activity. Also described is a composition
CC comprising the isolated peptide or polypeptide, and a carrier, excipient
CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
CC polypeptides. The peptide or polypeptide is useful for treating HIV
CC infection, and tumour. This is the amino acid sequence of Gelonium anti-
CC HIV protein 30kDa (MAP30).
XX
XX Sequence 251 AA;
```

Query Match 99.4%; Score 1269; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 2.7e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYTYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
Db 1 GLDTSVSTKGTATYTYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVVVGQVVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
Db 61 GOLAEIAIDVTSVVVGQVVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNPKYPTBIASLLVVIOMVSEARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNPKYPTBIASLLVVIOMVSEARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 6
ABG71551
ID ABG71551 standard; protein; 316 AA.
AC ABG71551;
DT 08-JAN-2003 (first entry)
DE G. multiflorum recombinant gelonin (rGel) toxin.
KW Modified protein; reduced antigenicity; modified toxin; gelonin;
KW designer toxin; immunotoxin; proteinaceous compound; cancer;
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW inflammatory disease; cardiovascular disease; diabetes;
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW recombinant gelonin; rGel.
OS Gelonium multiflorum.
XX WO200269886-A2.
PN 12-SEP-2002.
XX 12-FEB-2002; 2002WO-US004195.
XX 12-FEB-2001; 2001US-0268402P.
XX (RERE-) RES DEV FOUND.
XX Rosenblum MG, Cheung L;
PI WPI; 2002-750431/81.
DR N-PSDB; ABS56021.
XX Generating a modified protein with reduced antigenicity for treating
PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
PT antigenic in the first subject using antiserum from either the first or a
PT second subject.
XX Claim 63; Page 169-170; 176pp; English.
XX The present invention relates to a method of generating a modified
CC protein with reduced antigenicity while maintaining its biological
CC activity. The method comprises identifying a region of the protein that
CC is antigenic in a first subject using antiserum from either the first

CC subject or a second subject of the same species as the first subject. In
CC particular the invention discloses modified toxin compounds, for example
CC gelonin toxin derived from Gelonium multiflorum, that are truncated
CC and/or possess reduced antigenicity. Such designer toxins have
CC therapeutic, diagnostic, and preventative benefits, particularly as
CC immunotoxins. The method of the invention is useful for generating
CC proteinaceous compounds with less antigenicity. The immunotoxin and
CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
CC compositions of the invention are also useful for treating microbial
CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
CC diseases, hyperproliferative disorders including cancer, leukaemias,
CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
CC diseases, and diabetes. The method provides less antigenic proteins, the
CC peptides and polypeptides, which are more effective than prior art. The
CC present sequence represents G. multiflorum recombinant gelonin (rGel).
XX
SQ Sequence 316 AA;

Query Match 99.4%; Score 1269; DB 5; Length 316;
Best Local Similarity 99.2%; Pred. No. 3.8e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYTYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
Db 47 GLDTSVSTKGTATYTYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 106

QY 61 GOLAEIAIDVTSVVVGQVVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
Db 107 GOLAEIAIDVTSVVVGQVVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGSGYPSLEGEK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENADNPKYPTBIASLLVVIOMVSEARFTFIENQIRNN 180
Db 167 AYRETTDLGIEPLRIGIKKLDENADNPKYPTBIASLLVVIOMVSEARFTFIENQIRNN 226

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 227 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 286

QY 241 ALLKFVDKDPK 251
Db 287 ALLKFVDKDPK 297

RESULT 7
ABG71552
ID ABG71552 standard; protein; 507 AA.
XX ABG71552;
AC ABG71552;
XX 08-JAN-2003 (first entry)
DT Murine scfWEL/G. multiflorum rGel fusion protein.
DE Modified protein; reduced antigenicity; modified toxin; gelonin;
KW designer toxin; immunotoxin; proteinaceous compound; cancer;
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW inflammatory disease; cardiovascular disease; diabetes;
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW murine; single-chain ZMB-018 antibody; recombinant gelonin; rGel;
XX scfWEL/rGel; mutant; mutein.
OS Mus sp.
OS Gelonium multiflorum.
OS Synthetic.
OS Chimeric.
XX WO200269886-A2.
XX

PD 12-SEP-2002.
 XX
 PF 12-FEB-2002; 2002WO-US004195.
 XX
 PR 12-FEB-2001; 2001US-0268402P.
 XX
 PA (RERE-) RES DEV FOUND.
 XX
 PI Rosenblum MG, Cheung L;
 DR WPI; 2002-750431/81.
 DR N-PSDB; ABS56029.
 XX
 PT Generating a modified protein with reduced antigenicity for treating
 PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
 PT antigenic in the first subject using antiserum from either the first or a
 PT second subject.
 XX
 PS Disclosure; Page 174-176; 176pp; English.
 XX
 CC The present invention relates to a method of generating a modified
 CC protein with reduced antigenicity while maintaining its biological
 CC activity. The method comprises identifying a region of the protein that
 CC is antigenic in a first subject using antiserum from either the first
 CC subject or a second subject of the same species as the first subject. In
 CC particular the invention discloses modified toxin compounds, for example
 CC gelonin toxin derived from Gelonium multiflorum, that are truncated
 CC and/or possess reduced antigenicity. Such designer toxins have
 CC therapeutic, diagnostic, and preventative benefits, particularly as
 CC immunotoxins. The method of the invention is useful for generating
 CC proteinaceous compounds with less antigenicity. The immunotoxin and
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
 CC compositions of the invention are also useful for treating microbial
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
 CC diseases, hyperproliferative disorders including cancer, leukaemias,
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
 CC diseases, and diabetes. The method provides less antigenic proteins,
 CC peptides and polypeptides, which are more effective than prior art. The
 CC present sequence represents murine single-chain ZME-018 antibody/G.
 CC multiflorum recombinant gelonin (rgeI) (scfVMEI/rgeI) fusion protein
 XX
 SQ Sequence 507 AA;
 Query Match 99.4%; Score 1269; DB 5; Length 507;
 Best Local Similarity 99.2%; Pred. No. 7.3e-119;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GLDTSVSTKGTATYTYVNFNLRLVKLPKPGNSHGIPILRRKADDPGKAFVLVALSNDN 60
 DB 257 GLDTSVSTKGTATYTYVNFNLRLVKLPKPGNSHGIPILRRKADDPGKAFVLVALSNDN 316
 QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 DB 317 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 376
 QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 180
 DB 377 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 436
 QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 437 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 496
 QY 241 ALLKXFDKDPK 251
 DB 497 ALLKXFDKDPK 507
 RESULT 8
 AAW29300

AAW29300 standard; protein; 293 AA.
 AAW29300;
 20-APR-1998 (first entry)
 BPI peptide fusion protein pING3797 vector construct protein.
 Bactericidal/permeability increasing peptide; BPI; fusion protein;
 bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 fungicidal; recombinant DNA; vector.
 Synthetic.
 Pectobacterium carotovorum.
 Homo sapiens.
 Chimeric.
 WO9735009-A1.
 25-SEP-1997.
 18-MAR-1997; 97WO-US005287.
 22-MAR-1996; 96US-00621803.
 (XOMA) XOMA CORP.
 Better MD;
 WPI; 1997-480215/44.
 N-PSDB; AAT86336.
 Recombinant production of bactericidal/permeability increasing protein -
 by expression as a fusion protein in microbial host cells, then cleaving
 the BPI peptide from the carrier.
 Example 1; Page 160-161; 186pp; English.
 A new recombinant DNA vector construct has been developed which encodes a
 fusion protein and is suitable for introduction into a bacterial host.
 The vector comprises: (a) DNA encoding at least one cationic
 bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 located between (a) and (b). The present sequence represents the protein
 from the pING3797 vector construct which codes for a BPI fusion protein.
 The peptides have many uses including the treatment of bacterial and
 fungal infections. BPI peptides also bind to endotoxins and heparin,
 neutralising their effects. The peptides have further been shown to
 inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 proteins have been found to be expressed in large amounts without
 significant proteolysis, and in some cases are actually secreted from the
 host cells. This allows the indirect production of anti-microbial BPI
 peptides in microbial hosts

Query Match 99.1%; Score 1266; DB 2; Length 293;
 Best Local Similarity 98.8%; Pred. No. 6.8e-119;
 Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GLDTSVSTKGTATYTYVNFNLRLVKLPKPGNSHGIPILRRKADDPGKAFVLVALSNDN 60
 DB 23 GLDTSVSTKGTATYTYVNFNLRLVKLPKPGNSHGIPILRRKADDPGKAFVLVALSNDN 82
 QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 DB 83 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 142
 QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 180
 DB 143 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 202
 QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

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Db      203 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262
      |||||
Qy      241 ALLKFVDKDPK 251
      |||||
Db      263 ALLKFVDKDPK 273
      |||||

RESULT 9
AAW29303
ID      AAW29303 standard; protein; 309 AA.
XX
AC      AAW29303;
XX
DT      20-APR-1998 (first entry)
XX
DE      BPI peptide fusion protein PING3795 vector construct protein.
XX
KW      Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW      bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW      fungicidal; recombinant DNA; vector.
XX
OS      Synthetic.
OS      Pectobacterium carotovorum.
OS      Homo sapiens.
OS      Chimeric.
XX
PN      WO9735009-A1.
XX
XX
PD      25-SEP-1997.
XX
PF      18-MAR-1997; 97WO-US005287.
XX
PR      22-MAR-1996; 96US-00621803.
XX
PA      (XOMA ) XOMA CORP.
XX
PI      Better MD;
XX
DR      WPI; 1997-480215/44.
DR      N-PSDB; AAT86341.
XX
PT      Recombinant production of bactericidal/permeability increasing protein -
PT      by expression as a fusion protein in microbial host cells, then cleaving
PT      the BPI peptide from the carrier.
XX
PS      Example 1; Page 152-153; 186pp; English.
XX
CC      A new recombinant DNA vector construct has been developed which encodes a
CC      fusion protein and is suitable for introduction into a bacterial host.
CC      The vector comprises: (a) DNA encoding at least one cationic
CC      bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC      carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC      located between (a) and (b). The present sequence represents the protein
CC      from the PING3795 vector construct which codes for a BPI fusion protein.
CC      The peptides have many uses including the treatment of bacterial and
CC      fungal infections. BPI peptides also bind to endotoxins and heparin,
CC      neutralising their effects. The peptides have further been shown to
CC      inhibit angiogenesis (partly due to heparin-binding activity). The fusion
CC      proteins have been found to be expressed in large amounts without
CC      significant proteolysis, and in some cases are actually secreted from the
CC      host cells. This allows the indirect production of anti-microbial BPI
CC      peptides in microbial hosts
XX
SQ      Sequence 309 AA;
      Query Match 99.1%; Score 1266; DB 2; Length 309;
      Best Local Similarity 98.8%; Pred. No. 7.3e-119; Indels 0; Gaps 0;
      Matches 248; Conservative 1; Mismatches 2;

Qy      1 GLDTSFSTKGATYITYNFLNELRVKLPKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
      |||||
Db      23 GLDTSFSTKGATYITYNFLNELRVKLPKPEGNHGIPLLRKADDPGKAFVLVALSNDN 82
      |||||

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Qy      61 QQLAEIAIDVTSVVVGVQVNRNRYFFKDAADAAVEGLFKNTIKTRLHFGGSGYPSLEGK 120
      |||||
Db      83 QQLAEIAIDVTSVVVGVQVNRNRYFFKDAADAAVEGLFKNTIKTRLHFGGSGYPSLEGK 142
      |||||
Qy      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTPIENQIRNN 180
      |||||
Db      143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTPIENQIRNN 202
      |||||
Qy      181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
      |||||
Db      203 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262
      |||||
Qy      241 ALLKFVDKDPK 251
      |||||
Db      263 ALLKFVDKDPK 273
      |||||

RESULT 10
AAW29294
ID      AAW29294 standard; protein; 332 AA.
XX
AC      AAW29294;
XX
DT      20-APR-1998 (first entry)
XX
DE      BPI peptide fusion protein PING3793 vector construct protein.
XX
KW      Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW      bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW      fungicidal; recombinant DNA; vector.
XX
OS      Synthetic.
OS      Pectobacterium carotovorum.
OS      Homo sapiens.
OS      Chimeric.
XX
PN      WO9735009-A1.
XX
PD      25-SEP-1997.
XX
PF      18-MAR-1997; 97WO-US005287.
XX
PR      22-MAR-1996; 96US-00621803.
XX
PA      (XOMA ) XOMA CORP.
XX
PI      Better MD;
XX
DR      WPI; 1997-480215/44.
DR      N-PSDB; AAT86332.
XX
PT      Recombinant production of bactericidal/permeability increasing protein -
PT      by expression as a fusion protein in microbial host cells, then cleaving
PT      the BPI peptide from the carrier.
XX
PS      Example 1; Page 148-150; 186pp; English.
XX
CC      A new recombinant DNA vector construct has been developed which encodes a
CC      fusion protein and is suitable for introduction into a bacterial host.
CC      The vector comprises: (a) DNA encoding at least one cationic
CC      bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC      carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC      located between (a) and (b). The present sequence represents the protein
CC      from the PING3793 vector construct which codes for a BPI fusion protein.
CC      The peptides have many uses including the treatment of bacterial and
CC      fungal infections. BPI peptides also bind to endotoxins and heparin,
CC      neutralising their effects. The peptides have further been shown to
CC      inhibit angiogenesis (partly due to heparin-binding activity). The fusion
CC      proteins have been found to be expressed in large amounts without
CC      significant proteolysis, and in some cases are actually secreted from the
CC      host cells. This allows the indirect production of anti-microbial BPI
CC      peptides in microbial hosts

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XX Sequence 332 AA;
SQ
Query Match 99.1%; Score 1266; DB 2; Length 332;
Best Local Similarity 98.8%; Pred. No. 8.1e-119;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTSFSFGATYITYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 23 GLDTSFSFGATYITYVNFNLRLVKLPKGNHGIPLLRKADDPGKCFVLVALSNDN 82
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 83 GLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 142
QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 202
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYTAVDQVKPKI 240
DB 203 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYTAVDQVKPKI 262
QY 241 ALLKFVDKDPK 251
DB 263 ALLKFVDKDPK 273
RESULT 11
AAR63923
ID AAR63923 standard; protein; 251 AA.
XX
AC AAR63923;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C103).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 187-188; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
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CC correct PN field.)
XX
SQ Sequence 251 AA;
Query Match 99.0%; Score 1264; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 8.7e-119;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSFGATYITYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSFGATYITYVNFNLRLVKLPKGNHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVYTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 12
AAR63921
ID AAR63921 standard; protein; 251 AA.
XX
AC AAR63921;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C10).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 186; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
```

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 1 GLDTSFSTKATYTYVNFNLRLVKLPKPNHSHGIPLLRKKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
AAR63918
ID AAR63918 standard; protein; 251 AA.
XX
AC AAR63918;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I RIP gelonin analog Gel (C248).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 183-184; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the

CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSTKATYTYVNFNLRLVKLPKPNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKATYTYVNFNLRLVKLPKPNHSHGIPLLRKKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
AAR63920
ID AAR63920 standard; protein; 251 AA.
XX
AC AAR63920;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I RIP gelonin analog Gel (C244).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 185; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the

CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
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DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 15

AAR63919
ID AAR63919 standard; protein; 251 AA.

XX AC AAR63919;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel(C239).

XX Type I ribosome-inactivating proteins; RIPS; gelonin;
XX cytotoxic therapeutic agents; autoimmune disease; cancer;
XX graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

XX PA PA

XX Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which

XX are suitable for use as components of cytotoxic therapeutic agents.

XX Example 3; Page 184; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
XX protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
XX RIPS are key components of cytotoxic therapeutic agents (CTAs), which
XX include gene fusion products and immunconjugates. CTAs may be used to
XX selectively eliminate any cell type to which a RIP component is

CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.7e-118;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:16:45
Job time : 118 secs

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GenCore version 5.1.6
Copyright (C) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 09:20:52 ; Search time 105.5 Seconds

(without alignments)
913.544 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDVSFSTKGTATITVNF.....AVDQVKPKIALLKFDKDKPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1277	100.0	251	17	US-10-717-243-101
3	1273	99.7	251	14	US-10-127-890-99
4	1273	99.7	251	14	US-10-127-890-100
5	1273	99.7	251	17	US-10-717-243-99
6	1273	99.7	251	17	US-10-717-243-100
7	1269	99.4	251	9	US-09-765-527-247
8	1269	99.4	251	14	US-10-127-890-2
9	1269	99.4	251	14	US-10-127-890-110
10	1269	99.4	251	17	US-10-717-243-2
11	1269	99.4	251	17	US-10-717-243-110
					Sequence 101, App
					Sequence 101, App
					Sequence 99, Appl
					Sequence 100, App
					Sequence 99, Appl
					Sequence 100, App
					Sequence 247, App
					Sequence 2, Appli
					Sequence 110, App
					Sequence 2, Appli
					Sequence 110, App

12 1269 99.4 316 14 US-10-074-596-1 Sequence 1, Appli
13 1269 99.4 507 14 US-10-074-596-11 Sequence 11, Appl
14 1266 99.1 293 9 US-09-765-527-259 Sequence 259, App
15 1266 99.1 309 9 US-09-765-527-253 Sequence 253, App
16 1266 99.1 332 9 US-09-765-527-251 Sequence 251, App
17 1264 99.0 251 14 US-10-127-890-108 Sequence 108, App
18 1264 99.0 251 17 US-10-717-243-108 Sequence 108, App
19 1261 98.7 251 14 US-10-127-890-103 Sequence 103, App
20 1261 98.7 251 14 US-10-127-890-104 Sequence 104, App
21 1261 98.7 251 14 US-10-127-890-105 Sequence 105, App
22 1261 98.7 251 14 US-10-127-890-106 Sequence 106, App
23 1261 98.7 251 14 US-10-127-890-109 Sequence 109, App
24 1261 98.7 251 17 US-10-717-243-103 Sequence 103, App
25 1261 98.7 251 17 US-10-717-243-104 Sequence 104, App
26 1261 98.7 251 17 US-10-717-243-105 Sequence 105, App
27 1261 98.7 251 17 US-10-717-243-106 Sequence 106, App
28 1261 98.7 251 17 US-10-717-243-109 Sequence 109, App
29 1260 98.7 251 14 US-10-127-890-102 Sequence 102, App
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34 1260 98.7 251 17 US-10-717-243-111 Sequence 111, App
35 348 27.3 263 14 US-10-127-890-4 Sequence 4, Appli
36 348 27.3 263 17 US-10-717-243-4 Sequence 4, Appli
37 346 27.1 267 14 US-10-282-935-1 Sequence 1, Appli
38 346 27.1 267 14 US-10-127-890-1 Sequence 1, Appli
39 346 27.1 267 15 US-10-440-796-1 Sequence 1, Appli
40 346 27.1 267 17 US-10-717-243-1 Sequence 1, Appli
41 346 27.1 576 14 US-10-083-336A-1 Sequence 1, Appli
42 326.5 25.6 312 16 US-10-467-009-2 Sequence 2, Appli
43 323 25.3 247 9 US-09-792-793A-39 Sequence 39, Appli
44 323 25.3 247 15 US-10-375-209A-39 Sequence 39, Appli
45 323 25.3 289 14 US-10-280-679B-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-127-890-101

; Sequence 101, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-127-890-101

Query Match 100.0%; Score 1277; DB 14; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 120

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DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2

US-10-717-243-101
Sequence 101, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243

FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-717-243-101

Query Match 100.0%; Score 1277; DB 17; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180

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DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3

US-10-127-890-99
Sequence 99, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois

;;
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/10/127,890
;; FILING DATE: 23-Apr-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;;
;; INFORMATION FOR SEQ ID NO: 99:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99

Query Match 99.7%; Score 1273; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60
DB |||||
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB |||||
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB |||||
QY 121 AYRETTDLGIEPLRIGIKKLDENAINYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
DB |||||
QY 121 AYRETTDLGIEPLRIGIKKLDENAINYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
DB |||||
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 240
DB |||||
QY 241 ALLKFVDKDPK 251
DB |||||
QY 241 ALLKFVDKDPK 251
DB |||||

RESULT 4
US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroil, Stephen F.

;; Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/127,890
;; FILING DATE: 23-Apr-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEFAX: 312/707-8889
;; TELEX: 650 388-1248
;;
;; INFORMATION FOR SEQ ID NO: 100:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100

Query Match 99.7%; Score 1273; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60
DB |||||
QY 1 GLDTSFSTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60
DB |||||
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB |||||
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB |||||
QY 121 AYRETTDLGIEPLRIGIKKLDENAINYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
DB |||||
QY 121 AYRETTDLGIEPLRIGIKKLDENAINYKPTETASSLLVVIQMVSEAAFTFIENQIRNN 180
DB |||||
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 240
DB |||||
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADQVKPKI 240
DB |||||
QY 241 ALLKFVDKDPK 251
DB |||||
QY 241 ALLKFVDKDPK 251
DB |||||

RESULT 5
US-10-717-243-99
; Sequence 99, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-717-243-99
Query Match 99.7%; Score 1273; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GQAGIAIDVTSVYVGVQVRNRSYFFKDPAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
DB 61 GQAGIAIDVTSVYVGVQVRNRSYFFKDPAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180

Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFOIRTSYGANGMSEAVELEFRANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFOIRTSYGANGMSEAVELEFRANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 6
US-10-717-243-100
; Sequence 100, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100
Query Match 99.7%; Score 1273; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLKPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

Db 1 GLDTSFSTKATYIYVNFLELRLVKLPENSHGIPILRRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSFAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSFAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
RESULT 7
US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247
Query Match 99.4%; Score 1269; DB 9; Length 251;
Best Local Similarity 99.2%; Pred. No. 6.7e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTSFSTKATYIYVNFLELRLVKLPENSHGIPILRRKADDPGKCFVLVALSNDN 60
Db 1 GLDTSFSTKATYIYVNFLELRLVKLPENSHGIPILRRKADDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Db 61 GQLAEIAIDVTSYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSFAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSFAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
RESULT 8
US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

Query Match 99.4%; Score 1269; DB 14; Length 251;
Best Local Similarity 99.2%; Pred. No. 6.7e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYIYVNFLELRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTVSFSTKGATYIYVNFLELRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 9
US-10-127-890-110
; Sequence 110, Application US/10127890
; Publication No US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; PROTEINS
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248

Query Match 99.4%; Score 1269; DB 14; Length 251;
Best Local Similarity 99.2%; Pred. No. 6.7e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYIYVNFLELRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTVSFSTKGATYIYVNFLELRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 10
US-10-717-243-2
; Sequence 2, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; PROTEINS
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567

ATTORNEY/AGENT INFORMATION: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match 99.4%; Score 1269; DB 17; Length 251;
Best Local Similarity 99.2%; Pred. No. 6.7e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITYVNFNLRLVRLKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGATYITYVNFNLRLVRLKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVMSAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVMSAARFTFIENQIRNN 180
QY 181 FQOIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
US-10-717-243-110
Sequence 110, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-717-243-110

Query Match 99.4%; Score 1269; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 6.7e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITYVNFNLRLVRLKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGATYITYVNFNLRLVRLKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVMSAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVMSAARFTFIENQIRNN 180
QY 181 FQOIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12
US-10-074-596-1
Sequence 1, Application US/10074596
Publication No. US20030176331A1
GENERAL INFORMATION:
APPLICANT: ROSENBLUM, MICHAEL G.
APPLICANT: CHEUNG, LAWRENCE
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF MAKING THEREOF
FILE REFERENCE: CLFR:007US
CURRENT APPLICATION NUMBER: US/10/074,596
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/268,402
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 316
TYPE: PRT
ORGANISM: Gelonium multiflorum
US-10-074-596-1

Query Match 99.4%; Score 1269; DB 14; Length 316;
Best Local Similarity 99.2%; Pred. No. 9.2e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 47 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKCFVLVALSNDN 106

QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 107 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 167 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 226

QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 227 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 286

QY 241 ALLKFVDKDPK 251
DB 287 ALLKFVDKDPK 297

RESULT 13
US-10-074-596-11
; Sequence 11, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF MAKING THEREOF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-074-596-11

Query Match 99.4%; Score 1269; DB 14; Length 507;
Best Local Similarity 99.2%; Pred. No. 1.8e-114;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 257 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKCFVLVALSNDN 316

QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 317 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 376

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 377 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 436

QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 437 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 496

QY 241 ALLKFVDKDPK 251
DB 497 ALLKFVDKDPK 507

RESULT 14
US-09-765-527-259
; Sequence 259, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match 99.1%; Score 1266; DB 9; Length 293;
Best Local Similarity 98.8%; Pred. No. 1.6e-114;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 23 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKCFVLVALSNDN 82

QY 61 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 83 GOLAEIAIDVTSVYVVGQVRRNSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 142

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 202

QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 203 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262

QY 241 ALLKFVDKDPK 251
DB 263 ALLKFVDKDPK 273

RESULT 15
US-09-765-527-253

; Sequence 253, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/765,527
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-765-527-253

Query Match 99.1%; Score 1266; DB 9; Length 309;
Best Local Similarity 98.8%; Pred. No. 1.7e-114;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHSGIPLLRKKADDPGKAFVLVALSNDN 60
DB 23 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHSGIPLLRKKADDPGKAFVLVALSNDN 82

QY 61 GLAEIAIDVTSYVVGYYQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 83 GLAEIAIDVTSYVVGYYQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGTYPSPLEGEK 142

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAIASSLLVVIQWVSEAAFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAIASSLLVVIQWVSEAAFTFIENQIRNN 202

QY 181 FQORIRPANTTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTVADQVKPKI 240
DB 203 FQORIRPANTTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTVADQVKPKI 262

QY 241 ALLKFVDKDPK 251
DB 263 ALLKFVDKDPK 273

Search completed: June 20, 2005, 09:39:27
Job time : 106.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 17:36:19 ; Search time 122 Seconds
(without alignments)
375.539 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACAAAGACTTCATTGGC 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 924010

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/6C COMB.seq.*
6: /cgn2_6/prodata/1/ina/6D COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	1	US-07-988-430-61
2	28	100.0	28	1	Sequence 61, Appl
3	28	100.0	28	1	Sequence 59, Appl
4	28	100.0	28	1	Sequence 59, Appl
5	28	100.0	28	2	US-08-477-484B-59
6	28	100.0	28	2	Sequence 59, Appl
7	28	100.0	28	3	US-08-839-765-59
8	28	100.0	28	3	Sequence 59, Appl
9	28	100.0	28	4	US-09-610-838-59
10	28	100.0	28	4	Sequence 59, Appl
11	15.6	55.7	25	5	PCT-US92-09487-61
12	14.2	50.7	25	4	US-09-396-196G-105925
13	14	50.0	27	4	US-09-396-196G-114261
14	13.8	49.3	20	3	US-08-597A-3
15	13.8	49.3	20	4	US-09-756-541-18
16	13.6	48.6	24	2	US-08-370-319C-6
17	13.6	48.6	24	3	US-09-224-834-6
18	13.6	48.6	25	4	US-09-396-196G-10271
19	13.6	48.6	27	3	US-09-552-322-27
20	13.4	47.9	20	4	US-09-198-452A-3846
21	13.4	47.9	23	3	US-08-755-587-163
22	13.4	47.9	25	4	US-09-396-196G-1783
23	13.4	47.9	25	4	US-09-396-196G-125558
24	13.2	47.1	20	3	US-09-418-640-74
25	13.2	47.1	25	4	US-09-396-196G-5918
26	13.2	47.1	25	4	US-09-396-196G-21250
27	13.2	47.1	25	4	US-09-396-196G-36903

Sequence 122538, A
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 37209, A
Sequence 50918, A
Sequence 55823, A
Sequence 11795, A
Sequence 3184, Ap
Sequence 28343, A
Sequence 67606, A
Sequence 67607, A
Sequence 67608, A
Sequence 74968, A

25 4 US-09-396-196G-122538
24 1 US-07-741-940-55
24 1 US-08-289-548A-55
24 1 US-08-452-654-55
24 1 US-08-452-655B-55
24 3 US-08-450-582-55
24 3 US-08-449-731-55
25 4 US-09-396-196G-37209
25 4 US-09-396-196G-50918
25 4 US-09-396-196G-55823
20 4 US-09-422-978-11795
23 3 US-09-368-588-6
25 4 US-09-396-196G-3184
25 4 US-09-396-196G-28343
25 4 US-09-396-196G-67606
25 4 US-09-396-196G-67607
25 4 US-09-396-196G-67608
25 4 US-09-396-196G-74968

ALIGNMENTS

RESULT 1

US-07-988-430-61

Sequence 61, Application US/07988430

Patent No. 5416202

GENERAL INFORMATION:

APPLICANT: Bernhardt, Susan L.

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Lane, Julie A.

APPLICANT: Lei, Shau-Ping

TITLE OF INVENTION: Materials Comprising and Methods of

TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell

STREET: Two First National Plaza, 20 South Clark

STREET: Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/988,430

FILING DATE: 19921209

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. 5416202and, Greta E.

REGISTRATION NUMBER: 35302

REFERENCE/DOCKET NUMBER: 31133

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-988-430-61

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTGGC 28
|||||
DB 1 CACATGTAACAAACAGACTTCATTTGGC 28

RESULT 2

US-08-425-336-59
; Sequence 59, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-425-336-59

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTGGC 28
|||||
DB 1 CACATGTAACAAACAGACTTCATTTGGC 28

RESULT 3

US-08-488-113B-59
; Sequence 59, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-113B-59

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTGGC 28
|||||
DB 1 CACATGTAACAAACAGACTTCATTTGGC 28

RESULT 4

US-08-477-484B-59
; Sequence 59, Application US/08477484B
; Patent No. 5756699

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-477-484B-59

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
DB 1 CACATGTAACAAAGACTTCATTTCGC 28

RESULT 5
US-08-646-360-59
Sequence 59, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-360-59

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
DB 1 CACATGTAACAAAGACTTCATTTCGC 28

RESULT 6
US-08-839-765-59
Sequence 59, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor

;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60661
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent In Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA: US/08/839,765
;/ APPLICATION NUMBER: US/08/839,765
;/ FILING DATE: 15-APR-1997
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/425,336
;/ FILING DATE: 18-APR-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/064,691
;/ FILING DATE: 12-MAY-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/988,430
;/ FILING DATE: 09-DEC-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/901,707
;/ FILING DATE: 19-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/787,567
;/ FILING DATE: 04-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: McNicholas, Janet M.
;/ REGISTRATION NUMBER: 32,918
;/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 312/707-8889
;/ TELEFAX: 312/707-9155
;/ TELEX: 650 388-1248
;/ INFORMATION FOR SEQ ID NO: 59:
;/ TYPE: nucleic acid
;/ LENGTH: 28 base pairs
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA
;/ US-08-839-765-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CACATGTAACAAACAGACTTCATTTCATTTGGC 28

RESULT 7
US-09-136-389-59
; Sequence 59, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent In Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA: US/09/136,389
;/ APPLICATION NUMBER: US/09/136,389
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/646,360
;/ FILING DATE: 13-MAY-1996
;/ APPLICATION NUMBER: PCT/US94/05348
;/ FILING DATE: 12-MAY-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/064,691
;/ FILING DATE: 12-MAY-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/988,430
;/ FILING DATE: 09-DEC-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/901,707
;/ FILING DATE: 19-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/787,567
;/ FILING DATE: 04-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: McNicholas, Janet M.
;/ REGISTRATION NUMBER: 32,918
;/ REFERENCE/DOCKET NUMBER: 200-70.P4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 312/707-8889
;/ TELEFAX: 312/707-9155
;/ TELEX: 650 388-1248
;/ INFORMATION FOR SEQ ID NO: 59:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 28 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA
;/ US-09-136-389-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTCATTTGGC 28
Db 1 CACATGTAACAAACAGACTTCATTTCATTTGGC 28

RESULT 8
US-09-610-838-59
; Sequence 59, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/610,838
/ FILING DATE: 06-JUL-2000
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389
/ FILING DATE: 18-AUG-1998
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-09-610-838-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTGTC 28
Db 1 CACATGTAACAAAGACTTCATTGTC 28

RESULT 9
US-09-711-485-59
/ Sequence 59, Application US/09711485
/ Patent No. 6649742
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
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/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/839,765
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-09-711-485-59

Query Match 100.0%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTGTC 28
Db 1 CACATGTAACAAAGACTTCATTGTC 28

RESULT 10
PCT-US92-09487-61
/ Sequence 61, Application PC/TUS9209487
/ GENERAL INFORMATION:
/ APPLICANT: Bernhard, Susan L.
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Lane, Julie A.
/ APPLICANT: Lei, Shau-Ping
/ TITLE OF INVENTION: Materials Comprising and Methods of
/ TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
/ NUMBER OF SEQUENCES: 101
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ STREET: Street
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/09487
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; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US92-09487-61

Query Match          100.0%; Score 28; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAAGACTTCATTTGGC 28
Db 1 CACATGTAATAACAAGACTTCATTTGGC 28

RESULT 11
US-09-396-196G-105925
; Sequence 105925, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-105925

Query Match          55.7%; Score 15.6; DB 4; Length 25;
Best Local Similarity 81.8%; Pred. No. 9.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGTATAACAAGACTTCATTTTG 26
Db 1 TTTAAGCACGACTTCATGTTG 22

RESULT 12
US-09-396-196G-114261/c
; Sequence 114261, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: David Mack
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; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114261
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-114261

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Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ATGTATAACAAGACTTCAT 22
Db 24 ATCTATAACAAGACTTCAT 6

RESULT 13
US-09-682-597A-3
; Sequence 3, Application US/09682597A
; Patent No. 6689880
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Chen, Guilan
; APPLICANT: Hironaka, Catherine
; APPLICANT: Zhou, Hua-Ping
; TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Methods
; FILE REFERENCE: 38-21(52232)A
; CURRENT APPLICATION NUMBER: US/09/682,597A
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-682-597A-3

Query Match          50.0%; Score 14; DB 4; Length 27;
Best Local Similarity 77.3%; Pred. No. 5.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CATGTATAACAAGACTTCATTT 24
Db 1 CATGTAATGCATGACGTTATTT 22

RESULT 14
US-08-899-330-18
; Sequence 18, Application US/08899330
; Patent No. 6177275
; GENERAL INFORMATION:
; APPLICANT: CORUZZI, GLORIA
; APPLICANT: LAM, HON-MING
; APPLICANT: HSIEH, MING-HSIUN
; TITLE OF INVENTION: PLANT NITROGEN REGULATORY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,330
FILING DATE: 23-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/022,328
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-042-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-08-899-330-18

Query Match 49.3%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACATGTAAACCAAGACT 18
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Db 3 ACAGGTAAACCAAGACT 19

RESULT 15
US-09-756-541-18
Sequence 18, Application US/09756541
Patent No. 6822079
GENERAL INFORMATION:
APPLICANT: CORUZZI, GLORIA
LAM, HON-MING
HSIEH, MING-HSIUN
TITLE OF INVENTION: PLANT NITROGEN REGULATORY
P-PII GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,541
FILING DATE: 08-Jan-2001
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/899,330
FILING DATE: 23-JUL-1997
APPLICATION NUMBER: 60/022,328
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-042-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-756-541-18

Query Match 49.3%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 3 ACAGGTAAACCAAGACT 19

Search completed: June 21, 2005, 19:15:10
Job time : 125 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 18:22:59 ; Search time 527 Seconds
(without alignments)
329.813 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACAAAGACTTCATTGGC 28

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Total number of hits satisfying chosen parameters: 5500628

Minimum DB seq length: 0

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	28	100.0	28	21	US-10-717-243-59
3	16.6	59.3	25	15	US-10-719-900-839652
4	15.6	55.7	25	15	US-10-098-2638-17282
5	15.6	55.7	25	21	US-10-809-189-105925
6	15.4	55.0	25	21	US-10-956-157-93516
7	15.4	55.0	25	21	US-10-956-157-231959

8	15.4	55.0	25	21	US-10-956-157-265753
9	15.2	54.3	25	21	US-10-719-900-342034
10	15.2	54.3	25	21	US-10-719-900-898965
11	15	53.6	25	21	US-10-719-900-292506
12	15	53.6	25	21	US-10-719-900-463285
13	15	53.6	25	21	US-10-719-900-839653
14	15	53.6	25	21	US-10-719-900-933648
15	15	53.6	25	21	US-10-956-157-93524
16	15	53.6	25	21	US-10-956-157-273438
17	14.8	52.9	25	15	US-10-098-2638-70112
18	14.6	52.1	25	15	US-10-098-2638-19337
19	14.6	52.1	25	21	US-10-719-900-396595
20	14.6	52.1	25	21	US-10-719-900-396596
21	14.6	52.1	25	21	US-10-719-900-697924
22	14.6	52.1	25	21	US-10-719-900-697925
23	14.6	52.1	25	21	US-10-719-900-845346
24	14.6	52.1	25	21	US-10-956-157-153378
25	14.6	52.1	25	21	US-10-956-157-157214
26	14.6	52.1	25	21	US-10-956-157-158946
27	14.6	52.1	25	21	US-10-956-157-170735
28	14.6	52.1	25	21	US-10-956-157-244754
29	14.4	51.4	25	21	US-10-719-900-107315
30	14.4	51.4	25	21	US-10-719-900-465260
31	14.4	51.4	25	21	US-10-719-900-465261
32	14.4	51.4	25	21	US-10-719-900-565390
33	14.4	51.4	25	21	US-10-719-900-571211
34	14.4	51.4	25	21	US-10-719-900-844034
35	14.4	51.4	25	21	US-10-956-157-93519
36	14.4	51.4	25	21	US-10-956-157-170647
37	14.2	50.7	25	18	US-10-210-281-172
38	14.2	50.7	25	21	US-10-719-900-107507
39	14.2	50.7	25	21	US-10-719-900-113415
40	14.2	50.7	25	21	US-10-719-900-270253
41	14.2	50.7	25	21	US-10-719-900-273465
42	14.2	50.7	25	21	US-10-719-900-282140
43	14.2	50.7	25	21	US-10-719-900-325939
44	14.2	50.7	25	21	US-10-719-900-402443
45	14.2	50.7	25	21	US-10-719-900-402444

ALIGNMENTS

RESULT 1

US-10-127-890-59
; Sequence 59, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

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/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-127-890-59

Query Match      100.0%; Score 28; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTGGC 28
Db 1 CACATGTAACAAAGACTTCATTGGC 28

RESULT 2
US-10-717-243-59
/ Sequence 59, Application US/10717243
/ Publication No. US20050054835A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Carroll, Stephen F.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/717,243
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
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/
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-717-243-59

Query Match      100.0%; Score 28; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTGGC 28
Db 1 CACATGTAACAAAGACTTCATTGGC 28

RESULT 3
US-10-719-900-839652
/ Sequence 839652, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 839652
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-839652

Query Match      59.3%; Score 16.6; DB 21; Length 25;
Best Local Similarity 82.6%; Pred. No. 3.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CATGTAAACAAAGACTTCATTTT 25
Db 2 CTTGTAAACAAAGACTTTCCTTT 24

RESULT 4
US-10-098-263B-17282/c
/ Sequence 17282, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Mittman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 17282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-17282

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Query Match	55.7%	Score 15.6;	DB 15;
Best Local Similarity	81.8%	Pred. No. 8.7e+03;	Length 25;
Matches 18;	Conservative	0;	Mismatches 4;
			Indels 0;
			Gaps 0;

Qy 2 ACATGTAAAAACAAGACTTCATT 23
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Db 23 ATATGTAACCAACACCTCGTT 2

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RESULT 5
US-10-809-189-105925
; Sequence 105925, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-105925

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Query Match	55.7%	Score 15.6;	DB 21;	Length 25;
Best Local Similarity	81.8%	Pred. No. 8.7e+03;		
Matches 18;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy

5 TGTAACAAGACTTCATTTTG 26
| | | | | | | | | | | | | | | | | | | | | | | | | |
Dd

1 TTATAAGCACGACTTCATGTGG 22

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RESULT 6
US-10-956-157-93516
; Sequence 93516, Application US/10956157-
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 1010
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-93516

```

Query Match	55.0%	Score 15.4;	DB 21;	Length 25;
Best Local Similarity	76.0%;	Pred. No. 1.1e+04;		
Matches 19;	Conservative	0;	Mismatches 6;	Indels 0;
	Gaps	0;		

Qy 4 ATGTAAACAAGACTTCATTTTGGC 28
|||||
Db 1 ATGTTATACTAGACTCCATTGTGCC 25

RESULT 7

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RESULT 7
US-10-956-157-231959
; Sequence 231959, Application US/10956157
; Publication NO. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEAR ACID ARRAYS FOR
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 231959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-231959

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Query Match	55.0%	Score 15.4;	DB 21;	Length 25;
Best Local Similarity	94.1%;	Pred. No. 1.1e+04;		
Matches 16;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 8 AAAACAAGACTTCATT 24
|||||
Db 6 AAAACGAGACTTCATT 22

RESULTS AND DISCUSSION

```

US-10-956-157-265753
; Sequence 265753, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHR
; FILE REFERENCE: 031896-043000 (AM 10108
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 265753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-265753

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Query Match	55.0%	Score 15.4;	DB 21;	Length 25;
Best Local Similarity	94.1%	Pred. No. 1.1e+04;		
Matches 16;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 8 AAAACAAGACTTCATT 24
||||| ||||| ||||| |||||
Db 7 AAAACGAGACTTCATT 23

RESIST 9

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US-10-719-900-342034
; Sequence 342034, Application US/10719900
; Publication No. US20050026184A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10719.900

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; AFFILIATION: AUCI REG. 2003-11-20
;
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;
; FILE REFERENCE: 3528.1
;
; CURRENT APPLICATION NUMBER: US/10/719,900
;
; CURRENT FILING DATE: 2003-11-20
;

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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 933648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-933648

Query Match 53.6%; Score 15; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CAAGACTTCATTG 26
DB 21 CAAGACTTCATTG 7

RESULT 15
US-10-956-157-93524
; Sequence 93524, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-93524

Query Match 53.6%; Score 15; DB 21; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 ATGTAAACACAGACTTCATTG 26
DB 2 ATGTATACAGACTTCATTG 24

Search completed: June 21, 2005, 20:43:48
Job time : 530 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 14:27:12 ; Search time 128 Seconds
(without alignments)
357.936 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACAAAGACTTCATTGTC 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	1	US-07-988-430-61
2	28	100.0	28	1	US-08-425-336-59
3	28	100.0	28	1	US-08-488-113B-59
4	28	100.0	28	1	US-08-477-484B-59
5	28	100.0	28	2	US-08-646-360-59
6	28	100.0	28	3	US-08-839-765-59
7	28	100.0	28	3	US-09-136-389-59
8	28	100.0	28	3	US-09-610-838-59
9	28	100.0	28	4	US-09-711-485-59
10	28	100.0	28	5	PCT-US92-09487-61
11	24.8	88.6	813	1	US-07-901-707-11
12	24.8	88.6	813	1	US-07-901-707-57
13	24.8	88.6	813	1	US-07-988-430-11
14	24.8	88.6	813	1	US-07-988-430-57
15	24.8	88.6	813	1	US-08-425-336-11
16	24.8	88.6	813	1	US-08-488-113B-11
17	24.8	88.6	813	1	US-08-477-484B-11
18	24.8	88.6	813	2	US-08-646-360-11
19	24.8	88.6	813	2	US-08-621-803-246
20	24.8	88.6	813	3	US-08-839-765-11
21	24.8	88.6	813	3	US-09-136-389-11
22	24.8	88.6	813	3	US-09-217-352-246
23	24.8	88.6	813	3	US-09-610-838-11
24	24.8	88.6	813	4	US-09-711-485-11
25	24.8	88.6	813	5	PCT-US92-09487-11
26	24.8	88.6	813	5	PCT-US92-09487-57
27	24.8	88.6	955	2	US-08-621-803-258

28 24.8 88.6 955 3 US-09-217-352-258 Sequence 258, App
29 24.8 88.6 1003 2 US-08-621-803-252 Sequence 252, App
30 24.8 88.6 1003 3 US-09-217-352-252 Sequence 252, App
31 24.8 88.6 1072 2 US-08-621-803-250 Sequence 250, App
32 24.8 88.6 1072 3 US-09-217-352-250 Sequence 250, App
33 20.2 72.1 2187 4 US-08-956-171E-329 Sequence 329, App
34 20.2 72.1 2187 4 US-08-781-986A-329 Sequence 329, App
35 20 71.4 11298 1 US-07-869-933-31 Sequence 31, Appl
36 20 71.4 11298 1 US-08-201-879A-2 Sequence 2, Appl
37 20 71.4 11298 3 US-09-103-663-31 Sequence 31, Appl
38 20 71.4 98567 4 US-09-949-016-11750 Sequence 11750, A
39 20 71.4 100567 4 US-09-949-016-16934 Sequence 16934, A
40 19.6 70.0 3132 1 US-08-167-919A-9 Sequence 9, Appl
41 19.6 70.0 3132 3 US-08-715-106-9 Sequence 9, Appl
42 19.6 70.0 3132 4 US-09-442-649-9 Sequence 9, Appl
C 43 19.6 70.0 126982 4 US-09-949-016-16597 Sequence 16597, A
C 44 19.4 69.3 36 1 US-07-988-430-62 Sequence 62, Appl
C 45 19.4 69.3 36 1 US-08-425-336-60 Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-07-988-430-61

; Sequence 61, Application US/07988430

; Patent No. 5416202

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Lane, Julie A.

; APPLICANT: Lei, Shau-Ping

; TITLE OF INVENTION: Materials Comprising and Methods of

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/988,430

; FILING DATE: 19921209

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5416202and, Greta E.

; REGISTRATION NUMBER: 35302

; REFERENCE/DOCKET NUMBER: 31133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-988-430-61

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTGGC 28
|||||
Db 1 CACATGTAACAAAGACTTCATTTGGC 28

RESULT 2

US-08-425-336-59
; Sequence 59, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-425-336-59

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTGGC 28
|||||
Db 1 CACATGTAACAAAGACTTCATTTGGC 28

RESULT 3

US-08-488-113B-59
; Sequence 59, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-113B-59

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTGGC 28
|||||
Db 1 CACATGTAACAAAGACTTCATTTGGC 28

RESULT 4

US-08-477-484B-59
; Sequence 59, Application US/08477484B
; Patent No. 5756699

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-477-484B-59

Query Match 100.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTCGC 28
DB 1 CACATGTAACAAGACTTCATTTCGC 28

RESULT 5
US-08-646-360-59
Sequence 59, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-360-59

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTCGC 28
DB 1 CACATGTAACAAGACTTCATTTCGC 28

RESULT 6
US-08-839-765-59
Sequence 59, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-839-765-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTTGGC 28
DB 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 7
US-09-136-389-59
Sequence 59, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-136-389-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTTGGC 28
DB 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 8
US-09-610-838-59
Sequence 59, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/09/136,389
; APPLICATION DATA:
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-610-838-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
Db 1 CACATGTAACAAAGACTTCATTTCGC 28

RESULT 9
US-09-711-485-59
; Sequence 59, Application US/09/11485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: PCT/US92/09487
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/839,765
; APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-711-485-59

Query Match 100.0%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
Db 1 CACATGTAACAAAGACTTCATTTCGC 28

RESULT 10
PCT-US92-09487-61
; Sequence 61, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
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/ FILING DATE: 19921104
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Noland, Greta E.
/ REGISTRATION NUMBER: 35302
/ REFERENCE/DOCKET NUMBER: 31133
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
PCT-US92-09487-61

Query Match 100.0%; Score 28; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 11
US-07-901-707-11
; Sequence 11, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,707
; FILING DATE: 19920619
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5376546and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27129/30910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
```

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/ TELEFAX: (312) 984-5750
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 813 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-07-901-707-11

Query Match 88.6%; Score 24.8; DB 1; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
Db 303 CACATGTAACAAGACTTCATTGGC 330

RESULT 12
US-07-901-707-57
; Sequence 57, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,707
; FILING DATE: 19920619
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5376546and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27129/30910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-901-707-57

Query Match 88.6%; Score 24.8; DB 1; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CACATGTAACAAAGACTTCATTTCGC 28
|||||
Db 303 CACAATTAACAAAGACTTCATTTCGC 330

RESULT 13
US-07-988-430-11
; Sequence 11, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 04-NOV-1991
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-988-430-11

Query Match 88.6%; Score 24.8; DB 1; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
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Db 303 CACAATTAACAAAGACTTCATTTCGC 330

RESULT 14
US-07-988-430-57
; Sequence 57, Application US/07988430
; Patent No. 5416202

; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 04-NOV-1991
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-988-430-57

Query Match 88.6%; Score 24.8; DB 1; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
|||||
Db 303 CACAATTAACAAAGACTTCATTTCGC 330

RESULT 15
US-08-425-336-11
; Sequence 11, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Searns Tower, 233 South Wacker Drive

/: CITY: Chicago
/: STATE: Illinois
/: COUNTRY: USA
/: ZIP: 60606-6402
/: COMPUTER READABLE FORM:
/: MEDIUM TYPE: Floppy disk
/: COMPUTER: IBM PC compatible
/: OPERATING SYSTEM: PC-DOS/MS-DOS
/: SOFTWARE: PatentIn Release #1.0, Version #1.25
/: CURRENT APPLICATION DATA:
/: APPLICATION NUMBER: US/08/425,336
/: FILING DATE: 18-APR-1995
/: CLASSIFICATION: 530
/: PRIOR APPLICATION DATA:
/: APPLICATION NUMBER: 08/064,691
/: FILING DATE: 12-MAY-1993
/: APPLICATION NUMBER: US 07/901,707
/: FILING DATE: 19-JUN-1992
/: PRIOR APPLICATION DATA:
/: APPLICATION NUMBER: US 07/787,567
/: FILING DATE: 04-NOV-1991
/: ATTORNEY/AGENT INFORMATION:
/: NAME: Meyers, Thomas C.
/: REGISTRATION NUMBER: P-36,989
/: REFERENCE/DOCKET NUMBER: 31394
/: TELECOMMUNICATION INFORMATION:
/: TELEPHONE: 312/474-6300
/: TELEFAX: 312/474-0448
/: TELEX: 25-3856
/: INFORMATION FOR SEQ ID NO: 11:
/: SEQUENCE CHARACTERISTICS:
/: LENGTH: 813 base pairs
/: TYPE: nucleic acid
/: STRANDEDNESS: single
/: TOPOLOGY: linear
/: MOLECULE TYPE: cDNA
US-08-425-336-11

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Best Local Similarity 92.9%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTGGC 28
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Db 303 CACAATTAAACAAACAGACTTCATTGGC 330

Search completed: June 21, 2005, 16:14:04
Job time : 130 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 16:14:13 ; Search time 1800 Seconds
(without alignments)
753.748 Million cell updates/sec

Title: US-10-717-243-59
Perfect score: 28
Sequence: 1 CACATGTAACAAACAGACTTCATTGGC 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1339764

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sv:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	28	100.0	28	AR003767 Sequence
2	28	100.0	28	AR010103 Sequence
3	28	100.0	28	AR055309 Sequence
4	28	100.0	28	AR141238 Sequence
5	28	100.0	28	AR141475 Sequence
6	28	100.0	28	I11949 Sequence 61
7	28	100.0	28	I40520 Sequence 59
8	28	100.0	28	AR368004 Sequence
9	28	100.0	28	AR430985 Sequence
10	15.8	56.4	28	A04644 Nucleotide
11	15.8	56.4	28	A34707 Synthetic P
12	15.2	54.3	27	AX115024 Sequence
13	14.8	52.9	23	CQ799733 Sequence
14	14.6	52.1	24	BD087988 A method
15	14.6	52.1	24	AB068695 Synthetic
16	14.6	52.1	25	E64639 Method for
17	14.2	50.7	25	CQ857743 Sequence
18	14	50.0	27	AR474262 Sequence
19	14	50.0	27	AX040131 Sequence

20	14	50.0	27	6	AX430080 Sequence
21	13.8	49.3	20	6	AR125594 Sequence
22	13.8	49.3	24	6	ES1281 Disease tol
23	13.6	48.6	24	6	AR026369 Sequence
c 24	13.6	48.6	24	6	AX119462 Sequence
25	13.6	48.6	27	6	AX711378 Sequence
26	13.4	47.9	20	6	AR313309 Sequence
c 27	13.4	47.9	23	6	A62922 Sequence 16
c 28	13.2	47.1	20	6	AR117677 Sequence
c 29	13.2	47.1	22	11	DOGC00501A
c 30	13	46.4	24	6	AR019570 Sequence
c 31	13	46.4	24	6	AR109531 Sequence
c 32	13	46.4	24	6	I55702 Sequence 55
c 33	13	46.4	24	6	I76479 Sequence 55
c 34	13	46.4	24	6	AR217044 Sequence
c 35	13	46.4	25	6	AX117622 Sequence
c 36	13	46.4	26	6	BD183259 Marker fo
c 37	13	46.4	27	6	AX045258 Sequence
c 38	13	46.4	27	6	AX449768 Sequence
39	12.8	45.7	20	6	AR300060 Sequence
40	12.8	45.7	23	6	AX253213 Sequence
41	12.8	45.7	24	6	CQ848654 Sequence
c 42	12.8	45.7	24	6	CQ866958 Sequence
c 43	12.8	45.7	24	6	AX493405 Sequence
44	12.8	45.7	25	6	AX609703 Sequence
45	12.8	45.7	25	6	AX610219 Sequence

ALIGNMENTS

RESULT 1	AR003767	Sequence 59 from patent US 5744580.	28 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR003767	Sequence 59 from patent US 5744580.				
DEFINITION	AR003767					
ACCESSION	AR003767.1	GI:3965026				
VERSION	AR003767.1	GI:3965026				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 28)					
AUTHORS	Better M.D., Carroll S.F. and Studnicka G.M.					
TITLE	Immunotoxins, comprising ribosome-inactivating proteins					
JOURNAL	Patent: US 5744580-A 59 28-APR-1998;					
FEATURES	Location/Qualifiers					
source	1..28					
ORIGIN	/organism="unknown"					
	/mol_type="unassigned DNA"					

Query Match	100.0%;	Score 28;	DB 6;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 0.36;		
Matches	28;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

Qy	1	CACATGTAACAAACAGACTTCATTGGC	28
Db	1	CACATGTAACAAACAGACTTCATTGGC	28

RESULT 2	AR010103	Sequence 59 from patent US 5756699.	28 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR010103	Sequence 59 from patent US 5756699.				
DEFINITION	AR010103					
ACCESSION	AR010103					
VERSION	AR010103.1	GI:3968908				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 28)					
AUTHORS	Better M.D., Carroll S.F. and Studnicka G.M.					
TITLE	Immunotoxins, comprising ribosome-inactivating proteins					

JOURNAL Patent: US 5756699-A 59 26-MAY-1998;
 FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACCAAGACTTCATTGGC 28
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 Db 1 CACATGTAACCAAGACTTCATTGGC 28

RESULT 3
 LOCUS AR055309 28 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 59 from patent US 5837491.
 ACCESSION AR055309
 VERSION AR055309.1 GI:5980886
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
 TITLE Polynucleotides encoding gelonin sequences
 JOURNAL Patent: US 5837491-A 59 17-NOV-1998;
 FEATURES Location/Qualifiers
 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACCAAGACTTCATTGGC 28
 |||||
 Db 1 CACATGTAACCAAGACTTCATTGGC 28

RESULT 4
 LOCUS AR141238 28 bp DNA PAT 08-AUG-2001
 DEFINITION Sequence 59 from patent US 6146631.
 ACCESSION AR141238
 VERSION AR141238.1 GI:15100755
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
 TITLE Immunotoxins comprising ribosome-inactivating proteins
 JOURNAL Patent: US 6146631-A 59 14-NOV-2000;
 FEATURES Location/Qualifiers
 1..28
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ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACCAAGACTTCATTGGC 28
 |||||
 Db 1 CACATGTAACCAAGACTTCATTGGC 28

JOURNAL Patent: US 5756699-A 59 26-MAY-1998;
 FEATURES Location/Qualifiers
 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACCAAGACTTCATTGGC 28
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 Db 1 CACATGTAACCAAGACTTCATTGGC 28

RESULT 5
 LOCUS AR141475 28 bp DNA PAT 08-AUG-2001
 DEFINITION Sequence 59 from patent US 6146850.
 ACCESSION AR141475
 VERSION AR141475.1 GI:15100991
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Better,M.D. and Carroll,S.F.
 TITLE Proteins encoding gelonin sequences
 JOURNAL Patent: US 6146850-A 59 14-NOV-2000;
 FEATURES Location/Qualifiers
 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"

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Query Match 100.0%; Score 28; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACCAAGACTTCATTGGC 28
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 Db 1 CACATGTAACCAAGACTTCATTGGC 28

RESULT 6
 LOCUS I11949 28 bp DNA PAT 26-JUL-1995
 DEFINITION Sequence 61 from Patent US 5416202.
 ACCESSION I11949
 VERSION I11949.1 GI:909392
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.-P.
 TITLE Materials comprising and methods of preparation and use for
 ribosome-inactivating proteins
 JOURNAL Patent: US 5416202-A 61 16-MAY-1995;
 FEATURES Location/Qualifiers
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 /organism="unknown"
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ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACCAAGACTTCATTGGC 28
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 Db 1 CACATGTAACCAAGACTTCATTGGC 28

RESULT 7
 LOCUS I40520 28 bp DNA PAT 13-MAY-1997
 DEFINITION Sequence 59 from patent US 5621083.
 ACCESSION I40520
 VERSION I40520.1 GI:2082812
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
 TITLE Immunotoxins comprising ribosome-inactivating proteins

JOURNAL Patent: US 5621083-A 59 15-APR-1997;
FEATURES Location/Qualifiers
source 1..28
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/mol_type="unassigned DNA"

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Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY 1 CACATGTAACAAAGACTTCATTTCGGC 28
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Db 1 CACATGTAACAAAGACTTCATTTCGGC 28

RESULT 8
LOCUS AR368004 28 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 59 from patent US 5376217.
ACCESSION AR368004
VERSION AR368004.1 GI:34601515
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D. and Carroll,S.F.
TITLE Fusion proteins and polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5376217-A 59 23-APR-2002;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY 1 CACATGTAACAAAGACTTCATTTCGGC 28
|||||
Db 1 CACATGTAACAAAGACTTCATTTCGGC 28

RESULT 9
LOCUS AR430985 28 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 59 from patent US 5649742.
ACCESSION AR430985
VERSION AR430985.1 GI:40192816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5649742-A 59 18-NOV-2003;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY 1 CACATGTAACAAAGACTTCATTTCGGC 28
|||||
Db 1 CACATGTAACAAAGACTTCATTTCGGC 28

RESULT 10
LOCUS A04644 28 bp DNA linear PAT 02-DEC-1993
DEFINITION Nucleotide sequence 19 from patent number EP0140762.
ACCESSION A04644
VERSION A04644.1 GI:490368
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 28)
AUTHORS Lathe,R., Kieny,M.P., Lemoine,Y., Loison,G., Aigle,M. and Lecocq,J.P.
TITLE Vectors for the expression of an antigenic rabies protein in eukaryotic cells, and their use in the preparation of a vaccine
JOURNAL Patent: EP 0140762-A 19 08-MAY-1985;
FEATURES Location/Qualifiers
source 1..28
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Best Local Similarity 74.1%; Pred. No. 6.3e+04; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 7;

QY 1 CACATGTAACAAAGACTTCATTTCGG 27
|||||
Db 1 CAAATATAAAACAAGATCTAATATGG 27

RESULT 11
LOCUS A34707 28 bp DNA linear PAT 20-JUN-1996
DEFINITION Synthetic PKG promoter/glycoprotein cDNA fusion.
ACCESSION A34707
VERSION A34707.1 GI:1568264
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 28)
AUTHORS
TITLE VECTORS FOR THE EXPRESSION OF AN ANTIGENIC PROTEIN OF RABIES IN EUKARYOTIC CELLS AND APPLICATION THEREOF TO THE PREPARATION OF A VACCINE
JOURNAL Patent: WO 8501516-A 19 11-APR-1985;
FEATURES Location/Qualifiers
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Best Local Similarity 74.1%; Pred. No. 6.3e+04; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 7;

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Db 1 CAAATATAAAACAAGATCTAATATGG 27

RESULT 12
LOCUS AX115024 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 147 from Patent WO0129262.
ACCESSION AX115024
VERSION AX115024.1 GI:14031966
KEYWORDS

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Picoult-Newburg,L. and Pohl,M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 147 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES    Location/Qualifiers
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            /note="n = C3 linker"
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Best Local Similarity 81.0%; Pred. No. 1.1e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 GTAAACAAGACTTCATTG 26
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DB      3 GTAAAAAAGATTTCATTGTG 23

RESULT 13
LOCUS   CQ799733/c          23 bp      DNA          linear      PAT 28-APR-2004
DEFINITION
Sequence 383 from Patent WO2004031413.
ACCESSION CQ799733
VERSION   CQ799733.1 GI:46848680
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Nakamura,Y., Daigo,Y. and Nakatsuru,S.
TITLE     Method for diagnosing non-small cell lung cancers
JOURNAL   Patent: WO 2004031413-A 383 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
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Query Match      52.9%; Score 14.8; DB 6; Length 23;
Best Local Similarity 88.9%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CACATGTAAACAAGACT 18
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RESULT 14
LOCUS   BD087988          24 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION
A method of arraying genome clone.
ACCESSION BD087988
VERSION   BD087988.1 GI:226333598
KEYWORDS  JP 2001321190-A/232.
SOURCE    synthetic construct
ORGANISM  synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS   Soeda,E.

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Picoult-Newburg,L. and Pohl,M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 147 26-APR-2001;
            Orchid Biosciences, Inc. (US)
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Query Match      54.3%; Score 15.2; DB 6; Length 27;
Best Local Similarity 81.0%; Pred. No. 1.1e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 GTAAACAAGACTTCATTG 26
      ||||| || ||||| ||
DB      3 GTAAAAAAGATTTCATTGTG 23

RESULT 13
LOCUS   CQ799733/c          23 bp      DNA          linear      PAT 28-APR-2004
DEFINITION
Sequence 383 from Patent WO2004031413.
ACCESSION CQ799733
VERSION   CQ799733.1 GI:46848680
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Nakamura,Y., Daigo,Y. and Nakatsuru,S.
TITLE     Method for diagnosing non-small cell lung cancers
JOURNAL   Patent: WO 2004031413-A 383 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES  Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CACATGTAAACAAGACT 18
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DB      18 CACAGTAAACCAAGACT 1

RESULT 14
LOCUS   BD087988          24 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION
A method of arraying genome clone.
ACCESSION BD087988
VERSION   BD087988.1 GI:226333598
KEYWORDS  JP 2001321190-A/232.
SOURCE    synthetic construct
ORGANISM  synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS   Soeda,E.

TITLE      A method of arraying genome clone
JOURNAL    Patent: JP 2001321190-A 232 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT    OS Artificial Sequence
            PN JP 2001321190-A/232
            PD 20-NOV-2001
            PF 12-MAR-2001 JP 2001069285
            PI EIICHI SOEDA
            PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
            C12N15/00,
            PC C12N15/00
            CC Description of Artificial Sequence:Synthetic DNA FH Key
            Location/Qualifiers
            FT source
            1..24
            /organism='Artificial Sequence'.
            FT Location/Qualifiers
            1..24
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      52.1%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 2.1e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      7 TAAACAAGACTTCATTG 27
      ||||| ||||| ||||| |||||
DB      2 TCATACAAGACTGATTG 22

RESULT 15
LOCUS   AB068695          24 bp      DNA          linear      SYN 21-MAY-2003
DEFINITION
Synthetic construct DNA, reverse primer for human STS sts-SGC33042
at 1p36.
ACCESSION AB068695
VERSION   AB068695.1 GI:15129499
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Chen,Y.Z., Hayaashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
JOURNAL   Genomics 74 (1), 55-70 (2001)
MEDLINE   21269192
PUBMED    11374902
REFERENCE 2 (bases 1 to 24)
AUTHORS   Horii,A.
TITLE     Direct Submission
JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES  Location/Qualifiers
            source
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            misc_feature
            1..24
            /note="reverse primer for human STS sts-SGC33042 at 1p36
            sts-SGC33042 obtained from clones B46M21, B126K2, B35001,
            Human BAC library RPC1-11"
ORIGIN
Query Match      52.1%; Score 14.6; DB 12; Length 24;
Best Local Similarity 81.0%; Pred. No. 2.1e+05;

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Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TAAACACAGACTTCATTTGG 27

Db 2 TCATACAGACCTGATTTGG 22

Search completed: June 21, 2005, 18:22:42
Job time : 1807 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 21, 2005, 17:20:55 ; Search time 3005 Seconds
(without alignments)
354.675 Million cell updates/sec

Title: US-10-717-243-59
Perfect score: 28
Sequence: 1 CACATGTAACACAGACTTCATTTTGGC 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 39394

Minimum DB seq length: 0
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.8	45.7	24	8	AZ351302 IM0089117
C 2	12.8	45.7	28	8	BZ665403 SALK_1114
C 3	12.8	45.7	28	8	BZ665404 SALK_1114
C 4	12.6	45.0	27	9	TA140C03P
C 5	12.4	44.3	22	9	AG202132
C 6	12.4	44.3	27	8	BH863433
C 7	12.4	44.3	27	8	BZ382660 SALK_1186
C 8	12.4	44.3	27	8	BZ763517
C 9	12.4	44.3	28	1	AI431201
C 10	12.2	43.6	18	5	BQ590149
C 11	12.2	43.6	24	8	AZ784713
C 12	12.2	43.6	25	8	AZ804962
C 13	12.2	42.9	24	1	AJ668296
C 14	12.2	42.9	26	8	AZ803453
C 15	11.8	42.1	25	6	CD532369
C 16	11.8	42.1	25	9	AJ593422
C 17	11.6	41.4	20	1	AU014317
C 18	11.6	41.4	20	5	BQ59288
C 19	11.6	41.4	20	9	AJ591973
C 20	11.6	41.4	27	1	AU260224
C 21	11.6	41.4	28	9	AG189325
C 22	11.4	40.7	26	5	BQ584385
C 23	11.4	40.7	26	6	CD576873
C 24	11.4	40.7	26	8	AZ759583

C 25	11.4	40.7	28	1	AJ666432
C 26	11.4	40.7	28	1	AU257173
C 27	11.2	40.0	16	9	AJ592989
C 28	11.2	40.0	19	8	AZ345489
C 29	11.2	40.0	21	5	BX567143
C 30	11.2	40.0	23	8	AZ579508
C 31	11.2	40.0	24	7	CF298945
C 32	11.2	40.0	24	8	BH910951
C 33	11.2	40.0	25	8	AZ798040
C 34	11.2	40.0	27	8	AZ378215
C 35	11.2	40.0	27	8	AZ970619
C 36	11.2	40.0	28	1	AA867596
C 37	11.2	40.0	28	1	AA915770
C 38	11.2	40.0	28	1	AI573848
C 39	11.2	39.3	22	8	AZ372259
C 40	11.2	39.3	22	9	AJ590979
C 41	11.2	39.3	25	8	AZ877656
C 42	11.2	39.3	26	1	AU258699
C 43	11.2	39.3	27	1	AU258483
C 44	11.2	39.3	27	8	BZ356916
C 45	10.8	38.6	22	8	AZ387833

ALIGNMENTS

RESULT 1
AZ351302/c
LOCUS
DEFINITION
IM0089117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089117 F, genomic survey sequence.

ACCESSION
AZ351302
VERSION
AZ351302.1
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: 1 column: 17
Seq primer: CCGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source

1..24
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089117"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 24;
Best Local Similarity 87.5%; Pred. No. 8.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGA 16
|||||
Db 17 CACATGTAACAAATAGA 2

RESULT 2

BZ665403 28 bp DNA linear GSS 31-JAN-2003
LOCUS SALK_111481.23.75.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_111481.23.75.x, genomic survey sequence.

ACCESSION BZ665403.1 GI:28183007
VERSION BZ665403
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE AUTHORS

1 (bases 1 to 28)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of

At5g54020.

Class: TDNA tagged.

Location/Qualifiers

source

1. .28

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_111481.23.75.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

.ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 28;
Best Local Similarity 87.5%; Pred. No. 9.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACAAGACTT 19
|||||
Db 13 ATGTAAACAAGACTT 28

RESULT 3

BZ665404 28 bp DNA linear GSS 31-JAN-2003
LOCUS SALK_111483.22.35.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_111483.22.35.x, genomic survey sequence.

ACCESSION BZ665404
VERSION BZ665404.1 GI:28183008
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE AUTHORS

1 (bases 1 to 28)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of

At5g54020.

Class: TDNA tagged.

Location/Qualifiers

source

1. .28

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_111483.22.35.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 28;
Best Local Similarity 87.5%; Pred. No. 9.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACAAGACTT 19
|||||
Db 13 ATGTAAACAAGACTT 28

RESULT 4

TA140C03P/c 27 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140c03, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL466420


```

VERSION      AL466420.1  GI:11835775
KEYWORDS     GSS.
SOURCE       Trypanosoma brucei
ORGANISM     Trypanosoma brucei
REFERENCE    1 (bases 1 to 27)
AUTHORS      Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
              Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
              Melville, S.E., Rajadream, M.A. and Barrell, B.G.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES     source
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                  /mol_type="genomic DNA"
                  /strain="TREU927"
                  /db_xref="taxon:5691"
                  /clone="I40c03"

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Best Local Similarity 78.9%; Pred.No. 1.1e+06;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  5  TGTAAACACAGACTTCATT 23
    ||||| ||| ||| |||
DB   27 TGTAAAGCAGATTACATT 9

RESULT 5
AG202132
LOCUS      AG202132             22 bp    DNA    linear    GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-085C03.TJ, genomic survey
sequence.
ACCESSION  AG202132
VERSION     AG202132.1  GI:45234307
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes

REFERENCE   1
AUTHORS     Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
              Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE       BAC end sequences of Library RP-43
JOURNAL     Unpublished
AUTHORS     Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
              Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE       Direct Submission
JOURNAL     Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
              Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
              52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
              (E-mail:redstone@mail.kribb.re.kr, URL:http://pbs.grc.kribb.re.kr/,
              Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
              end was generated during the R&D process and may have higher chance

of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI.
R.Site 2    : EcoRI.
FEATURES     source
              Location/Qualifiers
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                  /mol_type="genomic DNA"
                  /db_xref="taxon:9598"
                  /clone="RP43-085C03.TJ"
                  /sex="male"
                  /cell_type="lymphocytes"
                  /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match      44.3%; Score 12.4; DB 9; Length 22;
Best Local Similarity 72.7%; Pred.No. 1.3e+06;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  4  ATGTAACACAGACTTCATTT 25
    ||||| ||| ||| |||
DB   1  ATTAAAAAGAACTGCTTTT 22

RESULT 6
BH863433/c
LOCUS      BH863433             27 bp    DNA    linear    GSS 05-AUG-2002
DEFINITION SALK 093870 Arabidopsis thaliana TDNA insertion lines Arabidopsis
              thaliana genomic clone SALK_093870, genomic survey sequence.
ACCESSION  BH863433
VERSION     BH863433.1  GI:22099046
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana

REFERENCE   1 (bases 1 to 27)
AUTHORS     Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
              Gadrian, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
              Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE       A Sequence-indexed Library of Insertion Mutations in the
              Arabidopsis Genome
JOURNAL     Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGNAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
              Tel: 858 453 4100 x1752
              Fax: 858 558 6379
              Email: ecker@salk.edu
              This is single pass sequence recovered from the left border of
              TDNA.
              Class: TDNA tagged.
              Location/Qualifiers
                1..27
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                  /mol_type="genomic DNA"
                  /ecotype="Col-0"
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                  /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
                  each of which contains one or more TDNA insertion
                  elements. The resultant fragment for each line was
                  directly sequenced to determine the genomic sequence at
                  the site of insertion. Details of the protocols used can
                  be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES     source
              Location/Qualifiers
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                  /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
                  each of which contains one or more TDNA insertion
                  elements. The resultant fragment for each line was
                  directly sequenced to determine the genomic sequence at
                  the site of insertion. Details of the protocols used can
                  be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

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Query Match      44.3%; Score 12.4; DB 8; Length 27;
Best Local Similarity 72.7%; Pred. No. 1.3e+06;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 ATGTAACACAGACTTCATTTT 25
DB 26 ATTATAACAAATTAAGATT 5

RESULT 7
BZ382660/c
LOCUS BZ382660.27 bp DNA linear GSS 26-NOV-2002
DEFINITION SALK_118629.27.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_118629.27.30.x, genomic
survey sequence.
ACCESSION BZ382660
VERSION BZ382660.1 GI:25477908
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 27)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g22800.
Class: TDNA tagged.
FEATURES
source
location/Qualifiers
1..27
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      44.3%; Score 12.4; DB 8; Length 27;
Best Local Similarity 72.7%; Pred. No. 1.3e+06;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCAT 22
DB 23 CATACTATAACAAAGTTTAT 2

RESULT 9
AI431201
LOCUS AI431201
DEFINITION 28 bp mRNA linear EST 23-JUL-2004
sa22f07.v2 Gm-cl006 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl006-62 5' similar to SW:ATP6_TRYBB P24499 ATP SYNTHASE A CHAIN
; mRNA sequence.
ACCESSION AI431201
VERSION AI431201.1 GI:4277037
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schuck,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project

```

```

source
1. .18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189975"
/db_xrefs="taxon:161934"
/clone="024-019-B19"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPI2-ADIS-024-storage root"
/notes="Vector: pCMWSPORT6; Site1: Sali; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match      43.8%; Score 12.2; DB 5; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.5e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACATGTAAAAACAGACT 18
    ||||| ||||| |||||
Db 2 ACATGGAAAGATACT 18
    ||||| ||||| |||||

RESULT 11
AZ784713/c
LOCUS
DEFINITION
2M0027K21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0027K21 R, genomic survey sequence.
ACCESSION
AZ784713
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: K column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7EL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0027K21"
/sex="Male"
FEATURES
source

```

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 43.6%; Score 12.2; DB 8; Length 24;
 Best Local Similarity 82.4%; Pred. No. 1.6e+06;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CACATGTAAACAAGAC 17
 |||||
 DB 17 CACATGTAGAAAAGGC 1

RESULT 12

AZ804962/c

LOCUS

DEFINITION 2M0066E10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0066E10 F, genomic survey sequence.

ACCESSION

AZ804962

VERSION

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0066 row: E column: 10
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0066E10"
 /sex="Male"

FEATURES

source

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 43.6%; Score 12.2; DB 8; Length 25;
 Best Local Similarity 82.4%; Pred. No. 1.6e+06;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AAACAAGACTTCATTTT 25
 |||||
 DB 24 ATAAAGAGTTCATTTT 8

RESULT 13

AJ668296/c

LOCUS

DEFINITION AJ668296 CSEQRAN09 Sus scrofa cDNA clone C0000045_J12, mRNA
 sequence.

ACCESSION

AJ668296

VERSION

AJ668296.1

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

1 (bases 1 to 24)

AUTHORS

Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

TITLE

Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle

JOURNAL

Unpublished (2004)

COMMENT

Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred
 v0.020425.c. Vector identified by cross match with the -minscore 20
 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
 EcoRI R. Site 2: NotI Description: Normalised library constructed
 from pooled tissue from day 30 placentas. Clones available from UK
 Centre for Functional Genomics in Farm Animals, Roslin Institute,
 Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source

1..24

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0000045_J12"

/tissue type="placenta"

/clone lib="CSEQRAN09"

/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
 NotI; Single pass sequencing. Normalised library
 constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 42.9%; Score 12; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 AAAACAAGACTTCATTTCG 27
| | | | | | | | | | | | | | | | | | | | |
DB 24 AAAAAAAAAATTTTTCG 5

RESULT 14
AZ803453/c
LOCUS
DEFINITION 26 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0063D19 R, genomic survey sequence.
ACCESSION AZ803453
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: D column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES
source
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0063D19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GII4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 12; DB 8; Length 26;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACATGTAAACAAGACTTCA 21
| | | | | | | | | | | | | | | | | | | | |
DB 23 ATATAGAAAAGAAGACTACA 4

RESULT 15
CD532369/c
LOCUS
DEFINITION 25 bp mRNA linear EST 31-DEC-2003
26O17 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
3', mRNA sequence.
ACCESSION CD532369
VERSION
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 25)
AUTHORS Guo, Y., Cai, Z. and Gan, S.
TITLE Transcriptome of Arabidopsis leaf senescence
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT Contact: Susheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
Insert Length: 25 Std Error: 0.00
Seq primer: T7
POLVA=No.

FEATURES
source
1. .25
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/tissue_type="Leaf"
/dev_stage="yellow Leaf With Greenish Base Area"
/clone_host="E. coli"
/clone_lib="Arabidopsis Leaf Senescence Library"
/note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

ORIGIN

Query Match 42.1%; Score 11.8; DB 6; Length 25;
Best Local Similarity 69.6%; Pred. No. 2.3e+06;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CATGTAAACAAGACTTCATTTT 25
| | | | | | | | | | | | | | | | | | | | |
DB 23 CATGTAAACAAGACTTCATTTT 1

Search completed: June 21, 2005, 19:13:00
Job time : 3012 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 16:11:58 ; Search time 417 Seconds
(without alignments)
397.489 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACACAGACTTCATTGGC 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 3386362

Minimum DB seq length: 0

Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004as: *
13: Geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	2	AAQ42253 PCR prime
C	16.6	59.3	28	10	ACF04990 Hair papi
3	15.8	56.4	28	1	AAN50399 Sequence
C	15.6	55.7	25	9	ACI17291 Human mic
5	15.2	54.3	27	4	AAH37351 SNP speci
C	14.8	52.9	23	12	ADN35702 Human NSC
7	14.8	52.9	25	9	ACI70121 Human mic
C	14.8	52.9	28	2	AAQ42253 PCR prime
9	14.6	52.1	25	6	ABL43188 Human chr
C	14.6	52.1	25	3	AAZ89383 A. thalia
11	14.6	52.1	25	9	ACI19346 Human mic
C	14.4	51.4	24	12	ADQ31135 C-fos mRN
13	14.4	51.4	24	12	ADQ31044 C-fos mRN
C	14.2	50.7	20	12	ADK72984 Chimeric
15	14.2	50.7	20	12	ADK72983 Chimeric
C	14.2	50.7	20	12	ADK73036 Chimeric
17	14.2	50.7	20	12	ADK73099 Chimeric
C	14.2	50.7	22	12	ADJ51107 Human NOV
19	14.2	50.7	25	13	ADR20628 Human oes
C	14	50.0	25	9	ACK15826 Human mic

C	21	14	50.0	25	9	ACI17290 Human mic
	22	14	50.0	27	6	AA2128022 Arabidops
	23	13.8	49.3	20	4	AAF58586 Arabidops
	24	13.8	49.3	20	12	ADI19115 Arabidops
	25	13.8	49.3	24	3	AAA40065 Rice dise
	26	13.8	49.3	25	6	AAI17875 FC-1 forw
C	27	13.8	49.3	25	9	ACI84703 Human mic
	28	13.8	49.3	25	9	ACI42430 Human mic
C	29	13.8	49.3	25	10	ADG92070 Schizophr
C	30	13.6	48.6	20	9	ABZ81587 PKA regul
C	31	13.6	48.6	20	12	ADH18270 2'-MOE ga
C	32	13.6	48.6	20	12	ADK72943 Chimeric
C	33	13.6	48.6	20	12	ADK72748 Chimeric
C	34	13.6	48.6	20	12	ADK72793 Chimeric
C	35	13.6	48.6	20	12	ADL58504 Human ESN
C	36	13.6	48.6	20	12	ADL58418 Human ESN
C	37	13.6	48.6	20	12	ADO32811 Antisense
C	38	13.6	48.6	24	4	AAO5019 Neurofibr
C	39	13.6	48.6	24	6	AAI47475 Human zin
	40	13.6	48.6	24	6	ABA04869 Human PCR
	41	13.6	48.6	25	9	ACI77522 Human mic
C	42	13.6	48.6	25	9	ACI54916 Human mic
	43	13.6	48.6	25	9	ACI85790 Human mic
C	44	13.6	48.6	27	3	AAQ68513 Mitochond
	45	13.6	48.6	27	8	ABX13209 DNA encod

ALIGNMENTS

RESULT 1
AAQ42253
ID AAQ42253 standard; cDNA; 28 BP.

XX AAQ42253;
XX
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1993 (first entry)

XX PCR primer GeloC-20 to replace Ile103 of gelonin with Cys.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin;
KW mutagenic polymerase chain reaction; ss.

XX Synthetic.

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

XX Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo.

XX Example 3; Page 35; 163pp; English.

XX Fifteen analogues of gelonin were constructed. Ten non-cysteine residues in surface positions and available for conjugation to a second protein were targeted for substn. In the other analogues, one or both of the native Cys residues present in gelonin were substd. Overlap extension PCR was used to construct the various analogues. Primer GeloC-20 was used in

CC the substn. of Ile103 of gelonin by Cys. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 28 BP; 10 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAAGACTTCATTGGC 28
DB 1 CACATGTAATAACAAGACTTCATTGGC 28

RESULT 2
ACF04990/c
ID ACF04990 standard; DNA; 28 BP.
XX
AC ACF04990;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hair papilla cell growth promoter related probe SEQ ID NO: 55.
XX
KW Human; hair growth; stimulant; tonic; hair papilla cell growth; promoter;
KW WNT-5A; endocrine-gen; PCR; primer; probe; ss.
XX
OS Unidentified.
XX
PN WO2003086334-A1.
XX
PD 23-OCT-2003.
XX
PF 17-APR-2003; 2003WO-JP004884.
XX
PR 17-APR-2002; 2002JP-00115529.
XX
PA (TAIS) TAISHO PHARM CO LTD.
XX
PI Ikeda A, Shionosaga H, Fujimoto N, Kasai Y;
XX
DR WPI; 2003-845259/78.
XX
PT Hair growth tonics or hair stimulants containing hair papilla cell growth
PT factors like Echinon chlamydia-originated macrolide compounds
PT capable of inhibiting function of WNT-5A, useful in drugs and cosmetics.
XX
PS Disclosure; Page 118; Opp; Japanese.
XX
CC The present invention relates to hair papilla cell growth promoters which
CC contain compounds with inhibitory activity on the function of WNT-5A. The
CC hair growth tonics and hair stimulants are useful in drugs and cosmetics.
CC The present sequence is a primer/probe shown in the exemplification of
CC the invention
XX
SQ Sequence 28 BP; 10 A; 5 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 59.3%; Score 16.6; DB 10; Length 28;
Best Local Similarity 82.6%; Pred. No. 2.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACATGTAAACAAGACTTCATT 24
DB 24 AAAGGTAATACAGACTTCTTTT 2

RESULT 3
AAN50399
ID AAN50399 standard; DNA; 28 BP.
XX
AC AAN50399;
XX
DT 24-OCT-2003 (revised)

DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-OCT-1991 (first entry)
XX
XX Sequence of the junction between yeast PKG gene promoter and rabies
DE glycoprotein gene.
XX
KW Rabies antigen; vaccine; immunogen; epitope; ss.
XX
OS Saccharomyces cerevisiae.
OS Rabies virus.
XX
FH Key Location/Qualifiers
FT promoter 14..19 /*tag= a
FT CDS 23..28 /*tag= b
FT /product= "rabies glycoprotein N-terminal"
XX
PN FR2552776-A.
XX
PD 05-APR-1985.
XX
PF 03-OCT-1983; 83FR-00315716.
XX
PR 03-OCT-1983; 83FR-00015716.
PR 27-MAR-1984; 84FR-00004754.
PR 03-OCT-1984; 84FR-00015716.
XX
PA (TRGE) TRANSGENE SA.
XX
PI Lathe R, Kiemy MP, Lemoine Y, Loison M, Aigle J, Lecoc P;
XX
DR WPI; 1985-112444/19.
XX
PT Expression vector contg. DNA sequence for antigenic rabies protein - and
PT viral or yeast expression elements, for transforming eucaryotic cells.
XX
PS Example; Fig 18; 29pp; French.
XX
CC The inventors claim vectors which express a rabies virus antigenic
CC protein in eucaryotic cells. AAN50399 is part of a vector designed for
CC expression in yeast. (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 28 BP; 14 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 56.4%; Score 15.8; DB 1; Length 28;
Best Local Similarity 74.1%; Pred. No. 6.2e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CACATGTAAACAAGACTTCATTGGG 27
DB 1 CAATATATAACAAGACTCTAATATGGG 27

RESULT 4
AC117291/c
ID AC117291 standard; DNA; 25 BP.
XX
AC AC117291;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 17282.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.


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XX US2003104410-A1.
XX
XX
XX PD 05-JUN-2003.
XX
XX PF 15-MAR-2002; 2002US-00098263.
XX
XX PR 16-MAR-2001; 2001US-0276759P.
XX
XX PA (AFFY-) AFFYMETRIX INC.
XX
XX PI Mittmann MP;
XX
XX DR WPI; 2003-567953/53.
XX
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
XX PS Claim 1; SEQ ID NO 17282; 9pp; English.
XX
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying allelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
XX
XX SQ Sequence 25 BP; 7 A; 3 C; 5 G; 10 T; 0 U; 0 Other;
    Query Match 55.7%; Score 15.6; DB 9; Length 25;
    Best Local Similarity 81.8%; Pred. No. 7.4e+03;
    Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
    QY 2 ACATGTAACCAAGACTTCATT 23
    Db 23 ATATGTAACCAACACCTCGTT 2
    RESULT 5
    AAH37351
    ID AAH37351 standard; DNA; 27 BP.
    XX
    XX AAH37351;
    AC
    XX
    XX 14-AUG-2001 (first entry)
    DT
    XX
    XX SNP specific SNPE primer SEQ ID 147.
    DE
    XX
    XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
    KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
    KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
    KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
    KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
    KW inflammation; forensic investigation; paternity analysis; primer; ss.
    XX

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OS Homo sapiens.
XX WO200129262-A2.
XX
XX PD 26-APR-2001.
XX
XX PF 13-OCT-2000; 2000WO-US028436.
XX
XX PR 15-OCT-1999; 99US-0160096P.
XX
XX PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX PI Picoult-Newburg L, Pohl M;
XX
XX DR WPI; 2001-290930/30.
XX
XX PT New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX PS Claim 1; Page 50; 83pp; English.
XX
XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a single nucleotide
XX primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence
XX
XX SQ Sequence 27 BP; 10 A; 1 C; 5 G; 10 T; 0 U; 1 Other;
    Query Match 54.3%; Score 15.2; DB 4; Length 27;
    Best Local Similarity 81.0%; Pred. No. 1.1e+04;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
    QY 6 GTAAACACAGACTTCATTTTG 26
    Db 3 GTAAAAAANGATTTCATTGTG 23
    RESULT 6
    ADN35702/c
    ID ADN35702 standard; DNA; 23 BP.
    XX
    XX ADN35702;
    AC
    XX
    XX 01-JUL-2004 (first entry)
    DT
    XX
    XX Human NSCLC gene semi-quantitative PCR primer forward primer #191.
    KW ss; primer; cytostatic; gene therapy; vaccine;
    KW non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1.
    XX
    XX Homo sapiens.
    OS

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PN WO2004031413-A2.
 XX 15-APR-2004.
 XX 22-SEP-2003; 2003WO-JP012072.
 PF 30-SEP-2002; 2002US-0414673P.
 PR 28-FEB-2003; 2003US-0451374P.
 PR 28-APR-2003; 2003US-0466100P.
 XX (ONCO-) ONCOTHERAPY SCI INC.
 PA (UYTY) UNIV TOKYO.
 XX Nakamura Y, Daigo Y, Nakatsuru S;
 PI WPI; 2004-330206/30.
 DR WPI; 2004-330206/30.
 XX Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)
 PT comprises determining an expression level of an NSCLC-associated gene in
 PT a sample.
 XX Disclosure; SEQ ID NO 383; 394pp; English.
 XX The invention relates to a method of diagnosing non-small cell lung
 CC cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
 CC determining the expression level of a NSCLC-associated gene in a
 CC biological sample derived from the subject, where an increase or decrease
 CC of the level compared to a normal control level of the gene indicates
 CC that the subject suffers from or is at risk of developing NSCLC. The
 CC method is useful in diagnosing NSCLC or a predisposition to developing
 CC NSCLC in a subject. The compound, polynucleotide and the encoded
 CC polypeptide and composition are useful in treating or preventing NSCLC.
 CC This sequence corresponds to a primer for semi-quantitative PCR
 CC amplification of genes that are differentially expressed in NSCLC cells.
 XX
 SQ Sequence 23 BP; 3 A; 4 C; 7 G; 9 T; 0 U; 0 Other;
 Query Match 52.9%; Score 14.8; DB 12; Length 23;
 Best Local Similarity 88.9%; Pred. No. 1.6e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CACATGTTAAACCAAGACT 18
 Db 18 CACAGGTTAAACCAAGACT 1
 RESULT 7
 ACI70121/c
 ID ACI70121 standard; DNA; 25 BP.
 XX ACI70121;
 AC ACI70121;
 XX 14-OCT-2003 (first entry)
 DT Human microarray DNA oligonucleotide SEQ ID NO 70112.
 DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
 XX genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX Homo sapiens.
 OS US2003104410-A1.
 PN 05-JUN-2003.
 XX 15-MAR-2002; 2002US-00098263.
 PF 16-MAR-2001; 2001US-0276759P.
 PR (AFFY-) AFFYMETRIX INC.
 PA Mittmann MP;
 XX

XX WPI; 2003-567953/53.
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX Claim 1; SEQ ID NO 70112; 9pp; English.
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 5 A; 5 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 52.9%; Score 14.8; DB 9; Length 25;
 Best Local Similarity 88.9%; Pred. No. 1.6e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 GTAAACCAAGACTTCATT 23
 Db 22 GTAAACCAAGACGTCCTT 5
 RESULT 8
 AAX10106/c
 ID AAX10106 standard; DNA; 28 BP.
 XX AAX10106;
 AC AAX10106;
 XX 24-MAR-1999 (first entry)
 DT Human biallelic polymorphic marker downstream primer #412.
 DE Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
 KW treatment; marker; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 OS WO9820165-A2.
 PN 14-MAY-1998.
 XX 05-NOV-1997; 97WO-US020313.
 PF 06-NOV-1996; 96US-0030455P.
 PR (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA Lander ES, Wang D, Hudson T;
 XX
 PI

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XX DR WPI; 1998-286974/25.
XX PT New isolated nucleic acid segments from the human genome - used for
XX PT determining polymorphic forms for use in e.g. forensics, paternity
XX PT testing or phenotypic typing for disease.
XX PS Claim 16; Page 201; 310pp; English.
XX CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the
XX CC isolation of various biallelic polymorphic markers found in the human
XX CC genome (represented in AAX10269-X12937). These primers can be used in a
XX CC method for determining polymorphic forms in an individual for use in e.g.
XX CC forensics, paternity testing or for phenotypic typing for diseases such
XX CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
XX CC hypercholesterolemia, polycystic kidney disease, hereditary
XX CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
XX CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
XX CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
XX CC autoimmune diseases, inflammation, cancer, diseases of the nervous
XX CC system, infection by pathogenic microorganisms, and characteristics such
XX CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
XX CC endurance, fertility, and susceptibility or receptivity to particular
XX CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
XX CC segments can also be used to produce medicaments for the treatment or
XX CC prophylaxis of such diseases
XX SQ Sequence 28 BP; 12 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 2; Length 28;
Best Local Similarity 88.9%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AAACAGACTTCATTGG 26
Db 18 AAACGATACCTCATTGG 1

RESULT 9
ABL43188
ID ABL43188 standard; DNA; 24 BP.
AC ABL43188;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:232.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 4; Page 9; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in

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CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
XX Sequence 24 BP; 7 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TAAACAGACTTCATTGG 27
Db 2 TCATACAGACCTGATTGG 22

RESULT 10
AAZ89383/c
ID AAZ89383 standard; DNA; 25 BP.
XX
XX AAZ89383;
XX
XX 15-JUN-2000 (first entry)
XX
XX A. thaliana ACW1 PCR primer 4.
XX
XX ACW1; plant cell wall; digestion efficiency; crop; agriculture;
XX PCR primer; ss.
XX
XX Arabidopsis thaliana.
XX
XX JP2000041685-A.
XX
XX 15-FEB-2000.
XX
XX 23-MAR-1999; 99JP-00077502.
XX
XX 29-MAY-1998; 98JP-00166174.
XX
XX (QJTP) OJI PAPER CO.
XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX
XX WPI; 2000-274045/24.
XX
XX Modification of the cell wall components of a plant - useful for
XX improving digestion efficiency of crops and feed crops.
XX
XX Example 1; Page 21; 24pp; Japanese.
XX
XX This invention describes a novel nucleic acid used for modifying the cell
XX wall components of a plant. The modification is used for the improvement
XX in digestion efficiency of useful crops and feed crops. The DNA is useful
XX in agriculture, industry and gardening. AAZ89380-289385 represent PCR
XX primers used in the amplification of the Arabidopsis thaliana ACW1
XX protein which is described in the method of the invention
XX
XX Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

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Query Match      52.1%; Score 14.6; DB 3; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGTAATAACAGACTTCATTTT 25
   ||||| ||| ||| ||| ||| |||
DB 22 TGTAACACATGAATTCATGTT 2

RESULT 11
ACI19346
ID ACI19346 standard; DNA; 25 BP.
XX
AC ACI19346;
XX
XX 13-OCT-2003 (first entry)
DE Human microarray DNA oligonucleotide SEQ ID NO 19337.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 19337; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 6 A; 4 C; 4 G; 11 T; 0 U; 0 Other;

Query Match      52.1%; Score 14.6; DB 3; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.9e+04;

QY 5 TGTAATAACAGACTTCATTTT 25
   ||||| ||| ||| ||| ||| |||
DB 22 TGTAACACATGAATTCATGTT 2

RESULT 12
ADQ31135/c
ID ADQ31135 standard; DNA; 24 BP.
XX
AC ADQ31135;
XX
XX 23-SEP-2004 (first entry)
DE C-fos mRNA detection related oligonucleotide.
XX
XX analyte detection; detection; probe; detection probe; reporter; human;
KW c-fos; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004057023-A1.
XX
XX 08-JUL-2004.
XX
PF 19-DEC-2003; 2003WO-EP014661.
XX
PR 20-DEC-2002; 2002EP-00028582.
PR 13-JAN-2003; 2003US-0439439P.
XX
PA (EVOT-) EVOTEC OAI AG.
XX
PI Hannah S, Lambrue D, Droegge S, Jaeger S, Gall K;
XX
DR WPI; 2004-543305/52.
XX
PT Detecting an analyte such as protein or nucleic acid, useful for
PT screening drugs, comprises probe detection of captured analyte where
PT surplus probe signal is quenched and/or differential emission wavelength
PT of labeled support is measured.
XX
PS Disclosure; Fig 4; 61pp; English.
XX
CC The present invention describes a method for detecting an analyte in a
CC sample. The method comprises: (a) providing detection probes being
CC labelled with a first reporter, where the detection probes are capable of
CC binding to the analyte; (b) providing a solid support; (c) providing
CC capture probes being bound or capable of binding to the solid support,
CC where the capture probes are capable of binding to the analyte, and so
CC concentrating the analyte on the solid support; (d) contacting the sample
CC with the detection probes, the solid support and the capture probes; and
CC (e) detecting the detection probes where (i) the detection of detection
CC probes is conducted in the presence of quenching probes binding to
CC surplus detection probes not being bound to the analyte and thereby
CC quenching at least partially an emission of the first reporter of said
CC surplus detection probes, and/or (ii) the solid support is labelled with
CC a second reporter different from the first reporter, imaging the sample
CC at an emission wavelength of the second reporter, generating a mask
CC obtained from imaging the sample at the emission wavelength of the second
CC reporter and applying this mask to an image of the sample used for
CC detecting the detection probes. The present sequence represents an
CC oligonucleotide used in the detection of c-fos mRNA, which is used in an
CC example from the present invention.
XX
SQ Sequence 24 BP; 5 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match      51.4%; Score 14.4; DB 12; Length 24;
Best Local Similarity 75.0%; Pred. No. 2.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 ATGTAATAACAGACTTCATTTTGG 27
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Db      24 AGGAAAACTAGAGTTTCATCTGG 1
      | | | | | | | | | | | | | | | |
RESULT 13
ADQ31044/c
ID ADQ31044 standard; DNA; 24 BP.
XX
AC ADQ31044;
XX
DT 23-SEP-2004 (first entry)
XX
DE C-fos mRNA detection capture oligonucleotide.
XX
KW analyte detection; detection; probe; detection probe; reporter;
KW capture oligonucleotide; human; c-fos; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "5, labelled with rhodamine-6G (Rh6G)"
XX
PN WO2004057023-A1.
XX
XX 08-JUL-2004.
XX
XX 19-DEC-2003; 2003WO-EP014661.
XX
XX 20-DEC-2002; 2002EP-00028582.
XX
XX 13-JAN-2003; 2003US-0439439P.
XX
XX (EVOT-) EVOTEC OAI AG.
XX
XX Hinmah S, Lambrue D, Droege S, Jaeger S, Gall K;
XX WPI; 2004-543305/52.
XX
PT Detecting an analyte such as protein or nucleic acid, useful for
PT screening drugs, comprises probe detection of captured analyte where
PT surplus probe signal is quenched and/or differential emission wavelength
PT of labeled support is measured.
XX
XX Example 1; Page 19; 61pp; English.
XX
CC The present invention describes a method for detecting an analyte in a
CC sample. The method comprises: (a) providing detection probes being
CC labelled with a first reporter, where the detection probes are capable of
CC binding to the analyte; (b) providing a solid support; (c) providing
CC capture probes being bound or capable of binding to the solid support,
CC where the capture probes are capable of binding to the analyte, and so
CC concentrating the analyte on the solid support; (d) contacting the sample
CC with the detection probes, the solid support and the capture probes; and
CC (e) detecting the detection probes where (i) the detection of detection
CC probes is conducted in the presence of quenching probes binding to
CC surplus detection probes not being bound to the analyte and thereby
CC quenching at least partially an emission of the first reporter of said
CC surplus detection probes, and/or (ii) the solid support is labelled with
CC a second reporter different from the first reporter, imaging the sample
CC at an emission wavelength of the second reporter, generating a mask
CC obtained from imaging the sample at the emission wavelength of the second
CC reporter and applying this mask to an image of the sample used for
CC detecting the detection probes. The present sequence represents a capture
CC oligonucleotide used in the detection of c-fos mRNA, which is used in an
CC example from the present invention.
XX
XX Sequence 24 BP; 5 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 51.4%; Score 14.4; DB 12; Length 24;
Best Local Similarity 75.0%; Pred. No. 2.4e+04;

Matches 24 BP; 5 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 4 ATGTAACAAACAGACTTCATTGG 27
DB 24 AGGAAAACTAGAGTTTCATCTGG 1
      | | | | | | | | | | | | | | | |
RESULT 14
ADK72984/c
ID ADK72984 standard; DNA; 20 BP.
XX
AC ADK72984;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #318.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 318; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 50.7%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 TAAACAAACAGCTTCATTTT 25
DB 19 TAAACAAACAGCATGATTAT 1
      | | | | | | | | | | | | | | | |
RESULT 15
ADK72983/c
ID ADK72983 standard; DNA; 20 BP.

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XX ADK72983;
XX AC
XX DT 20-MAY-2004 (first entry)
XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #317.
XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX KW diabetic neuropathy; arthritic pain; migraine headache;
XX KW infantile epilepsy; ataxia; ss.
XX OS Synthetic.
XX PN WO2004016754-A2.
XX PD 26-FEB-2004.
XX PF 14-AUG-2003; 2003WO-US025465.
XX PR 14-AUG-2002; 2002US-0403416P.
XX PA (PHAA) PHARMACIA CORP.
XX PI Roberds SL;
XX DR WPI; 2004-203785/19.
XX PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX PS Claim 4; SEQ ID NO 317; 417pp; English.
XX CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX SQ Sequence 20 BP; 5 A; 2 C; 3 G; 10 T; 0 U; 0 Other;
Query Match 50.7%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 TGTAAACACAGACTTCATT 23
DB 19 TATAAACACAGACATGATT 1

Search completed: June 21, 2005, 17:52:28
Job time : 423 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 15:19:32 ; Search time 543 Seconds
(without alignments)
320.094 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACACAGACTTCATTGGC 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	16	US-10-127-890-59
2	28	100.0	28	21	US-10-717-243-59
3	24.8	88.6	813	9	US-09-765-527-246
4	24.8	88.6	813	16	US-10-127-890-11
5	24.8	88.6	813	21	US-10-717-243-11
6	24.8	88.6	855	9	US-09-765-527-258
7	24.8	88.6	1003	9	US-09-765-527-252

8	24.8	88.6	1072	9	US-09-765-527-250	Sequence 250, Appl
9	24.8	88.6	1176	16	US-10-074-586-2	Sequence 2, Appl
10	24.8	88.6	1527	16	US-10-074-586-10	Sequence 10, Appl
11	20.6	73.6	38142	20	US-10-417-375-55	Sequence 55, Appl
12	20.2	72.1	2187	8	US-08-781-986A-329	Sequence 329, Appl
13	20.2	72.1	2187	18	US-10-329-624-329	Sequence 329, Appl
14	20	71.4	11298	10	US-09-960-706-705	Sequence 705, Appl
15	19.8	70.7	349	18	US-10-424-599-12953	Sequence 12953, A
16	19.8	70.7	742	13	US-10-027-632-141533	Sequence 141533, A
17	19.8	70.7	742	13	US-10-027-632-141533	Sequence 141533, A
18	19.8	70.7	742	17	US-10-027-632-141533	Sequence 141533, A
19	19.8	70.7	742	17	US-10-027-632-141533	Sequence 141533, A
20	19.8	70.7	13886	21	US-10-741-600-17592	Sequence 17592, A
21	19.6	70.0	2100	9	US-09-771-161A-45	Sequence 45, Appl
22	19.6	70.0	2793	21	US-10-794-514A-470	Sequence 470, Appl
23	19.6	70.0	2952	15	US-10-345-680-3	Sequence 3, Appl
24	19.6	70.0	2953	19	US-10-384-339C-3	Sequence 3, Appl
25	19.6	70.0	3149	15	US-10-205-823-96	Sequence 96, Appl
26	19.6	70.0	3149	15	US-10-345-680-1	Sequence 1, Appl
27	19.6	70.0	3149	17	US-10-295-027-601	Sequence 601, Appl
28	19.6	70.0	3149	20	US-10-473-974-220	Sequence 220, Appl
29	19.6	70.0	5799	21	US-10-794-514A-468	Sequence 468, Appl
30	19.6	70.0	5835	20	US-10-723-860-6909	Sequence 6909, Ap
31	19.4	69.3	36	16	US-10-127-890-60	Sequence 60, Appl
32	19.4	69.3	36	21	US-10-717-243-60	Sequence 60, Appl
33	19.4	69.3	1223197	13	US-10-027-632-179264	Sequence 179264, A
34	19.4	69.3	1223197	17	US-10-027-632-179264	Sequence 179264, A
35	19.2	68.6	179	9	US-09-783-590-2798	Sequence 2798, Ap
36	19.2	68.6	543	13	US-10-027-632-195566	Sequence 195566, A
37	19.2	68.6	543	17	US-10-027-632-195566	Sequence 195566, A
38	19.2	68.6	672	19	US-10-437-963-44159	Sequence 44159, A
39	19.2	68.6	1244	13	US-10-027-632-124417	Sequence 124417, A
40	19.2	68.6	1244	17	US-10-027-632-124417	Sequence 124417, A
41	19.2	68.6	5886	15	US-10-311-455-2185	Sequence 2185, Ap
42	19.2	68.6	99090	20	US-10-656-394A-13	Sequence 13, Appl
43	19.2	68.6	290547	19	US-10-367-094-77	Sequence 77, Appl
44	19.2	68.6	1503841	9	US-09-795-668-1	Sequence 1, Appl
45	19.2	68.6	1503841	9	US-09-795-668-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-127-890-59
; Sequence 59, Application US/10127890
; Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/127,890

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

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/
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-127-890-59

Query Match      100.0%; Score 28; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTTTGGC 28
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Db 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 2
US-10-717-243-59
/ Sequence 59, Application US/10717243
/ Publication NO. US20050054835A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Carroll, Stephen F.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/717,243
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992

/
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-717-243-59

Query Match      100.0%; Score 28; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 3
US-09-765-527-246
/ Sequence 246, Application US/09765527
/ Patent No. US20020006638A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ TITLE OF INVENTION: Methods for Recombinant Microbial Production of
/ Fusion Proteins and BPI-Derived Peptides
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/765,527
/ FILING DATE: 18-Jan-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/621,803
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Borun, Michael F.
/ REGISTRATION NUMBER: 25,447
/ REFERENCE/DOCKET NUMBER: 27129/33199
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 246:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 813 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
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/
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: "gelonin"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-765-527-246

Query Match      88.6%; Score 24.8; DB 9; Length 813;
Best Local Similarity 92.9%; Pred. No. 2.3;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTGGC 28
    ||| ||||| ||||| ||||| |||||
Db 303 CACAATTAACAAAGACTTCATTGGC 330

RESULT 4
US-10-127-890-11
; Sequence 11, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroli, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-127-890-11

QY 1 CACATGTAACAAAGACTTCATTGGC 28
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "gelonin"
SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-765-527-246

Query Match      88.6%; Score 24.8; DB 9; Length 813;
Best Local Similarity 92.9%; Pred. No. 2.3;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTGGC 28
    ||| ||||| ||||| ||||| |||||
Db 303 CACAATTAACAAAGACTTCATTGGC 330

RESULT 5
US-10-717-243-11
; Sequence 11, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroli, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-NOV-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-717-243-11

QY 1 CACATGTAACAAAGACTTCATTGGC 28
    ||| ||||| ||||| ||||| |||||
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Db 303 CACAATTAAACAAGACTTCATTTGGC 330

RESULT 6

US-09-765-527-258

; Sequence 258, Application US/09765527

; Patent No. US20020006638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/765,527

; FILING DATE: 18-Jan-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 258:

SEQUENCE CHARACTERISTICS:

LENGTH: 955 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: CDS

LOCATION: 66..944

FEATURE:

NAME/KEY: misc feature

LOCATION: residues 1-65

OTHER INFORMATION: /label= EcoRI

/note="residues 1-65 comprise EcoRI site to beginning of pel B."

FEATURE:

NAME/KEY: misc feature

LOCATION: AA 1-22

OTHER INFORMATION: /label= pel B

/note="pel B is the leader sequence from the pectate lyase gene of Erwinia caratovora."

FEATURE:

NAME/KEY: misc feature

LOCATION: AA 23-273

OTHER INFORMATION: /label= "gelonin"

/note="gelonin (see U.S. Patent No. 5,416,202)."

FEATURE:

NAME/KEY: misc feature

LOCATION: AA 274-275

OTHER INFORMATION: /label= EagI

/note="EagI cloning site."

FEATURE:

NAME/KEY: misc feature

LOCATION: AA 276-279

OTHER INFORMATION: /label= cleavage linker

/note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage site."

FEATURE:

NAME/KEY: misc feature

LOCATION: AA 280-293

OTHER INFORMATION: /label= peptide sequence

/note="BPI-derived peptide."

FEATURE:

NAME/KEY: misc feature

LOCATION: residues 945-954

OTHER INFORMATION: /label= XhoI

/note="residues 945-955 comprise stop codon and XhoI site."

SEQUENCE DESCRIPTION: SEQ ID NO: 258:

US-09-765-527-258

Query Match 88.6%; Score 24.8; DB 9; Length 955;

Best Local Similarity 92.9%; Pred. No. 2.3;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAAGACTTCATTTGGC 28

Db 434 CACAATTAAACAAGACTTCATTTGGC 461

RESULT 7

US-09-765-527-252

; Sequence 252, Application US/09765527

; Patent No. US20020006638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/765,527

; FILING DATE: 18-Jan-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 1003 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: CDS

LOCATION: 66..992

FEATURE:

NAME/KEY: misc feature

LOCATION: residues 1-65

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/
/ OTHER INFORMATION: /label= EcoRI
/ /note="residues 1-65 comprise EcoRI site to beginning of pel
/ B."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 1-22
/ OTHER INFORMATION: /label= pel B
/ /note="pel B is the leader sequence from the pectate lyase
/ gene of Erwinia caratovora."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 23-273
/ OTHER INFORMATION: /label= "gelonin"
/ /note="gelonin (see U.S. Patent No. 5,416,202)."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 274-275
/ OTHER INFORMATION: /label= EagI
/ /note="EagI cloning site."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 276-279
/ OTHER INFORMATION: /label= cleavage linker
/ /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
/ site."
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/ NAME/KEY: misc feature
/ LOCATION: AA 280-309
/ OTHER INFORMATION: /label= peptide sequence
/ /note="BPI-derived peptide."
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: residues 993-1011
/ OTHER INFORMATION: /label= XhoI
/ /note="residues 993-1003 comprise stop codon and XhoI site."
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 252:
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/ US-09-765-527-252
/
/ Query Match 88.6%; Score 24.8; DB 9; Length 1003;
/ Best Local Similarity 92.9%; Pred. No. 2.3;
/ Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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/ QY 1 CACATGTAACAAAGACTTCATTTCGC 28
/ ||||| ||||| ||||| ||||| |||||
/ Db 434 CACATTAACAAAGACTTCATTTCGC 461
/
/ RESULT 8
/ US-09-765-527-250
/ Sequence 250, Application US/09765527
/ Patent No. US20020008638A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ TITLE OF INVENTION: Methods for Recombinant Microbial Production of
/ Fusion Proteins and BPI-Derived Peptides
/
/ NUMBER OF SEQUENCES: 265
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ ZIP: 60606-6402
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/765,527
/ FILING DATE: 18-Jan-2001
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/621,803
```

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/
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Borun, Michael F.
/ REGISTRATION NUMBER: 25,447
/ REFERENCE/DOCKET NUMBER: 27129/33199
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 25-3856
/
/ INFORMATION FOR SEQ ID NO: 250:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1072 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 66..1061
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: residues 1-85
/ OTHER INFORMATION: /label= EcoRI
/ /note="residues 1-65 comprise EcoRI site to beginning of pel
/ B."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 1-22
/ OTHER INFORMATION: /label= pel B
/ /note="pel B is the leader sequence from the pectate lyase
/ gene of Erwinia caratovora."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 23-273
/ OTHER INFORMATION: /label= "gelonin"
/ /note="gelonin (see U.S. Patent No. 5,416,202)."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 274-276
/ OTHER INFORMATION: /label= EagI
/ /note="EagI cloning site."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 277-296
/ OTHER INFORMATION: /label= SLT linker
/ /note="SLT from shiga-like-toxin gene."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 297-298
/ OTHER INFORMATION: /label= FspI/ScaI
/ /note="FspI and ScaI cloning sites."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 299-302
/ OTHER INFORMATION: /label= cleavage linker
/ /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
/ site."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: AA 303-332
/ OTHER INFORMATION: /label= peptide sequence
/ /note="BPI-derived peptide."
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: residues 1062-1072
/ OTHER INFORMATION: /label= XhoI
/ /note="residues 1062-1072 comprise stop codon and XhoI site."
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 250:
/
/ US-09-765-527-250
/
/ Query Match 88.6%; Score 24.8; DB 9; Length 1072;
/ Best Local Similarity 92.9%; Pred. No. 2.4;
/ Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; TITLE: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 705
; LENGTH: 11298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 M89796
; NAME/KEY: unsure
; LOCATION: (1)..(11298)
; OTHER INFORMATION: n = a or c or g or t
US-09-960-706-705

Query Match 71.4%; Score 20; DB 10; Length 11298;
Best Local Similarity 82.1%; Pred. No. 3.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CACATGTAAACCAAGACTTCATTGTC 28
Db 4423 CACATTGAAACCAAGACTTCATTGTC 4450

RESULT 15
US-10-424-599-12953/c
; Sequence 12953, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 12953
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_111702C.1
US-10-424-599-12953

Query Match 70.7%; Score 19.8; DB 18; Length 349;
Best Local Similarity 91.3%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CATGTAAACCAAGACTTCATTTT 25
Db 117 CACGAAAAACCAAGACTTCATTTT 95

Search completed: June 21, 2005, 17:45:18
Job time : 549 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 13:39:31 ; Search time 426 Seconds
(without alignments)
389.091 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACACAGACTTCATTTCGC 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	AAQ42253	PCR prime
2	24.8	88.6	813	AAQ48031	Encodes p
3	24.8	88.6	813	AAQ42253	Encodes p
4	24.8	88.6	813	AAQ75532	Type I ri
5	24.8	88.6	813	AAQ92342	Type I ri
6	24.8	88.6	955	AAT86336	BPI pepti
7	24.8	88.6	1003	AAT86341	BPI pepti
8	24.8	88.6	1072	AAT86332	BPI pepti
9	24.8	88.6	1176	ABSS6021	cDNA enco
10	24.8	88.6	1527	ABSS6029	DNA enco
11	20.6	73.6	38142	13 ABD32682	Abd32682 Mouse can
12	20.2	72.1	2103	8 ACPT73271	Acft73271 Staphyloc
13	20.2	72.1	2187	2 AAV74640	AAV74640 Staphyloc
14	20	71.4	11298	2 AAT86756	Human hig
15	20	71.4	11298	2 AAV54661	Human bet
16	20	71.4	11298	3 AAA34815	Human ade
17	20	71.4	11298	3 AAF20937	Human hig
18	20	71.4	11298	4 AAF92144	Human IGE
19	20	71.4	11298	10 AAB96631	Human hig
20	20	71.4	11298	11 ABD19056	Human hig

21	20	71.4	11357	2	AAQ51024	Human FCE
22	20	71.4	21742	3	AAQ34816	Human ade
23	20	71.4	21742	3	AAF20938	Human hig
24	20	71.4	21742	10	ABZ96632	Human hig
25	20	71.4	21742	11	ABD19051	Human hig
26	20	71.4	33030	5	AAF29337	Atopy rel
27	20	71.4	117608	10	ABZ97129	Human rec
28	20	71.4	117609	3	AAF21435	Human rec
29	20	71.4	117609	11	ABD17968	Human rec
C 30	19.8	70.7	1637	6	AAD43749	Human AGT
C 31	19.8	70.7	2361	6	AAD43751	Human AGT
C 32	19.8	70.7	2361	6	AAD43821	Human AGT
33	19.8	70.7	4102	6	AAI18667	Reference
34	19.8	70.7	4788	2	AAQ85367	MTP-1-1p
35	19.6	70.0	2349	8	ACF03675	Human Epn
36	19.6	70.0	2953	6	ABV78119	Human eph
37	19.6	70.0	2953	6	ABZ35695	Human eph
38	19.6	70.0	2953	6	ABX09938	Human eph
39	19.6	70.0	2953	6	ABL91660	Human pol
40	19.6	70.0	3132	2	AAQ34513	HEK codin
41	19.6	70.0	3149	3	AAA64458	cDNA enco
42	19.6	70.0	3149	8	ABZ34862	Coding se
43	19.6	70.0	3149	10	AAZ58484	Human rec
44	19.6	70.0	3149	10	ADB75272	Prostate
45	19.6	70.0	3149	11	ADN39283	Cancer/an

ALIGNMENTS

RESULT 1

AAQ42253
ID AAQ42253 standard; cDNA; 28 BP.

XX AAQ42253;

XX 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX PCR primer GeloC-20 to replace Ile103 of gelonin with Cys.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;

XX autoimmune disease; cell killing; toxin;

XX Mutagenic polymerase chain reaction; ss.

XX Synthetic.

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic

XX agents, immuno toxins for treating auto immune diseases, cancer, graft

XX versus host disease and selective cell killing in-vivo.

XX Example 3; Page 35; 163pp; English.

XX Fifteen analogues of gelonin were constructed. Ten non-cysteine residues

XX in surface positions and available for conjugation to a second protein

XX were targeted for substn. In the other analogues, one or both of the

XX native Cys residues present in gelonin were substd. Overlap extension PCR

XX was used to construct the various analogues. Primer GeloC-20 was used in

CC the substn. of ile103 of gelonin by Cys. (Updated on 25-MAR-2003 to
 CC correct PN field.)

SQ Sequence 28 BP; 10 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.046;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTGGC 28

Db 1 CACATGTAACAAACAGACTTCATTGGC 28

RESULT 2

AAQ48031

ID AAQ48031 standard; cDNA; 813 BP.

XX AC AAQ48031;

XX 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX Encodes plant type I RIP Gelonin.

DE Type I ribosome-inactivating protein; ricin; immunoconjugate;

KW autoimmune disease; cell killing; toxin; Euphorbiaceae family.

XX Gelonium multiflorum.

OS WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

PR 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

PA Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic

PT agents, immuno toxins for treating auto immune diseases, cancer, graft

PT versus host disease and selective cell killing in-vivo.

XX Claim 85; Page 114; 163pp; English.

XX The invention covers analogues of Type I RIPs. Gelonin is a Type I RIP

CC and the analogues of the invention have a cysteine available for

CC intermolecular disulphide bonding at an amino acid position corresp. to a

CC position not naturally available for bonding; the cys residue is located

CC in the C-terminal region of the analogue between a position corresp. to

CC amino acid 251 and the C-terminus of ricin A chain. The analogues are

CC pref. joined via a disulphide linkage to a molecule which specifically

CC binds to a target cell, e.g. an antibody fragment. See AAR37291 for

CC gelonin amino acid sequence. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX Sequence 813 BP; 266 A; 150 C; 182 G; 215 T; 0 U; 0 Other;

SQ Query Match 88.6%; Score 24.8; DB 2; Length 813;

Best Local Similarity 92.9%; Pred. No. 1.4;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTGGC 28

Db 303 CACAATTAACAAACAGACTTCATTGGC 330

RESULT 3

AAQ42222

ID AAQ42222 standard; cDNA; 813 BP.

XX AC AAQ42222;

XX 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX Encodes plant type I RIP Gelonin.

DE Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;

XX autoimmune disease; cell killing; toxin; Euphorbiaceae family; ss.

XX Gelonium multiflorum.

OS WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

PR 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

PA Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic

CC agents, immuno toxins for treating auto immune diseases, cancer, graft

CC versus host disease and selective cell killing in-vivo.

XX Claim 85; Page 101; 163pp; English.

XX Proteolytic peptide fragments of native gelonin were sequenced. PCR

CC primers were designed based on these peptide fragments. The primers were

CC used to amplify segments of cDNA covering the 5'-terminal, middle and 3'-

CC terminal regions of the gelonin coding sequence. A composite gelonin gene

CC sequence was assembled from the overlapping gelonin DNA fragments (see

CC AAQ42222). Having cloned the gelonin gene, the development of gelonin

CC analogues and gene fusions is facilitated. See AAR37291 for gelonin amino

CC acid sequence. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

SQ Query Match 88.6%; Score 24.8; DB 2; Length 813;

Best Local Similarity 92.9%; Pred. No. 1.4;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAACAGACTTCATTGGC 28

Db 303 CACAATTAACAAACAGACTTCATTGGC 330

RESULT 4

AAQ75532

ID AAQ75532 standard; cDNA; 813 BP.

XX AC AAQ75532;

XX 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I ribosome-inactivating protein gelonin cDNA.

DE Type I ribosome-inactivating proteins; RIPS; gelonin;

XX cytotoxic therapeutic agents; autoimmune disease; cancer;

XX graft-versus-host disease; ss.

XX Gelonium multiflorum.

OS


```

XX FH Key Location/Qualifiers
FT mat_peptide 1..810
FT /tag= a
FT /transl_except= pos:754..810
FT /note= "no corresponding amino acids"
XX WO9426910-A1.
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US005348.
XX
XX 12-MAY-1993; 93US-00064691.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Carroll SF, Studnicka GM;
XX WPI: 1995-006804/01.
XX P-PSDB; AAR63903.
XX
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins -- which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX Example 1; Page 155; 221pp; English.
XX
XX AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
XX gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
XX components of cytotoxic therapeutic agents (CTAs), which include gene
XX fusion products and immunoconjugates. CTAs may be used to selectively
XX eliminate any cell type to which a RIP component is targeted, by the
XX specific binding capacity of the second component of the agent. They can
XX be used in the treatment of diseases where the elimination of a
XX particular cell type is desired, such as autoimmune disease, cancer and
XX graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 1.4;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAAGACTTCATTTCGTC 28
DB 303 CACATGTAATAACAAGACTTCATTTCGTC 330

RESULT 5
AAQ92342
XX AAQ92342 standard; DNA; 813 BP.
XX
XX AC AAQ92342;
XX
XX 25-MAR-2003 (revised)
XX 01-JAN-1996 (first entry)
XX
XX Type I ribosome-inactivating protein gelonin gene.
XX
XX Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin; ss.
XX
XX Gelonium multiflorum.
XX
XX US5416202-A.
XX
XX 16-MAY-1995.
XX
XX 09-DEC-1992; 92US-00988430.
XX
XX 04-NOV-1991; 91US-00787567.
XX 19-JUN-1992; 92US-00901707.
XX
XX (XOMA ) XOMA CORP.
XX
XX Lei S, Carroll SF, Lane JA, Bernhard SL, Better MD;
XX WPI: 1995-193480/25.
XX
XX Polynucleotide(s) encoding gelonin analogues - having a cysteine residue
XX for intermolecular bonding for the prodn. of immuno-toxin(s).
XX
XX Example; Col 71-72; 66pp; English.
XX
XX Analogues of Type I RIP are defined as non-naturally occurring
XX polypeptides that share the ribosome-inactivating activity of the natural
XX protein but differ in AA sequence. Preferred analogues have a Cys
XX available for disulfide bonding located at a posn. it its AA sequence
XX from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy
XX terminus of the analogue. (AAR74176 is the sequence of the Type I RIPs
XX gelonin, BRIP, momordin II, luffin [see Islam et al. Agricultural
XX Biological Chem., 54(5) 1343-45 1991], alphatrichosanthin [see Chow et
XX al., J. Biol. Chem., 265, 8670-74 1990], momordin I [see Ho et al., BBA,
XX 1088, 311-14 1991], Mirabilis antiviral protein [see Habuka et al., J.
XX Biol. Chem., 264(12) 6629-37 1989], pokeweed antiviral protein isolated
XX from seeds [see Kung et al., Agric. Biol. Chem., 54(12), 3301-18 1990]
XX and saporin [see Banatti et al., Eur. J. Biochem., 183, 465-70 1989] are
XX individually aligned with the primary sequence of the ricin A-chain [see
XX Halling et al., Nucleic Acids Res., 13, 8019-8033 1985] respectively in
XX Figures 1-9. The AAs invariant among the ricin A-chain and the Type I
XX RIPs are indicated in FT. Also indicated are the preferred sites of Cys
XX substitution. It is also preferred that the gelonin cysteine residues at
XX positions 44 and 50 be replaced with alanine residues. The complete DNA
XX sequence of the gelonin gene is set out in AAQ92342. (Updated on 25-MAR-
XX 2003 to correct PR field.)
XX
XX Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 1.4;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAAGACTTCATTTCGTC 28
DB 303 CACATGTAATAACAAGACTTCATTTCGTC 330

RESULT 6
AAT86336
XX AAT86336 standard; DNA; 955 BP.
XX
XX AC AAT86336;
XX
XX 20-APR-1998 (first entry)
XX
XX BPI peptide fusion protein pING3797 vector construct.
XX
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
XX fungicidal; recombinant DNA; vector; ss.
XX
XX Synthetic.
XX Pectobacterium carotovorum.
XX Homo sapiens.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX misc_signal 1..22
XX /tag= a
XX /label= pel_B
XX /standard_name= "Leader"
XX /note= "pel B is the leader sequence from the pectate
XX lyase gene of Erwinia caratovora"
XX misc_feature 23..273
XX /tag= b
XX /label= gelonin
XX

```

```

FT CDS /note= "gelonin - see U.S. Patent No. 5,416,202"
FT 66..944
FT /*tag= c
FT misc_feature 274..275
FT /*tag= d
FT /label= EagI
FT /note= "EagI cloning site"
FT 276..279
FT /*tag= g
FT /label= cleavage linker
FT /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
FT cleavage site"
FT 280..293
FT /*tag= h
FT /label= peptide sequence
FT /note= "BPI-derived peptide"
XX
PN WO9735009-A1.
XX
XX 25-SEP-1997.
PD
XX 18-MAR-1997; 97WO-US005287.
PF
XX 22-MAR-1996; 96US-00621803.
PR
XX (XOMA ) XOMA CORP.
PA
XX Better MD;
PI
XX WPI; 1997-480215/44.
DR
XX P-PSDB; AAW29300.
DR
XX Recombinant production of bactericidal/permeability increasing protein -
PT by expression as a fusion protein in microbial host cells, then cleaving
PT the BPI peptide from the carrier.
XX
XX Example 1; Page 160-161; 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
CC fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents the pING3797
CC vector construct coding for a BPI fusion protein. The peptides have many
CC uses including the treatment of bacterial and fungal infections. BPI
CC peptides also bind to endotoxins and heparin, neutralising their effects.
CC The peptides have further been shown to inhibit angiogenesis (partly due
CC to heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the indirect
CC production of anti-microbial BPI peptides in microbial hosts
XX
SQ Sequence 955 BP; 307 A; 189 C; 216 G; 243 T; 0 U; 0 Other;
Query Match 88.6%; Score 24.8; DB 2; Length 955;
Best Local Similarity 92.9%; Pred. No. 1.4;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CACATGTATAAACAAAGACTTCATTGTGGC 28
Db 434 CACATTATAAACAAAGACTTCATTGTGGC 461
RESULT 7
ID AAT86341
ID AAT86341 standard; DNA; 1003 BP.
XX
AC AAT86341;
XX
XX 20-APR-1998 (first entry)
DT
XX BPI peptide fusion protein pING3795 vector construct.
DE

```

```

XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW fungicidal; recombinant DNA; vector; ss.
XX
OS Synthetic.
OS Pectobacterium carotovorum.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT misc_signal 1..22
FT /*tag= a
FT /label= pel B
FT /standard_name= "Leader"
FT /note= "pel B is the leader sequence from the pectate
FT lyase gene of Erwinia caratovora"
FT 23..273
FT misc_feature
FT /*tag= b
FT /label= gelonin
FT /note= "gelonin - see U.S. Patent No. 5,416,202"
FT 56..992
FT /*tag= c
FT 274..275
FT /*tag= d
FT /label= EagI
FT /note= "EagI cloning site"
FT 276..279
FT /*tag= g
FT /label= cleavage linker
FT /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
FT cleavage site"
FT 280..309
FT /*tag= h
FT /label= peptide sequence
FT /note= "BPI-derived peptide"
XX
XX WO9735009-A1.
PN
XX 25-SEP-1997.
PD
XX 18-MAR-1997; 97WO-US005287.
PF
XX 22-MAR-1996; 96US-00621803.
PR
XX (XOMA ) XOMA CORP.
PA
XX Better MD;
PI
XX WPI; 1997-480215/44.
DR
XX P-PSDB; AAW29303.
DR
XX Recombinant production of bactericidal/permeability increasing protein -
PT by expression as a fusion protein in microbial host cells, then cleaving
PT the BPI peptide from the carrier.
XX
XX Example 1; Page 152-153; 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
CC fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents the pING3795
CC vector construct coding for a BPI fusion protein. The peptides have many
CC uses including the treatment of bacterial and fungal infections. BPI
CC peptides also bind to endotoxins and heparin, neutralising their effects.
CC The peptides have further been shown to inhibit angiogenesis (partly due
CC to heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the indirect
CC production of anti-microbial BPI peptides in microbial hosts
XX

```

SQ Sequence 1003 BP; 325 A; 194 C; 227 G; 257 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 1003;
 Best Local Similarity 92.9%; Pred. No. 1.4;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACATGTAACAAAGACTTCATTTGGC 28
 |||||
 Db 434 CACAATTAACAAAGACTTCATTTGGC 461

RESULT 8
 AAT86332
 ID AAT86332 standard; DNA; 1072 BP.
 AC AAT86332;
 DT 20-APR-1998 (first entry)
 DE BPI peptide fusion protein PING3793 vector construct.
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector; ss.
 OS Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.

XX Key Location/Qualifiers
 FT misc_signal 1..22
 FT /tag= a
 FT /label= pel B
 FT /standard name= "Leader"
 FT /note= "pel B is the leader sequence from the pectate
 FT lyase gene of Erwinia caratovora"
 FT 23..273
 FT /tag= b
 FT /label= gelonin
 FT /note= "Gelonin - see U.S. Patent No. 5,416,202"
 FT 66..1064
 FT /tag= c
 FT /tag= c
 FT 274..276
 FT /tag= d
 FT /label= EagI
 FT /note= "EagI cloning site"
 FT 277..296
 FT /tag= e
 FT /label= SLT linker
 FT /note= "SLT from shiga-like-toxin gene"
 FT 297..298
 FT /tag= f
 FT /label= FspI/ScaI
 FT /note= "FspI and ScaI cloning sites"
 FT 299..302
 FT /tag= g
 FT /label= cleavage linker
 FT /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
 FT cleavage site"
 FT 303..332
 FT /tag= h
 FT /label= peptide sequence
 FT /note= "BPI-derived peptide"

XX WO9735009-A1.
 XX 25-SEP-1997.
 XX 18-MAR-1997; 97WO-US005287.
 XX 22-MAR-1996; 96US-00621803.

PA (XOMA) XOMA CORP.
 PI Better MD;
 DR WPI; 1997-480215/44.
 DR P-PSDB; AAW29294.
 XX Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX
 PS Example 1; Page 148-150; 186pp; English.
 CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the PING3793
 CC vector construct coding for a BPI fusion protein. The peptides have many
 CC uses including the treatment of bacterial and fungal infections. BPI
 CC peptides also bind to endotoxins and heparin, neutralising their effects.
 CC The peptides have further been shown to inhibit angiogenesis (partly due
 CC to heparin-binding activity). The fusion proteins have been found to be
 CC expressed in large amounts without significant proteolysis, and in some
 CC cases are actually secreted from the host cells. This allows the indirect
 CC production of anti-microbial BPI peptides in microbial hosts
 XX
 SQ Sequence 1072 BP; 340 A; 210 C; 244 G; 278 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 1072;
 Best Local Similarity 92.9%; Pred. No. 1.4;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACATGTAACAAAGACTTCATTTGGC 28
 |||||
 Db 434 CACAATTAACAAAGACTTCATTTGGC 461

RESULT 9
 ABS56021
 ID ABS56021 standard; cDNA; 1176 BP.
 XX
 AC ABS56021;
 XX
 DT 08-JAN-2003 (first entry)
 DE
 DE cDNA encoding G. multiflorum recombinant gelonin (rGel) toxin.
 XX Modified protein; reduced antigenicity; modified toxin; gelonin;
 KW designer toxin; immunotoxin; proteinaceous compound; cancer;
 KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
 KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
 KW inflammatory disease; cardiovascular disease; diabetes;
 KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
 KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
 KW recombinant gelonin; rGel; gene; ss.
 XX
 OS Gelonium multiflorum.
 XX
 PH Key Location/Qualifiers
 FT CDS 24..974
 FT /tag= a
 FT /product= "rGel"

XX WO200269886-A2.
 XX 12-SEP-2002.
 XX 12-FEB-2002; 2002WO-US004195.
 XX 12-FEB-2001; 2001US-0268402P.
 XX


```
KW leukaemia; lymphoma; CAP.
XX Mus musculus.
OS WO2004074320-A2.
XX 02-SEP-2004.
XX 17-FEB-2004; 2004WO-US004730.
XX 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Morris DW, Malandro MS;
XX WPI; 2004-652914/63.
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX disclosure; seqid 236; 310pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 38142 BP; 10396 A; 8310 C; 8130 G; 10863 T; 0 U; 443 Other;
Query Match 73.6%; Score 20.6; DB 13; Length 38142;
Best Local Similarity 85.2%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CACATGTAACAAAGACTTCATTG 27
DB 16568 CAGATGTAACAAAGACTTCAGTGTG 16594
```

```
RESULT 12
ACF73271
ID ACF73271 standard; DNA; 2103 BP.
XX
AC ACF73271;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus DNA #951.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target; gene; ds.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
DR P-PSDB; ABW71711.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
XX S. aureus, e.g. sepsis.
PS Claim 6; SEQ ID NO 1901; 49pp; English.
XX
CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus genes of the invention
XX
SQ Sequence 2103 BP; 786 A; 330 C; 271 G; 716 T; 0 U; 0 Other;
Query Match 72.1%; Score 20.2; DB 8; Length 2103;
Best Local Similarity 88.0%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTAACAAAGACTTCATT 25
DB 1838 CAGACGTAACAAAGACTTCATT 1862
RESULT 13
AAV74640
ID AAV74640 standard; DNA; 2187 BP.
XX
AC AAV74640;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus contig SEQ ID #329.
XX
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX
```


CC (nucleotide 6843 in the Fc epsilon RI beta gene sequence of Kuster, et
al. 1992). Detection of the protein is useful for diagnosis of atopy. In
particular the E273G polymorphism may also define a subgroup of asthma
sufferers with a particular clinical course, in which case recognition of
the variant/polymorphism would be of value in defining asthma prognosis
and management. NB. This sequence was created using the sequence given in
Genbank M89796

XX
SQ Sequence 11298 BP; 3469 A; 2113 C; 2284 G; 3415 T; 0 U; 17 Other;
Query Match 71.4%; Score 20; DB 2; Length 11298;
Best Local Similarity 82.1%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGTGGC 28
Db 4423 CACATTGAAACAAGAACTCATTGTGGC 4450

RESULT 15
AAV54661
ID AAV54661 standard; DNA; 11298 BP.
XX AC AAV54661;
XX AC
DT 13-NOV-1998 (first entry)
XX DE Human beta subunit of Fc epsilon RI coding sequence.
XX DE Human beta subunit of Fc epsilon RI; ARAM; Fc epsilon RI beta chain;
KW antigen recognition activation motif; human beta subunit; allergy;
KW high-affinity immunoglobulin E receptor; ds.
XX OS Homo sapiens.

XX FH Location/Qualifiers
FH CDS 456..7322
FT /*tag= a
FT /product= "human Fc epsilon RI beta chain"
FT /note= "contains introns"
FT exon 456..511
FT /*tag= b
FT /*number= 1
FT intron 512..1380
FT /*tag= c
FT /*number= 1
FT exon 1381..1510
FT /*tag= d
FT /*number= 2
FT intron 1511..2025
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FT /*tag= q
XX US5807988-A.
XX 15-SEP-1998.
XX 24-FEB-1994; 94US-00201879.
XX 16-APR-1992; 92US-00869933.
XX 16-APR-1993; 93WO-US003419.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Jouvin M, Kinet J;
XX WPI; 1998-520207/44.
XX P-PSDB; AAW75918.
XX Human IgE receptor beta subunit protein - and corresponding peptide(s)
XX Human IgE receptor beta subunit protein.
XX Example; Fig 2A-Q; 55pp; English.
XX This represents the coding sequence of a human beta subunit of Fc epsilon
RI [high-affinity immunoglobulin E receptor]. The invention provides a
peptide fragment (AAW75917) from the human Fc epsilon RI beta subunit
protein that contains the amino acid sequence of an ARAM [antigen
recognition activation motif]. Aspects of the invention are methods and
compositions to inhibit the function of human beta subunit, thereby
treating or preventing allergic reactions

XX SQ Sequence 11298 BP; 3470 A; 2113 C; 2283 G; 3415 T; 0 U; 17 Other;
Query Match 71.4%; Score 20; DB 2; Length 11298;
Best Local Similarity 82.1%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGTGGC 28
Db 4423 CACATTGAAACAAGAACTCATTGTGGC 4450

Search completed: June 21, 2005, 14:49:08
Job time : 433 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 14:23:52 ; Search time 3127 Seconds
(without alignments)
340.838 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACACAGACTTCATTTTGGC 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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2	21.6	77.1	835	9 CNS03C2M AL237271 Tetraodon
3	21.6	77.1	1013	8 CC279684 CH261-76J
4	21.6	77.1	1128	8 CC214234 CH261-74J
5	21.2	75.7	834	7 CO646793 ILLUMIGEN
6	21.2	75.7	942	3 AY066661 Schmidt
7	20.8	74.3	464	2 BE581909 K56C05.y
8	20.8	74.3	642	9 BX199941 Danio rer
9	20.8	74.3	652	9 CE147952 tigr-gss-
10	20.6	73.6	546	8 BH341834 CH230-64E
11	20.6	73.6	576	7 CN951902 Ha mx0.53
12	20.6	73.6	598	5 BX859292 EX859292
13	20.6	73.6	659	9 CR033848 Forward s
14	20.6	73.6	725	7 CN949957 Ha mx0.27
15	20.6	73.6	759	8 BZ462328 BOCAA76TR
16	20.6	73.6	768	4 BG921708 602825533
17	20.6	73.6	789	8 AQ049899 nbxb0003a
18	20.2	72.1	443	1 AV887297 AV887297
19	20.2	72.1	456	2 AV998061 AV998061
20	20.2	72.1	529	4 BG949978 PM2-BN013
21	20.2	72.1	556	6 CD665396 EtESTeg43
22	20.2	72.1	875	9 CNS02S80 Tetraodon
23	20.2	72.1	880	9 CL677144 PRI011cB
24	20.2	72.1	882	8 BZ229732 CH230-527

C 25	20	71.4	361	4	BG627700	cc-esf1cL
C 26	20	71.4	396	7	CO081295	GR_Ra45E
C 27	20	71.4	407	4	B1512446	B1512446 B1512446
C 28	20	71.4	466	4	B1511101	B1511101 B1511101
C 29	20	71.4	494	1	A1432231	th43c06.x
C 30	20	71.4	555	2	BF567678	UI-R-BOO-
C 31	20	71.4	555	7	CO099633	GR_Ra24K
C 32	20	71.4	651	7	CO094320	GR_Ra16F
C 33	20	71.4	663	4	BG127096	EST472742
C 34	20	71.4	688	7	CO091583	GR_Ra12C
C 35	20	71.4	851	5	BU411188	603153922
C 36	20	71.4	912	9	CE254446	Forward s
C 37	19.8	70.7	669	9	CE532287	tigr-gss-
C 38	19.8	70.7	782	7	CF147787	AGENCOURT
C 39	19.8	70.7	1015	6	CD248979	AGENCOURT
C 40	19.6	70.0	253	7	D79387	HUM237A04B
C 41	19.6	70.0	415	9	CW510328	Cot678 H1
C 42	19.6	70.0	421	9	CW510671	Cot678 H1
C 43	19.6	70.0	464	5	BP084435	BP084435
C 44	19.6	70.0	502	7	CK889633	SGP149855
C 45	19.6	70.0	528	5	BX299737	BX299737

ALIGNMENTS

RESULT 1
BX992195
LOCUS
DEFINITION BX992195 540 bp DNA linear GSS 05-JUL-2004
Forward strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPP232j24, genomic survey sequence.
ACCESSION BX992195
VERSION BX992195.1 GI:49723653
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 540)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
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/db_xref="taxon:10090"
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ORIGIN

Query Match 79.3%; Score 22.2; DB 9; Length 540;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTAAACACAGACTTCATTTTGG 27
DB 275 CACATGTAGCACAGACTTCATTTTGG 301

RESULT 2

CNS03C2M
LOCUS
DEFINITION CNS03C2M 835 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
013B17 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL237271
VERSION AL237271.1 GI:7896406
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis

RESULT 6
AY0666661/C

Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
NIAD, NIH (tnutman@nih.gov). DNA sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 262.
Location/Qualifiers

FEATURES

source
1. .464
/organism="Strongyloides stercoralis"
/mol_type="mrna"
/strain="Rhabbitiform larvae obtained from gerbils"
/db_xref="taxon:6248"
/lab_host="XL-1 Blue MRF" (Stratagene)"
/clone_lib="TM95TM-SSR"
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1:
EcoRI; Site 2: XhoI; mRNA was purified from 2 x 10E3
rhabbitiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the EcoRI site to the XhoI site. The library
has an unamplified titer of 1 x 10E5 pfu/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
average insert size of the unamplified library is 675 bp
(range, 100-1700)."

ORIGIN

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Best Local Similarity 91.7%; Pred. No. 7.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACACAGACTTCATTGG 27
DB 109 ATGTAAACACAGACTTCCTTTGG 132

RESULT 8
EX199941/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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/db_xref="taxon:7955"
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/note="vector pIndigoBAC-536"

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Best Local Similarity 91.7%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAAACACAGACTTCATT 24

DB 308 CACATGTAAACACAGACTTCATT 285

RESULT 9
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LOCUS
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KEYWORDS
SOURCE
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REFERENCE
AUTHORS
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MEDLINE
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/note="Site 1: BstXI; Libraries were prepared from
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Best Local Similarity 91.7%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACACAGACTTCATTGG 27
DB 309 ATGTAAACACAGACTTAATTGG 286

RESULT 10
BH341834
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ACCESSION
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KEYWORDS
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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1. .546
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/db_xref="taxon:10116"
/tissue type="Testis"
/note="vector pIndigoBAC-536"

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Best Local Similarity 91.7%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAAACACAGACTTCATT 24

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
749.998 Million cell updates/sec

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Perfect score: 28
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	100.0	28	6	AR010103
3	28	100.0	28	6	AR05309
4	28	100.0	28	6	AR141238
5	28	100.0	28	6	AR141475
6	28	100.0	28	6	I11949
7	28	100.0	28	6	I40520
8	28	100.0	28	6	AR368004
9	28	100.0	28	6	AR430985
10	24.8	88.6	813	6	AR003721
11	24.8	88.6	813	6	AR010057
12	24.8	88.6	813	6	AR05263
13	24.8	88.6	813	6	AR067747
14	24.8	88.6	813	6	AR141192
15	24.8	88.6	813	6	AR141429
16	24.8	88.6	813	6	AR164985
17	24.8	88.6	813	6	I11901
18	24.8	88.6	813	6	I11947
19	24.8	88.6	813	6	I40474

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21	24.8	88.6	813	6	AR430939	AR430939 Sequence	
22	24.8	88.6	955	6	AR067753	AR067753 Sequence	
23	24.8	88.6	955	6	AR164991	AR164991 Sequence	
24	24.8	88.6	1003	6	AR067750	AR067750 Sequence	
25	24.8	88.6	1003	6	AR164988	AR164988 Sequence	
26	24.8	88.6	1072	6	AR067749	AR067749 Sequence	
27	24.8	88.6	1072	6	AR164987	AR164987 Sequence	
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c	29	22.2	79.3	243191	2	AC098147	AC098147 Rattus no
30	22.2	79.3	251066	2	AC118400	AC118400 Rattus no	
31	21.8	77.9	110000	1	BX571856	Continuation (26 o	
32	21.6	77.1	150467	9	AC009541	Continuation (26 o	
c	33	21.6	77.1	172237	9	AC083869	AC009541 Human Chr
c	34	21.6	77.1	174775	5	BX284691	AC083869 Homo sapi
c	35	21.2	75.7	120870	2	AC149582	BX284691 Zebrafish
c	36	21.2	75.7	245377	2	AC095875	AC149582 Medicago
c	37	21.2	75.7	288636	2	AC130903	AC095875 Rattus no
38	21.2	75.7	293867	2	AC130587	AC130903 Rattus no	
39	20.8	74.3	714	11	PM4B2G	AC130587 Rattus no	
40	20.8	74.3	153572	5	BX323992	AL685801 Penicilli	
41	20.8	74.3	168773	10	AL731820	BX323992 Zebrafish	
c	42	20.8	74.3	177468	5	AL953916	AL731820 Mouse DNA
43	20.8	74.3	178425	5	BX255912	AL953916 Zebrafish	
c	44	20.8	74.3	194220	5	BX571880	BX255912 Zebrafish
c	45	20.8	74.3	208974	2	AC129625	BX571880 Zebrafish
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ALIGNMENTS

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DEFINITION	AR003767	Sequence 59 from patent US 5744580.	28 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR003767	Sequence 59 from patent US 5744580.	28 bp	DNA	linear	PAT 04-DEC-1998
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SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 28)					
AUTHORS	Better,M.D., Carroll,S.F. and Studnicka,G.M.					
TITLE	Immunotoxins comprising ribosome-inactivating proteins					
JOURNAL	Patent: US 5744580-A 59 28-APR-1998;					
FEATURES	Location/Qualifiers					
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DEFINITION	AR010103	Sequence 59 from patent US 5756699.	28 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR010103	Sequence 59 from patent US 5756699.	28 bp	DNA	linear	PAT 04-DEC-1998
VERSION	AR010103.1	GI:3968908				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 28)					
AUTHORS	Better,M.D., Carroll,S.F. and Studnicka,G.M.					
TITLE	Immunotoxins comprising ribosome-inactivating proteins					

JOURNAL Patent: US 5756699-A 59 26-MAY-1998;
FEATURES Location/Qualifiers
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LOCUS 28 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 59 from patent US 5837491.
ACCESSION AR055309
VERSION AR055309.1 GI:5980886
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better M.D., Carroll, S.F. and Studnicka, G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 59 17-NOV-1998;
FEATURES Location/Qualifiers
source
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CACATGTAACAAGACTTCATTGGC 28
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RESULT 4
AR141238
LOCUS 28 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6146631.
ACCESSION AR141238
VERSION AR141238.1 GI:15100755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better M.D., Carroll, S.F. and Studnicka, G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 6146631-A 59 14-NOV-2000;
FEATURES Location/Qualifiers
source
ORIGIN
Query Match 100.0%; Score 28; DB 6; Length 28;
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CACATGTAACAAGACTTCATTGGC 28
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RESULT 5
AR141475
LOCUS 28 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6146850.
ACCESSION AR141475
VERSION AR141475.1 GI:15100991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better M.D. and Carroll, S.F.
TITLE Proteins encoding gelonin sequences
JOURNAL Patent: US 6146850-A 59 14-NOV-2000;
FEATURES Location/Qualifiers
source
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Best Local Similarity 100.0%; Pred. No. 0.36; 0; Indels 0; Gaps 0;
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RESULT 6
I11949
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DEFINITION Sequence 61 from Patent US 5416202.
ACCESSION I11949
VERSION I11949.1 GI:909392
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Bernhardt, S.L., Better, M.D., Carroll, S.F., Lane, J.A. and Lei, S.-P.
TITLE Materials comprising and methods of preparation and use for ribosome-inactivating proteins
JOURNAL Patent: US 5416202-A 61 16-MAY-1995;
FEATURES Location/Qualifiers
source
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Best Local Similarity 100.0%; Pred. No. 0.36; 0; Indels 0; Gaps 0;
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Db 1 CACATGTAACAAGACTTCATTGGC 28
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LOCUS 28 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 59 from patent US 5621083.
ACCESSION I40520
VERSION I40520.1 GI:2082812
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better, M.D., Carroll, S.F. and Studnicka, G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins

JOURNAL Patent: US 5621083-A 59 15-APR-1997;
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RESULT 8
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LOCUS 28 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 59 from patent US 6376217.
ACCESSION AR368004
VERSION AR368004.1 GI:34601515
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D. and Carroll,S.F.
TITLE Fusion proteins and polynucleotides encoding gelonin sequences
JOURNAL Patent: US 6376217-A 59 23-APR-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN

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LOCUS 28 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 59 from patent US 6649742.
ACCESSION AR430985
VERSION AR430985.1 GI:40192816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 6649742-A 59 18-NOV-2003;
FEATURES Location/Qualifiers
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Db 1 CACATGTAACAAAGACTTCATTTCGC 28

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DEFINITION Sequence 11 from patent US 5744580.
ACCESSION AR003721
VERSION AR003721.1 GI:3964980
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 813)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5744580-A 11 28-APR-1998;
FEATURES Location/Qualifiers
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ORIGIN

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DEFINITION Sequence 11 from patent US 5756699.
ACCESSION AR010057
VERSION AR010057.1 GI:3968862
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 813)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 11 26-MAY-1998;
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ORIGIN

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DEFINITION Sequence 11 from patent US 5837491.
ACCESSION AR055263
VERSION AR055263.1 GI:5980840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 813)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 11 17-NOV-1998;

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Db 303 CACAATTAAACAACAGACTTCATTTTGGC 330

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DEFINITION Sequence 11 from patent US 6146631.
ACCESSION AR141192
VERSION AR141192.1 GI:15100709
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 813)
TITLE Better,M.D., Carroll,S.F. and Studnicka,G.M.
        Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 6146631-A 11 14-NOV-2000;
FEATURES Location/Qualifiers
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Best Local Similarity 92.9%; Pred. No. 5.7;
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Db 303 CACAATTAAACAACAGACTTCATTTTGGC 330

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GenCore version 5.1.6
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50.610 Million cell updates/sec

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Perfect score: 100

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Maximum DB seq length: 20

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	100	100.0	20	1 US-08-477-484B-57	Sequence 57, Appl
5	100	100.0	20	2 US-08-646-360-57	Sequence 57, Appl
6	100	100.0	20	3 US-08-839-765-57	Sequence 57, Appl
7	100	100.0	20	3 US-09-136-389-57	Sequence 57, Appl
8	100	100.0	20	3 US-09-610-838-57	Sequence 57, Appl
9	100	100.0	20	4 US-09-711-485-57	Sequence 57, Appl
10	100	100.0	20	5 PCT-US92-09487-59	Sequence 59, Appl
11	33	33.0	15	3 US-09-053-003-6	Sequence 6, Appl
12	33	33.0	15	4 US-09-818-094-6	Sequence 15, Appl
13	33	33.0	15	4 US-10-092-138A-15	Sequence 15, Appl
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15	31.5	31.5	20	4 US-09-636-215-494	Sequence 494, App
16	31.5	31.5	20	4 US-09-685-166A-494	Sequence 494, App
17	31.5	31.5	20	4 US-09-679-426-494	Sequence 494, App
18	31.5	31.5	20	4 US-09-759-143-494	Sequence 494, App
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21	31	31.0	14	5 PCT-US95-13794-2	Sequence 2, Appl
22	31	31.0	15	1 US-08-276-099A-10	Sequence 10, Appl
23	31	31.0	15	1 US-08-781-890-10	Sequence 10, Appl
24	30	30.0	10	3 US-09-291-803-18	Sequence 18, Appl
25	30	30.0	10	4 US-09-860-276-18	Sequence 18, Appl
26	30	30.0	10	4 US-09-860-395-18	Sequence 18, Appl
27	30	30.0	16	4 US-10-158-847-65	Sequence 65, Appl

28 30 30.0 19 4 US-09-441-502B-48 Sequence 48, Appl
29 30 30.0 20 3 US-08-467-023-44 Sequence 44, Appl
30 29 29.0 13 4 US-10-053-485-49 Sequence 49, Appl
31 29 29.0 18 3 US-08-390-353A-8 Sequence 8, Appl
32 29 29.0 18 4 US-09-101-059-8 Sequence 8, Appl
33 28 28.0 9 3 US-09-339-511-3 Sequence 3, Appl
34 28 28.0 12 2 US-09-066-227-5 Sequence 5, Appl
35 28 28.0 12 2 US-08-823-143-5 Sequence 5, Appl
36 28 28.0 12 4 US-09-410-889-3 Sequence 3, Appl
37 28 28.0 19 4 US-09-441-502B-20 Sequence 20, Appl
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39 27 27.0 10 2 US-08-436-772-25 Sequence 25, Appl
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42 27 27.0 10 3 US-09-291-803-17 Sequence 17, Appl
43 27 27.0 10 4 US-09-860-276-17 Sequence 17, Appl
44 27 27.0 10 4 US-09-860-395-17 Sequence 17, Appl
45 27 27.0 12 4 US-09-914-259-178 Sequence 178, App

ALIGNMENTS

RESULT 1

US-07-988-430-59

; Sequence 59, Application US/07988430

; Patent No. 5416202

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Lane, Julie A.

; APPLICANT: Lei, Shau-Ping

; TITLE OF INVENTION: Materials Comprising and Methods of

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/988,430

; FILING DATE: 19921209

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: NO. 5416202and, Greta E.

; REGISTRATION NUMBER: 35302

; REFERENCE/DOCKET NUMBER: 31133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

;
US-07-988-430-59

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSFNHAY 20
|||||

DB 1 PSGQAGAAASLSLFSFNHAY 20
|||||

RESULT 2

US-08-425-336-57
; Sequence 57, Application US/08425336
; Patent No. 5621083

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-425-336-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSFNHAY 20
|||||

DB 1 PSGQAGAAASLSLFSFNHAY 20
|||||

RESULT 3

US-08-488-113B-57

; Sequence 57, Application US/08488113B
; Patent No. 5744580

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-488-113B-57

Query Match 100.0%; Score 100; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSFNHAY 20
|||||

DB 1 PSGQAGAAASLSLFSFNHAY 20
|||||

RESULT 4

US-08-477-484B-57

; Sequence 57, Application US/08477484B
; Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-484B-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 5
US-08-646-360-57
Sequence 57, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-360-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 6
US-08-839-765-57
Sequence 57, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70. P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-839-765-57

Query Match 100.0%; Score 100; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
DB 1 PSGQAGAAASESLFISNHAY 20

RESULT 7
US-09-136-389-57
; Sequence 57, Application US/09136389
; Patent No. 614650
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389

/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-136-389-57

Query Match 100.0%; Score 100; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
DB 1 PSGQAGAAASESLFISNHAY 20

RESULT 8
US-09-610-838-57
; Sequence 57, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389

;/ FILING DATE: 18-AUG-1998
;/ APPLICATION NUMBER: 08/646,360
;/ FILING DATE: 13-MAY-1996
;/ APPLICATION NUMBER: PCT/US94/05348
;/ FILING DATE: 12-MAY-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/064,691
;/ FILING DATE: 12-MAY-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/988,430
;/ FILING DATE: 09-DEC-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/901,707
;/ FILING DATE: 19-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/787,567
;/ FILING DATE: 04-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: McNicholas, Janet M.
;/ REGISTRATION NUMBER: 32,918
;/ REFERENCE/DOCKET NUMBER: 200-70-P4
;/ TELEPHONE: 312/707-8889
;/ TELEFAX: 312/707-9155
;/ TELEX: 650 388-1248
;/ INFORMATION FOR SEQ ID NO: 57:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-09-610-838-57

Query Match 100.0%; Score 100; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
DB 1 PSGQAGAAASESLFISNHAY 20

RESULT 9

US-09-711-485-57
; Sequence 57, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: US 08/064,691
;/ FILING DATE: 12-MAY-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/988,430
;/ FILING DATE: 09-DEC-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/901,707
;/ FILING DATE: 19-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/787,567
;/ FILING DATE: 04-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: McNicholas, Janet M.
;/ REGISTRATION NUMBER: 32,918
;/ REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
;/ TELEPHONE: 312/707-8889
;/ TELEFAX: 312/707-9155
;/ TELEX: 650 388-1248
;/ INFORMATION FOR SEQ ID NO: 57:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-09-711-485-57

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
DB 1 PSGQAGAAASESLFISNHAY 20

RESULT 10

PCT-US92-09487-59
; Sequence 59, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09487-59

Query Match 100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 11
US-09-053-003-6
Sequence 6, Application US/09053003
Patent No. 6207391
GENERAL INFORMATION:
APPLICANT: Wu, Pengguang
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 018781-0008000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = phosphotyrosine"
US-09-053-003-6

Query Match 33.0%; Score 33; DB 3; Length 15;
Best Local Similarity 53.8%; Pred. No. 35;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESL 13
Db 2 PPGEAGXKAFSSL 14

RESULT 12
US-09-818-094-6
Sequence 6, Application US/09818094
Patent No. 6682898
GENERAL INFORMATION:
APPLICANT: Wu, Pengguang
McKinney, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
Modulators of STAT4 and STAT6 Activity
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,094
FILING DATE: 26-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/053,003
FILING DATE: 31-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 018781-0008000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = phosphotyrosine"
US-09-818-094-6

Query Match 33.0%; Score 33; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESL 13
Db 2 PPGEAGXKAFSSL 14

RESULT 13
US-10-092-138A-15
Sequence 15, Application US/10092138A
Patent No. 6743630
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki

; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; FILE REFERENCE: 65823/JPW/PT
; CURRENT APPLICATION NUMBER: US/10/092,138A
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:source:synthesized
US-10-092-138A-15

Query Match 33.0%; Score 33; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 ASESFLFSN 17
||| |||:
DB 4 ASEFLFSN 12

RESULT 14
US-09-439-313-494
; Sequence 494, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 494
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-494

Query Match 31.5%; Score 31.5; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 GQAGAAASE-SLFIS 16
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DB 6 GDTGGASSEDLSLMS 20

RESULT 15
US-09-636-215-494
; Sequence 494, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 494
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-636-215-494

Query Match 31.5%; Score 31.5; DB 4; Length 20;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 GQAGAAASE-SLFIS 16
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DB 6 GDTGGASSEDLSLMS 20

Search completed: June 20, 2005, 10:59:07
Job time : 30.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:46:29 ; Search time 104 Seconds
(without alignments)
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Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PFGQAGAAASLFTSNHAY 20

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Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	100	100.0	20	17	US-10-717-243-57 Sequence 57, Appl
3	38	38.0	7	14	US-10-022-066-40 Sequence 40, Appl
4	38	38.0	7	14	US-10-022-066-141 Sequence 141, Appl
5	38	38.0	7	14	US-10-022-066-443 Sequence 443, Appl
6	33	33.0	15	8	US-08-681-219-17 Sequence 17, Appl
7	33	33.0	15	9	US-09-818-094-6 Sequence 6, Appl
8	33	33.0	15	10	US-09-230-111C-15 Sequence 15, Appl
9	33	33.0	15	14	US-10-092-138-15 Sequence 15, Appl
10	33	33.0	15	16	US-10-820-403-15 Sequence 15, Appl
11	32	32.0	15	16	US-10-318-397-15 Sequence 15, Appl

12	32	32.0	15	16	US-10-317-747-15 Sequence 15, Appl
13	31.5	31.5	20	9	US-09-759-143-494 Sequence 494, Appl
14	31.5	31.5	20	9	US-09-780-663-494 Sequence 494, Appl
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18	31.5	31.5	20	13	US-10-012-896-494 Sequence 494, Appl
19	31.5	31.5	20	14	US-10-010-940-494 Sequence 494, Appl
20	31.5	31.5	20	14	US-10-144-678A-494 Sequence 494, Appl
21	31.5	31.5	20	14	US-10-294-025-494 Sequence 494, Appl
22	31	31.0	20	16	US-10-425-115-192880 Sequence 192880, Appl
23	30	30.0	10	10	US-09-860-276-18 Sequence 18, Appl
24	30	30.0	10	10	US-09-860-395-18 Sequence 18, Appl
25	30	30.0	16	14	US-10-158-847-65 Sequence 65, Appl
26	30	30.0	16	14	US-10-158-825-65 Sequence 65, Appl
27	30	30.0	16	15	US-10-264-309-142 Sequence 142, Appl
28	30	30.0	16	16	US-10-158-825-65 Sequence 65, Appl
29	30	30.0	20	14	US-10-076-622-613 Sequence 613, Appl
30	30	30.0	20	14	US-10-097-065-411 Sequence 411, Appl
31	30	30.0	20	14	US-10-124-805-613 Sequence 613, Appl
32	30	30.0	20	15	US-10-372-876-411 Sequence 411, Appl
33	29	29.0	13	14	US-10-053-485-49 Sequence 49, Appl
34	29	29.0	18	15	US-10-397-062-8 Sequence 8, Appl
35	29	29.0	19	14	US-10-225-567A-2124 Sequence 2124, Appl
36	29	29.0	20	16	US-10-240-430-11 Sequence 11, Appl
37	28	28.0	9	13	US-10-032-950-3 Sequence 3, Appl
38	28	28.0	10	10	US-09-572-404B-4172 Sequence 4172, Appl
39	28	28.0	10	15	US-10-430-685-236 Sequence 236, Appl
40	28	28.0	12	14	US-10-217-995-3 Sequence 3, Appl
41	28	28.0	12	16	US-10-363-552-25 Sequence 25, Appl
42	28	28.0	16	9	US-09-826-290-49 Sequence 49, Appl
43	28	28.0	16	9	US-09-826-290-227 Sequence 227, Appl
44	28	28.0	16	15	US-10-264-309-141 Sequence 141, Appl
45	28	28.0	18	9	US-09-848-967-26 Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-127-890-57

; Sequence 57, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Heid & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

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; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-127-890-57

Query Match      100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
DB 1 PSGQAGAAASESLFISNHAY 20

RESULT 2
US-10-717-243-57
; Sequence 57, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-NOV-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
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; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-717-243-57

Query Match      100.0%; Score 100; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
DB 1 PSGQAGAAASESLFISNHAY 20

RESULT 3
US-10-022-066-40
; Sequence 40, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022.066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-40

Query Match      38.0%; Score 38; DB 14; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FISNHAY 20
DB 1 FVSNHAY 7

RESULT 4
US-10-022-066-141
; Sequence 141, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
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US-08-681-219-17
; Sequence 17, Application US/08681219
; Publication No. US20020058607A1
; GENERAL INFORMATION:
; APPLICANT: Takaaki Sato and Junn Yanaoizawa
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,219
; FILING DATE: 22-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-219-17

Query Match 33.0%; Score 33; DB 8; Length 15;
Best Local Similarity 77.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gap

QY 9 ASESLFISN 17
   ||| ||| |||
DB 4 ASEFLFISN 12

RESULT 7
US-09-818-094-6
; Sequence 6, Application US/09818094
; Publication No. US20020039749A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Pengguang
; McKinney, Judi
; TITLE OF INVENTION: High-Throughput Screening Assays for
; Modulators of Stat4 and Stat6 Activity
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/818,094
; FILING DATE: 26-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,003
; FILING DATE: 31-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Timothy L.
; REGISTRATION NUMBER: 35,367
; REFERENCE/DOCKET NUMBER: 018781-0008000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /product= "OTHER"
; /note= "xaa = phosphotyrosine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-818-094-6

Query Match 33.0%; Score 33; DB 9; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 PSQAGAAASESL 13
DB 2 PPGEAGXKAFSSL 14

RESULT 8
US-09-230-111C-15
; Sequence 15, Application US/09230111C
; Publication No. US20030203414A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
; TITLE OF INVENTION: DOMAIN AND USES THEREOF
; FILE REFERENCE: 48962-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,111C
; CURRENT FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:source:synthesized
US-09-230-111C-15

Query Match 33.0%; Score 33; DB 10; Length 15;
Best Local Similarity 77.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 ASESLFISN 17
DB 4 ASEFLFLSN 12

RESULT 9
US-10-092-138-15
; Sequence 15, Application US/10092138
; Publication No. US20030170723A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 65823/JPW/PT
; CURRENT APPLICATION NUMBER: US/10/092,138
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:source:synthesized
US-10-092-138-15

Query Match 33.0%; Score 33; DB 14; Length 15;
Best Local Similarity 77.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 ASESLFISN 17
DB 4 ASEFLFLSN 12

RESULT 10
US-10-820-403-15
; Sequence 15, Application US/10820403
; Publication No. US20040229287A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 65823/JPW/PT
; CURRENT APPLICATION NUMBER: US/10/820,403
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/10/092,138
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:source:synthesized
US-10-820-403-15

Query Match 33.0%; Score 33; DB 16; Length 15;
Best Local Similarity 77.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 ASESLFISN 17
DB 4 ASEFLFLSN 12

RESULT 11
US-10-318-397-15
; Sequence 15, Application US/10318397
; Publication No. US20040115204A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fanger, Neil
; APPLICANT: King, David
; APPLICANT: Retter, Marc W.
; APPLICANT: Rock, Kenneth L.
; TITLE OF INVENTION: ANTIBODIES TO TREAT CANCER
; FILE REFERENCE: 07917-205001
```


; CURRENT APPLICATION NUMBER: US/10/318,397
 ; CURRENT FILING DATE: 2002-11-12
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Cricetulus migratorius
 US-10-318-397-15

Query Match 32.0%; Score 32; DB 16; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 ASESLSFISNHAY 20
 :|:|:|:|:|:|
 Db 2 SSQSLFSGNYNY 13

RESULT 12

US-10-317-747-15
 ; Sequence 15, Application US/10317747
 ; Publication No. US20040126378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Fanger, Neil
 ; APPLICANT: King, David
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Rock, Kenneth L.
 ; TITLE OF INVENTION: ANTIBODIES TO TREAT CANCER
 ; FILE REFERENCE: 07917-184001
 ; CURRENT APPLICATION NUMBER: US/10/317,747
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: US 60/339,736
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: US 60/388,956
 ; PRIOR FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: US 60/399,103
 ; PRIOR FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: US 60/400,958
 ; PRIOR FILING DATE: 2002-08-01
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Cricetulus migratorius
 US-10-317-747-15

Query Match 32.0%; Score 32; DB 16; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 ASESLSFISNHAY 20
 :|:|:|:|:|:|
 Db 2 SSQSLFSGNYNY 13

RESULT 13

US-09-759-143-494
 ; Sequence 494, Application US/09759143
 ; Patent No. US2002022248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 494
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-759-143-494

Query Match 31.5%; Score 31.5; DB 9; Length 20;
 Best Local Similarity 60.0%; Pred. No. 6.3e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 GQAGAAASE-SLFIS 16
 |:|:|:|:|:|:|
 Db 6 GDTGGASSEDLSLMS 20

RESULT 14

US-09-780-669-494
 ; Sequence 494, Application US/09780669
 ; Patent No. US20020051977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C24
 ; CURRENT APPLICATION NUMBER: US/09/780,669
 ; CURRENT FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 943
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 494
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-780-669-494

Query Match 31.5%; Score 31.5; DB 9; Length 20;
 Best Local Similarity 60.0%; Pred. No. 6.3e+02;

Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
QY 3 GOAGRAASE-SLFIS 16
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GDTGASSEDSLMIS 20

RESULT 15
US-09-822-827-494
; Sequence 494, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 494
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-822-827-494

Query Match 31.5%; Score 31.5; DB 9; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.3e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 GOAGRAASE-SLFIS 16
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GDTGASSEDSLMIS 20

Search completed: June 20, 2005, 11:15:09
Job time : 105 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:27:32 ; Search time 23 seconds
(without alignments)
83.667 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSCQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	28.0	12	2	A28856	fructose-bisphosph
2	26	26.0	13	2	A23695	myosin heavy chain
3	26	26.0	18	2	I73024	T cell receptor be
4	25	25.0	15	2	B56661	S-locus specific g
5	25	25.0	19	2	C56661	S-locus specific g
6	24	24.0	8	2	P70527	T-cell receptor be
7	24	24.0	17	2	S57519	T cell receptor be
8	24	24.0	17	2	S57556	T cell receptor be
9	23	23.0	8	2	I48934	apolipoprotein A-I
10	23	23.0	13	2	B61233	conceptus protein
11	23	23.0	13	2	I50173	alpha-2 collagen -
12	23	23.0	17	2	S18534	hypothetical prote
13	23	23.0	20	2	S27351	lysophospholipase
14	22	22.0	10	2	S23371	T-cell receptor al
15	22	22.0	13	2	PQ0491	self-incompatibili
16	22	22.0	13	2	S66558	serine proteinase
17	22	22.0	15	2	A56891	gamma 1 gliadin -
18	22	22.0	15	2	B56891	gamma 2 gliadin -
19	22	22.0	15	2	A61391	alpha-1-antitryps
20	22	22.0	16	2	PH1477	T-cell receptor be
21	22	22.0	16	2	PH1480	T-cell receptor be
22	22	22.0	17	2	PH0757	T-cell receptor be
23	22	22.0	18	2	S52125	gamma2-gliadin P25
24	22	22.0	18	2	B48839	T-cell receptor be
25	22	22.0	19	2	S43652	serpin WSZCI - whe
26	22	22.0	19	2	PQ0492	self-incompatibili
27	22	22.0	20	2	S33867	quinaldic acid 4-o
28	22	22.0	20	2	A49142	hyaluronidase (EC
29	21	21.0	13	2	D56661	S-locus specific g

30	21	21.0	14	2	PH0774	T-cell receptor be
31	21	21.0	14	2	S58866	botulinum neurotox
32	21	21.0	15	2	A49252	T-cell receptor be
33	21	21.0	16	2	PC4371	telomeric and tetr
34	21	21.0	16	2	PH1473	T-cell receptor be
35	21	21.0	18	2	C40433	NADA protein - Cya
36	21	21.0	19	2	A48408	21K high mobility
37	21	21.0	20	2	S46479	retinoid-X-recepto
38	21	21.0	20	2	B47642	T-cell surface gly
39	21	21.0	20	2	A40198	N-acetylneuraminate
40	20.5	20.5	16	2	CQRT	cerebellin - rat
41	20	20.0	6	2	P70687	T-cell receptor be
42	20	20.0	7	2	P70666	T-cell receptor be
43	20	20.0	7	2	P70655	T-cell receptor be
44	20	20.0	7	2	P70544	T-cell receptor be
45	20	20.0	8	2	P70631	T-cell receptor be

ALIGNMENTS

RESULT 1

A28856

fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 31-Oct-1997

C:Accession: A28856

R:Hannappel, E.; MacGregor, J.S.; Davoust, S.; Horecker, B.L.

Arch. Biochem. Biophys. 214, 293-298, 1982

A:Title: Limited proteolysis of liver and muscle aldolases: effects of subtilisin, cathel

A:Reference number: A28856; MUID:82205113; PMID:7044315

A:Accession: A28856

A:Molecule type: protein

A:Residues: 1-12 <HAN>

C:Superfamily: fructose-bisphosphate aldolase

C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; pent

Query Match 28.0%; Score 28; DB 2; Length 12;

Best Local Similarity 33.3%; Pred. No. 2.3e+02;

Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 ASESIFISNHAY 20

Db 1 STQSLEFASITY 12

RESULT 2

A23695

myosin heavy chain, smooth muscle - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004

C:Accession: A23695

R:Garabedian, T.E.; Yount, R.G.

J. Biol. Chem. 265, 22547-22553, 1990

A:Title: Direct photoaffinity labeling of gizzard myosin with [3H]uridine diphosphate pla

A:Reference number: A23695; MUID:91093106; PMID:1979981

A:Accession: A23695

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <GAR>

A:Cross-references: UNIPROT:Q02015; UNIPROT:Q9PS67

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: nucleotide binding; P-loop; smooth muscle

F;2-9/Region: nucleotide-binding motif A (P-loop)

Query Match 26.0%; Score 26; DB 2; Length 13;

Best Local Similarity 36.4%; Pred. No. 5.3e+02;

Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGQAGAAASES 12

Db 1 TGESGAGKTEN 11

RESULT 3

I73024
T cell receptor beta chain variable region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I73024
R:Wang, X.; Golikar, L.; Uyemura, K.; Ohmen, J.D.; Villahermosa, L.G.; Fajardo, T.T.
J. Immunol. 151, 7105-7116, 1993
A:Title: T cells bearing V beta 6 T cell receptors in the cell-mediated immune response
A:Reference number: I56207; MUID:94081361; PMID:8258714
A:Accession: I73024
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-18 <RES>
A:Cross-references: GB:S67656; NID:g459324; PIDN:AAB29242.1; PID:g459325
C:Genetics:
A:Gene: TCRBV6.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.0%; Score 26; DB 2; Length 18;
Best Local Similarity 46.2%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 SGOAGAAASESLF 14
||| ||| ||| |||
Db 3 SSLAGGAYNEQPF 15

RESULT 4

B56661
S-locus specific glycoprotein P57 beta - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C:Accession: B56661
R:Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal sequencing
A:Reference number: A56661; MUID:92090397; PMID:1752245
A:Accession: B56661
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GAU>
A:Cross-references: UNIPROT:Q9S924
A:Experimental source: stigma extracts, var. acephala, self-compatible line P57
A:Note: sequence extracted from NCBI backbone (NCBIP:72302)
C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in the
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein; polymorphism

Query Match 25.0%; Score 25; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 AASESLFIS 16
::||| |||
Db 7 SSESLETLIS 15

RESULT 5

C56661
S-locus specific glycoprotein (allele S9) - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C:Accession: C56661
R:Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal sequencing
A:Reference number: A56661; MUID:92090397; PMID:1752245
A:Accession: C56661
A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-19 <GAU>

A:Cross-references: UNIPROT:Q9S923

A:Experimental source: stigma extracts, var. acephala

A:Note: sequence extracted from NCBI backbone (NCBIP:72301)

C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in the
C:Keywords: glycoprotein; polymorphism

Query Match 25.0%; Score 25; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 AASESLFISN 17
::||| |||
Db 5 SSESLETLTN 14

RESULT 6

PT0527
T-cell receptor beta chain V-D-J region (100-41) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0527
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0527
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 24.0%; Score 24; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGOAGAA 8
||| |||
Db 2 SGDAGGA 8

RESULT 7

S57519
T cell receptor beta chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57519
R:Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified by
A:Reference number: S57494
A:Accession: S57519
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <BUR>
A:Cross-references: EMBL:Z49930; NID:g887494; PIDN:CAA90176.1; PID:g887495
C:Keywords: T-cell receptor

Query Match 24.0%; Score 24; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 AASESLFISNH 18
||| |||
Db 2 ASSQGLISSY 12

RESULT 8

S57556
T cell receptor beta chain V-D-J region (clone pP7 and clone TFL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

```
C:Accession: S57556; S57557
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A:Reference number: S57494
A:Accession: S57556
A:Molecule type: mRNA
A:Residues: 1-17 <BUR>
A:Cross-references: EMBL:Z49926; NID:G887498; PIDN:CAA90172.1; PID:G887499
A:Experimental source: clone PP7
A:Accession: S57557
A:Molecule type: mRNA
A:Residues: 1-17 <BUW>
A:Cross-references: EMBL:Z49928; NID:G887502; PIDN:CAA90174.1; PID:G887503
A:Experimental source: clone TFI
C:Keywords: T-cell receptor

Query Match      24.0%; Score 24; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 AAESLFIISNH 18
   |:|:| |:|:|
DB 2 ASSQGLAISY 12

RESULT 9
I48934
A:Accession: I48934
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R:AO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I48934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q60615; EMBL:U05691; NID:G497010; PIDN:AAB60462.1; PID:G6428

Query Match      23.0%; Score 23; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GOAGAAA 9
   |:|:|
DB 1 GETGSAA 7

RESULT 10
B61233
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
R:Thatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sieum, W.; Randal, S.
Biol. Reprod. 44, 108-120, 1991
A:Title: Characterization of feline conceptus proteins during pregnancy.
A:Reference number: A61233; MUID:91198359; PMID:2015342
A:Accession: B61233
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <THA>

Query Match      23.0%; Score 23; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GOAGAAASESL 13
   |:|:| |:|
DB 2 GLQGAAVQEX 12
```

RESULT 11

```
I50173
A:Title: alpha-2 collagen - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50173
R:Avvedimento, E.V.; Vogeli, G.; Yamada, Y.; Maizel, J.V.
Cell 21, 689-696, 1980
A:Title: Correlation between splicing sites within an intron and their sequence complemer
A:Reference number: I50172; MUID:81064671; PMID:6159982
A:Accession: I50173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-13 <AVV>
A:Cross-references: UNIPROT:P02467; GB:M10540; NID:G211324; PIDN:AAA48638.1; PID:G555428
C:Genetics:
A:Introns: 12/3
```

```
Query Match      23.0%; Score 23; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 PSGQAG 6
   |:|:|
DB 2 PSGKLG 7
```

RESULT 12

```
S18534
A:Title: hypothetical protein 7 (eryG 3' region) - Saccharopolyspora erythraea (fragment)
C:Species: Saccharopolyspora erythraea
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C:Accession: S18534
R:Haydock, S.F.; Dowson, J.A.; Dhillion, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
Mol. Gen. Genet. 230, 120-128, 1991
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in
methyitransferases.
A:Reference number: S18530; MUID:92079886; PMID:1840640
A:Accession: S18534
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <HAY>
A:Cross-references: EMBL:X60379
A:Note: the authors translated the codon CTG for residue 12 as Gly
```

```
Query Match      23.0%; Score 23; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 PSGQAGAAASES 12
   |:|:| |:|
DB 3 PAVASGGALEA 14
```

RESULT 13

```
S27351
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R:Garsetti, D.; Holtsberg, F.; Steiner, M.R.; Egan, R.W.; Clark, M.A.
Biochem. J. 288, 831-837, 1992
A:Title: Butyric acid-induced differentiation of HL-60 cells increases the expression of
A:Reference number: S27350; MUID:93111958; PMID:1471998
A:Accession: S27351
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GAR>
A:Cross-references: UNIPROT:P56643
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Query Match      23.0%; Score 23; DB 2; Length 20;
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Best Local Similarity 66.7%; Pred. NO. 2.6e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 ASESLFISN 17
|||
Db 2 ASISLYSN 10

RESULT 14
S23371
T-cell receptor alpha chain J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S23371
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
Eur. J. Immunol. 21, 2749-2754, 1991
A>Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
A;Reference number: S23364; MUID:92037820; PMID:1657615
A;Accession: S23371
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-10 <PLU>
A;Cross-references: EMBL:X58166
C;Keywords: T-cell receptor

Query Match 22.0%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. NO. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGQAG 6
|||
Db 2 SGEAG 6

RESULT 15
PQ0491
self-incompatibility locus glycoprotein delta - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PQ0491
R;Gaudet, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
Plant Cell 5, 75-86, 1993
A>Title: Expression of a self-incompatibility gene in a self-compatible line of Brassica
A;Reference number: JQ1733; MUID:93177215; PMID:8439745
A;Accession: PQ0491
A;Molecule type: protein
A;Residues: 1-13 <GAU>
A;Cross-references: UNIPROT:Q9SXH5; UNIPROT:Q9SXH7; UNIPROT:O23846; UNIPROT:O23837; UNIP
ROT:Q9SXH4; UNIPROT:O23833; UNIPROT:Q8S9B2; UNIPROT:Q9SXH6; UNIPROT:O23834; UNIPROT:Q8W
A;Experimental source: stigma, var. acephala P5781
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein
C;Keywords: glycoprotein

Query Match 22.0%; Score 22; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. NO. 2.4e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 AASESLFIS 16
:::|||||
Db 5 SSTELELIS 13

Search completed: June 20, 2005, 10:47:11
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:15:52 ; Search time 110.5 Seconds

(without alignments)
92.684 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSGQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	28.0	20	2	Q15988	Q15988 homo sapien
2	27.5	27.5	16	2	Q7TM78	Q7TM78 uncultured
3	27	27.0	16	2	P82453	P82453 spinacia ol
4	27	27.0	19	2	Q9TWJ8	Q9TWJ8 mytilus edu
5	26	26.0	15	2	Q9S8M9	Q9S8M9 raphanus sa
6	26	26.0	17	2	Q75L26	Q75L26 homo sapien
7	26	26.0	20	2	Q15989	Q15989 homo sapien
8	26	26.0	20	2	Q9TRM7	Q9TRM7 bos taurus
9	26	26.0	20	2	Q36584	Q36584 nicotiana g
10	25	25.0	12	2	Q9PS67	Q9PS67 gallus gall
11	25	25.0	15	2	Q9S924	Q9S924 brassica ol
12	25	25.0	16	2	Q9UC88	Q9UC88 homo sapien
13	25	25.0	16	2	Q9UCL0	Q9UCL0 homo sapien
14	25	25.0	18	2	Q6LBY3	Q6LBY3 homo sapien
15	25	25.0	18	2	Q7JJ51	Q7JJ51 canis faml
16	25	25.0	19	2	Q9S923	Q9S923 brassica ol
17	25	25.0	20	1	NF09 NAEFO	P83889 naegleria f
18	25	25.0	20	2	Q7JMY8	Q7JMY8 leishmania
19	25	25.0	20	2	Q48632	Q48632 lactococcus
20	24	24.0	13	2	Q9AIR1	Q9AIR1 pseudomonas
21	24	24.0	14	2	Q798V0	Q798V0 bacillus su
22	24	24.0	15	2	Q37016	Q37016 nicotiana a
23	24	24.0	15	2	Q7GEF3	Q7GEF3 nicotiana g
24	24	24.0	15	2	Q7GEF4	Q7GEF4 nicotiana t
25	24	24.0	16	2	Q9UCK9	Q9UCK9 homo sapien
26	24	24.0	16	2	Q9TR82	Q9TR82 sus scrofa
27	24	24.0	16	2	Q36789	Q36789 solanum nig
28	24	24.0	17	2	Q7RA69	Q7RA69 plasmodium
29	24	24.0	17	2	Q9AUB3	Q9AUB3 arabidopsis
30	24	24.0	18	2	Q9RAF5	Q9RAF5 aeromonas
31	24	24.0	19	2	Q36925	Q36925 nicotiana p

32	24	24.0	19	2	Q7GEF1	Q7GEF1 nicotiana v
33	24	24.0	19	2	Q7GEF2	Q7GEF2 nicotiana a
34	24	24.0	19	2	Q7TE17	Q7TE17 citrus tris
35	24	24.0	19	2	Q6QIF2	Q6QIF2 gallus gall
36	24	24.0	20	2	Q53345	Q53345 pseudomonas
37	23	23.0	8	2	Q60615	Q60615 mus musculu
38	23	23.0	10	2	P83161	P83161 anabaena sp
39	23	23.0	12	2	P92680	P92680 trimersu
40	23	23.0	14	2	Q945F2	Q945F2 cicet ariet
41	23	23.0	15	1	C1QA RAT	P31720 rattus norv
42	23	23.0	15	2	O00604	O00604 homo sapien
43	23	23.0	16	2	Q9UC54	Q9UC54 homo sapien
44	23	23.0	16	2	Q9TWK0	Q9TWK0 mytilus edu
45	23	23.0	17	2	Q96DJ6	Q96DJ6 homo sapien

ALIGNMENTS

RESULT 1

Q15988	PRELIMINARY;	PRT;	20 AA.
AC Q15988;			
DT 01-NOV-1996	(TREMBLrel. 01, Created)		
DT 01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT 01-MAY-1999	(TREMBLrel. 10, Last annotation update)		
DE HLX1 protein (Fragment).			
GN Name=HLX1;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=93194183; PubMed=8095486;			
RA Nishimura D.Y., Purchio A.F., Murray J.C.;			
RT "Linkage localization of TGFB2 and the human homeobox gene HLX1 to			
RT chromosome 1q.;"			
RL Genomics 15:357-364(1993).			
DR EMBL; S56767; AAD13883.1; -.			
FT NON TER 20 20			
SQ SEQUENCE 20 AA; 2012 MW; 6BB655F09B5B5AE4 CRC64;			

Query Match 28.0%; Score 28; DB 2; Length 20;
Best Local Similarity 63.6%; Pred. No. 2.5e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	PSGQAGAAASE 11
Db	2	PSGGAPADGE 12

RESULT 2

Q7TM78	PRELIMINARY;	PRT;	16 AA.
ID Q7TM78			
AC Q7TM78;			
DT 01-OCT-2003	(TREMBLrel. 25, Created)		
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)		
DT 01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE Ribulose-1,5-bisphosphate carboxylase large subunit			
DE (Fragment).			
GN Name=rbcL;			
OS uncultured organism.			
OC unclassified; environmental samples.			
OX NCBI_TaxID=155900;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=sample 2/01/4.8;			
RA Willerslev E., Hansen A.J., Binladen J., Brand T.B., Gilbert M.T.P.,			
RA Shairo B., Bunce M., Wiuf C., Gilchinsky D.A., Cooper A.;			
RT "Diverse plant and animal genetic records from holocene and			
RT pleistocene sediments.;"			
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			

```

DR EMBL; AY262604; AAP95185.1; -.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .; IEA.
DR GO; GO:0016984; P:ribulose-biphosphate carboxylase activity; IEA.
DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
DR InterPro; IPR000685; RuBisCO large.
DR Pfam; PF02788; RuBisCO_large_N; 1.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1452 MW; 25EB5989979F0406 CRC64;

Query Match      27.5%; Score 27.5; DB 2; Length 16;
Best Local Similarity 61.5%; Pred. No. 2.4e+03;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 PSGQAGAA-AGES 12
DB 4 PPEAGAAVAES 16

RESULT 3
ID P82453 PRELIMINARY; PRT; 16 AA.
AC P82453;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 60S ribosomal protein L21 (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1] SEQUENCE.
RC STRAIN=cv. Alvaro; TISSUE=leaf;
RA Yamaguchi K., Subramanian A.R.;
RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein L21.";
RL Submitted (APR-2000) TO Swiss-Prot.
CC -!- SIMILARITY: BELONGS TO THE L21E FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR InterPro; IPR001147; Ribosomal_L21e.
DR PROSITE; PS01171; RIBOSOMAL_L21E; PARTIAL.
KW Ribosomal protein.
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1752 MW; 654F1395EA8BDAF4 CRC64;

Query Match      27.0%; Score 27; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 2.9e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLF 14
DB 1 PAGHGARTRDLF 14

RESULT 4
Q9TWJ8 PRELIMINARY; PRT; 19 AA.
ID Q9TWJ8
AC Q9TWJ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proximal collagen (Fragment).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytilodea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1] SEQUENCE.
RP MEDLINE=95230211; PubMed=7714453;
RA Qin X., Waite J.H.;
RT "Exotic collagen gradients in the byssus of the mussel Mytilus edulis.";

RL J. Exp. Biol. 198;633-644(1995).
SQ SEQUENCE 19 AA; 1605 MW; 8DC1622E63973220 CRC64;

Query Match      27.0%; Score 27; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSGQAGA 7
DB 5 PSGPSGA 11

RESULT 5
Q9S8M9 PRELIMINARY; PRT; 15 AA.
ID Q9S8M9
AC Q9S8M9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ascorbate peroxidase homolog (Fragment).
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1] SEQUENCE.
RP MEDLINE=94272301; PubMed=8003938;
RX Lopez F., Vansuyt G., Derancourt J., Fourcroy P., Casse-Delbart F.;
RT "Identification by 2D-page analysis of salt-stress induced proteins in radish (Raphanus sativus).";
RL Cell. Mol. Biol. 40:85-90(1994).
RN [1] SEQUENCE.
SQ SEQUENCE 15 AA; 1683 MW; D3B5985EF892B4 CRC64;

Query Match      26.0%; Score 26; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.9e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 AAESLRFISNHA 19
DB 2 AADEAFADYA 13

RESULT 6
Q75L26 PRELIMINARY; PRT; 17 AA.
ID Q75L26
AC Q75L26;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein AUTS2 (Fragment).
GN Name=AUTS2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Sewell G.A., Delehaunt K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
RA Biriri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,

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RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
 RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,
 RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
 RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.,
 RT "The DNA sequence of human chromosome 7.";
 RL Nature 424:157-164(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cotton M., Holmes A., Spalding L.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Wilson R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC093679; AAS07486.1; -;
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 17
 FT NON TER 17
 SQ SEQUENCE 17 AA; 1823 MW; 0287D097DB58F55B CRC64;

Query Match 26.0%; Score 26; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGAAGASESLF 14
 | : : : : |
 Db 1 ASDASSEKLF 10

RESULT 7
 Q15989 PRELIMINARY; PRT; 20 AA.
 AC Q15989; Q15990;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE HLX1 protein (Fragment).
 GN Name-HLX1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93194183; PubMed=8095486;
 RA Nishimura D.Y., Purchio A.F., Murray J.C.;
 RT "Linkage localization of TGFB2 and the human homeobox gene HLX1 to
 RT chromosome 1q.";
 RL Genomics 15:357-364(1993).
 DR EMBL; S56768; AAD13884.1; -;
 DR EMBL; S56769; AAD13885.1; -;
 FT NON TER 20
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2028 MW; 6BB655F09B4036E4 CRC64;

Query Match 26.0%; Score 26; DB 2; Length 20;
 Best Local Similarity 63.8%; Pred. No. 5.3e+03;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PSQGAGAAASE 11
 | : : : : |
 Db 2 PSQGALAAAGE 12

RESULT 8
 Q9TRM7 PRELIMINARY; PRT; 20 AA.
 AC Q9TRM7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Inositol polyphosphate receptor, IPXREC (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93028388; PubMed=1329085;
 RA Timmerman A.P., Mayrleitner M.M., Lukas T.J., Chadwick C.C., Saito A.,
 RA Watterson D.M., Schindler H., Fleischer S.;
 RT "Inositol polyphosphate receptor and clathrin assembly protein AP-2
 RT are related proteins that form potassium-selective ion channels in
 RT planar lipid bilayers.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8976-8980(1992).
 DR PIR; B31596; B31596.
 DR GO; GO:0030125; C:clathrin vesicle coat; IEA.
 DR GO; GO:0006886; P:intracellular protein transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR011012; Longin_like.
 FT NON TER 20
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2310 MW; 546EDDD34940494B CRC64;

Query Match 26.0%; Score 26; DB 2; Length 20;
 Best Local Similarity 83.3%; Pred. No. 5.3e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LFISSH 18
 | : : : : |
 Db 5 LFIYNH 10

RESULT 9
 Q36584 PRELIMINARY; PRT; 20 AA.
 AC Q36584;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Rps19' protein (Fragment).
 GN Name-rps19';
 OS Nicotiana glauca (Glaucous tobacco) (Tree tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96397499; PubMed=8804393; DOI=10.1007/s004389670022;
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RT "Ebb and flow of the chloroplast inverted repeat.";
 RL Mol. Gen. Genet. 252:195-206(1996).
 DR EMBL; Z71244; CAA94954.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
 DR GO; GO:000412; P:protein biosynthesis; IEA.
 DR InterPro; IPR002222; Ribosomal_S19.
 DR Pfam; PF0203; Ribosomal_S19; I.
 KW Chloroplast.
 FT NON TER 20
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2388 MW; 2FC9AA300459DE1D CRC64;

Search completed: June 20, 2005, 10:46:19
Job time : 111.5 secs

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OY 3 GOAGAAASESL 13
Db 2 GPGGAAAEAI 12

RESULT 14
Q6LBY3
ID O6LBY3 PRELIMINARY; PRT; 18 AA.
AC O6LBY3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Pro-alpha 1(II) collagen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215609; PubMed=2987845;
RA Sangiorgi F.O., Benson-Chanda V., de Wet W.J., Sobel M.E.,
RA Tsipouras F., Ramirez F.;
RT "Isolation and partial characterization of the entire human pro alpha
RT 1(II) collagen gene."
RL Nucleic Acids Res. 13:2207-2225(1985).
DR EMBL; X02376; CAA26225.1; -.
KW Collagen.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1590 MW; 4D3CD1638CB03A1C CRC64;

Query Match 25.0%; Score 25; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.9e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSGQAGA 7
Db 8 PPGAGA 14

RESULT 15
Q7JJ51
ID Q7JJ51 PRELIMINARY; PRT; 18 AA.
AC Q7JJ51;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type II collagen (Fragment).
GN Name=COL2A1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99016714; PubMed=9800332;
RA Du F., Ray J.;
RT "A tetranucleotide polymorphism in the canine type II collagen gene
RT (COL2A1).";
RL Anim. Genet. 29:400-400(1998).
DR EMBL; AF036484; AAC24763.1; -.
KW Collagen.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1566 MW; 1C89D16A12DC286A CRC64;

Query Match 25.0%; Score 25; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 6.9e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSGQAGA 8
Db 8 PPGDGA 15
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:14:47 ; Search time 62.5 Seconds
(without alignments)
123.763 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSGQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesepc16Dec04:*

1: Genesepc1980s:*

2: Genesepc1990s:*

3: Genesepc2000s:*

4: Genesepc2001s:*

5: Genesepc2002s:*

6: Genesepc2003as:*

7: Genesepc2003bs:*

8: Genesepc2004s:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	AAR37301	Rabbit Mu
2	46	46.0	9	ADN63558	Adn63558 HLA bindi
3	46	46.0	9	ADN64270	Adn64270 HLA bindi
4	38	38.0	7	ABP55800	Abp55800 B15 class
5	38	38.0	7	ABP55717	Abp55717 B15 class
6	38	38.0	7	ABG96843	Abg96843 Human leu
7	38	38.0	7	ABG96597	Abg96597 Human leu
8	38	38.0	7	ABG96695	Abg96695 Human leu
9	38	38.0	7	ABG97023	Abg97023 Human leu
10	38	38.0	7	ADL98512	Adl98512 Human leu
11	38	38.0	7	ADL98370	Adl98370 Human leu
12	38	38.0	7	ADL98676	Adl98676 Human leu
13	38	38.0	7	ADL98857	Adl98857 Human leu
14	38	38.0	7	ADL98439	Adl98439 Human leu
15	37	37.0	20	ABG70560	Abg70560 A. oryzae
16	33	33.0	15	AAW50174	Aaw50174 Signal-tr
17	33	33.0	15	ADG65831	Adg65831 Library p
18	33	33.0	17	ADL46355	Adl46355 D-alanine
19	32	32.0	15	ABR82269	AbR82269 Anti-gang
20	32	32.0	15	ADP84124	Adp84124 Anti-mono
21	32	32.0	15	ADS31786	Ads31786 CDR1 regi
22	31.5	31.5	20	AAW01149	Aaw01149 Human pro
23	31.5	31.5	20	AAU69794	Aau69794 Human pro
24	31.5	31.5	20	AAG99034	Aag99034 Human pro
25	31.5	31.5	20	ABU71685	Abu71685 Prostate

26	31.5	31.5	20	5	ABR95254	AbR95254 Epitope m
27	31.5	31.5	20	6	ABR54366	AbR54366 Prostate
28	31.5	31.5	20	7	ADB13944	AdB13944 Human pro
29	31.5	31.5	20	7	ADG26360	AdG26360 Human pro
30	31	31.0	10	4	AAG87980	Aag87980 Saccharom
31	31	31.0	10	4	AAG87982	Aag87982 Saccharom
32	31	31.0	10	4	AAG87981	Aag87981 Saccharom
33	31	31.0	15	2	AAR88321	Aar88321 Cytokine
34	31	31.0	15	6	ABP58843	AbP58843 RNA bindi
35	31	31.0	15	8	ADE25841	Ade25841 Anti-alpha
36	31	31.0	20	5	AAU75276	Aau75276 Leucine-r
37	30	30.0	9	2	AAW49140	Aaw49140 Human leu
38	30	30.0	10	2	AAW42816	Aaw42816 Antigenic
39	30	30.0	10	2	AAV33475	Aav33475 HHV-8 kap
40	30	30.0	10	4	AAG93377	Aag93377 Procollag
41	30	30.0	10	4	AAG87983	Aag87983 Saccharom
42	30	30.0	16	6	ADA03267	Ada03267 Angiotens
43	30	30.0	16	6	ABR56637	AbR56637 Angiotens
44	30	30.0	16	6	ABR58791	AbR58791 Alzheimer
45	30	30.0	16	8	ADN31816	Adn31816 Human Alz

ALIGNMENTS

RESULT 1

AAR37301

ID AAR37301 standard; protein; 20 AA.

XX

AC AAR37301;

XX

DT 25-MAR-2003 (revised)

DT

DT 13-SEP-1993 (first entry)

XX

DE Rabbit Muscle aldolase peptide segment.

XX

KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; human engineered antibody; variable region; light chain; cell targeting; chimeric antibody; RMA; linker.

KW

OS

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT

FT Cleavage-site i. .20

FT

FT /note= "contains several potential cathepsin cleavage sites"

XX

PN WO9309130-Al.

XX

PD 13-MAY-1993.

XX

PF 04-NOV-1992; 92WO-US009487.

XX

PR 04-NOV-1991; 91US-00787567.

PR

PR 19-JUN-1992; 92US-00901707.

XX

PA (XOMA) XOMA CORP.

XX

PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX

DR WPI; 1993-167617/20.

XX

PT Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft

PT

PT versus host disease and selective cell killing in-vivo.

XX

PS Example 10; Page 115; 163pp; English.

XX

CC The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the

CC

CC analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules

CC are antibodies or their fragments, esp. human engineered H65 antibody
 CC fragments. Fusion constructs were assembled that included a natural
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an
 CC H65 light chain (kapapa) gene. A DNA linker encoding a peptide segment of
 CC the rabbit muscle aldolase was inserted between the gelonin gene and the
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 100; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQQAAGAAASESLFTSNHAY 20
 |||||
 Db 1 PSQQAAGAAASESLFTSNHAY 20
 |||||

RESULT 2
 ADN63558
 ID ADN63558 standard; peptide; 9 AA.
 XX
 AC ADN63558;

XX 01-JUL-2004 (first entry)
 XX
 DE HLA binding peptide #158.
 XX
 KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyoma acuminatum.
 XX

OS Unidentified.

XX WO2004031211-A2.

XX 15-APR-2004.

XX 03-OCT-2003; 2003WO-US031308.

XX 03-OCT-2002; 2002US-0416207P.

XX 08-OCT-2002; 2002US-0417269P.

XX (EPIM-) EPIMUNE INC.

XX Sidney J, Southwood S, Sette A;

XX WPI; 2004-347953/32.

XX New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.

PS Claim 1; SEQ ID NO 158; 186pp; English.

XX The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HLA epitope. It also comprises a spacer
 CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
 CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TKP). The composition is useful for preventing or treating viral

CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma
 CC acuminatum. The composition is also be used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.

XX Sequence 9 AA;

Query Match 46.0%; Score 46; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SLFTSNHAY 20
 |||:||||
 Db 1 SLFVSNHAY 9

RESULT 3
 ADN64270
 ID ADN64270 standard; peptide; 9 AA.

XX ADN64270;

XX 01-JUL-2004 (first entry)

XX HLA binding peptide #870.

XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyoma acuminatum.

OS Unidentified.

XX WO2004031211-A2.

XX 15-APR-2004.

XX 03-OCT-2003; 2003WO-US031308.

XX 03-OCT-2002; 2002US-0416207P.

XX 08-OCT-2002; 2002US-0417269P.

XX (EPIM-) EPIMUNE INC.

XX Sidney J, Southwood S, Sette A;

XX WPI; 2004-347953/32.

XX New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.

PS Claim 1; SEQ ID NO 870; 186pp; English.

XX The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HLA epitope. It also comprises a spacer
 CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
 CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TKP). The composition is useful for preventing or treating viral
 CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma
 CC acuminatum. The composition is also be used for diagnosing such diseases.

CC This sequence represents a peptide of the invention.

XX
SQ Sequence 9 AA;

Query Match 46.0%; Score 46; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 SLFVSNHAY 20
Db |||:|||||
1 SLFVSNHAY 9

RESULT 4
ABP55800
ID ABP55800 standard; peptide; 7 AA.
XX
AC ABP55800;
XX
DT 25-FEB-2003 (first entry)
XX
DE B15 class I sHLA molecule ligand related peptide #94.
XX
KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
XX
OS Synthetic.
XX
PN WO200269198-A2.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005298.
XX
PR 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.
XX
PI Hildebrand WH, Prilliman KR, Hickman HD;
XX
DR WPI; 2002-732755/79.
XX

PT Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.

XX Disclosure; Fig 5; 118pp; English.

XX The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated
CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands
CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC motifs of sequences, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent

CC amino acid sequences used in the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 38.0%; Score 38; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FVSNHAY 20
Db |:|||||
1 FVSNHAY 7

RESULT 5
ABP55717
ID ABP55717 standard; peptide; 7 AA.
XX

AC ABP55717;

DT 25-FEB-2003 (first entry)

DE B15 class I sHLA molecule ligand related peptide #11.

XX HLA ligand; human leukocyte antigen; predictive algorithm; database;

KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.

XX Synthetic.

XX WO200269198-A2.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WO-US005298.

PR 21-FEB-2001; 2001US-0270357P.

PR 10-OCT-2001; 2001US-00974366.

PR 18-DEC-2001; 2001US-00022066.

XX (HILD/) HILDEBRAND W H.

PA (PRIL/) PRILLIMAN K R.

PA (HICK/) HICKMAN H D.

XX Hildebrand WH, Prilliman KR, Hickman HD;

XX WPI; 2002-732755/79.

XX Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.

XX Disclosure; Fig 5; 118pp; English.

XX The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated
CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands
CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC motifs of sequences, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent

CC amino acid sequences used in the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 38.0%; Score 38; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FISNHAY 20
|:|||||
Db 1 FVSNHAY 7

RESULT 6
ABG96843
ID ABG96843 standard; peptide; 7 AA.
XX
AC ABG96843;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #168.
XX
KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
KW major histocompatibility complex; diagnostic development;
KW HLA class I polymorphism; HLA-B15 allotype; ligand.
XX
OS Homo sapiens.
XX
FN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
PR 18-DEC-2000; 2000US-0256410P.
PR 10-OCT-2001; 2001US-00974366.
XX
XX (HILD//) HILDEBRAND W H.
PA (PRIL//) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
XX WPI; 2002-698563/75.
DR
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.
XX
XX Disclosure; Page 178; 300pp; English.

The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (PI), inserting PI into mammalian expression vector; CC electroporating the plasmid into a host cell; inoculating the cell pharm CC with the host cell such that cell pharm produces sHLA. A multimeric HLA CC complex (I) is useful for testing functionality of peptide ligands bound CC by at least two soluble HLA molecules. (I) can be tested for its ability CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune CC responses in humans. (I) is useful for studying T cell responses to CC pathological conditions such as viral infections and cancer, and for CC modulating the human immune system to induce tolerance in autoimmune CC diseases. The individual secreted major histocompatibility complex (MHC) CC molecules produced are useful for studies of peptide loading (i.e., in CC vaccine development) and to the development of diagnostics. With the CC secreted MHC molecules, naturally loaded peptides can be eluted from the CC MHC molecule and characterised. The secreted MHC molecules allow the CC assessment of structural and functional impact of HLA class I CC polymorphism. The molecules are also useful to generate ligands and hence

CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to
CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX
SQ Sequence 7 AA;

Query Match 38.0%; Score 38; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FISNHAY 20
|:|||||
Db 1 FVSNHAY 7

RESULT 7
ABG96597
ID ABG96597 standard; peptide; 7 AA.
XX
AC ABG96597;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #20.
XX
KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
KW major histocompatibility complex; diagnostic development;
KW HLA class I polymorphism; HLA-B15 allotype; ligand.
XX
OS Homo sapiens.
XX
FN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
PR 18-DEC-2000; 2000US-0256410P.
PR 10-OCT-2001; 2001US-00974366.
XX
XX (HILD//) HILDEBRAND W H.
PA (PRIL//) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
XX WPI; 2002-698563/75.
DR
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.
XX
XX Disclosure; Page 159; 300pp; English.

The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (PI), inserting PI into mammalian expression vector; CC electroporating the plasmid into a host cell; inoculating the cell pharm CC with the host cell such that cell pharm produces sHLA. A multimeric HLA CC complex (I) is useful for testing functionality of peptide ligands bound CC by at least two soluble HLA molecules. (I) can be tested for its ability CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune CC responses in humans. (I) is useful for studying T cell responses to CC pathological conditions such as viral infections and cancer, and for CC modulating the human immune system to induce tolerance in autoimmune

CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterised. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterise the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
 XX
 XX Sequence 7 AA;

Query Match 38.0%; Score 38; DB 5; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FISNHAY 20
 Db 1 FVSNHAY 7
 |:|||||

RESULT 8
 ABG96695
 ID ABG96695 standard; peptide; 7 AA.
 AC ABG96695;
 XX
 DT 16-DEC-2002 (first entry)
 XX
 DE Human leukocyte antigen (HLA) B15 ligand #118.
 XX
 KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
 KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
 KW major histocompatibility complex; diagnostic development;
 KW HLA class I polymorphism; HLA-B15 allotype; ligand.
 XX
 OS Homo sapiens.

XX WO200262846-A2.
 XX 15-AUG-2002.
 XX 18-DEC-2001; 2001WO-US049744.
 XX 18-DEC-2000; 2000US-0256409P.
 XX 18-DEC-2000; 2000US-0256410P.
 XX 10-OCT-2001; 2001US-00974366.
 XX (HILD//) HILDEBRAND W H.
 XX (PRIL//) PRILLIMAN K R.
 XX Hildebrand WH, Prilliman KR;
 XX WPI; 2002-698563/75.
 XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 XX studies of peptide loading for characterizing human immune responses
 XX involves using HLA allelic cDNA or genomic DNA as starting material.
 XX Disclosure; Fig 26; 300pp; English.

XX The invention describes a method of producing soluble human leukocyte
 XX antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
 XX allelic DNA by PCR using a locus specific primer to produce truncated a
 XX PCR product (PI), inserting PI into mammalian expression vector, and
 XX electroporating the plasmid into a host cell; inoculating the cell pharm

CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterised. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterise the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
 XX
 XX Sequence 7 AA;

Query Match 38.0%; Score 38; DB 5; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FISNHAY 20
 Db 1 FVSNHAY 7
 |:|||||

RESULT 9
 ABG97023
 ID ABG97023 standard; peptide; 7 AA.
 AC ABG97023;
 XX
 DT 16-DEC-2002 (first entry)
 XX
 DE Human leukocyte antigen (HLA) B15 ligand #351.
 XX
 KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
 KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
 KW major histocompatibility complex; diagnostic development;
 KW HLA class I polymorphism; HLA-B15 allotype; ligand.

XX Homo sapiens.
 XX WO200262846-A2.
 XX 15-AUG-2002.
 XX 18-DEC-2001; 2001WO-US049744.
 XX 18-DEC-2000; 2000US-0256409P.
 XX 18-DEC-2000; 2000US-0256410P.
 XX 10-OCT-2001; 2001US-00974366.
 XX (HILD//) HILDEBRAND W H.
 XX (PRIL//) PRILLIMAN K R.
 XX Hildebrand WH, Prilliman KR;
 XX WPI; 2002-698563/75.

XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 XX studies of peptide loading for characterizing human immune responses
 XX involves using HLA allelic cDNA or genomic DNA as starting material.

PS Disclosure; Page 183; 300pp; English.

XX The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (shLA) in cell pharm involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector;
 CC electroporating the plasmid into a host cell; inoculating the cell pharm
 CC with the host cell such that cell pharm produces shLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterised. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B*15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterise the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
 XX Sequence 7 AA;

Query Match 38.0%; Score 38; DB 5; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FISNHAY 20
 Db 1 FVSNHAY 7
 |:|||||
 |:|||||

RESULT 10
 ADL98512
 ID ADL98512 standard; peptide; 7 AA.
 XX
 AC ADL98512;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human leukocyte antigen-B15 ligand #54.
 XX
 KW soluble human leukocyte antigen; HLA; locus-specific primer; truncation;
 KW multimeric HLA complex; bioreactor;
 KW major histocompatibility complex molecule; MHC; vaccine; HLA-B*15; ligand.
 XX
 OS Homo sapiens.
 XX
 FN US2003166057-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 18-DEC-2001; 2001US-00022066.
 XX
 PR 17-DEC-1999; 99US-00465321.
 PR 18-DEC-2000; 2000US-0256409P.
 PR 18-DEC-2000; 2000US-0256410P.
 PR 24-MAY-2001; 2001US-0293261P.
 PR 09-OCT-2001; 2001US-0327907P.
 PR 10-OCT-2001; 2001US-00974366.
 XX
 PA (HILD//) HILDEBRAND W H.
 PA (PRIL//) PRILLIMAN K R.
 XX

PI. Hildebrand WH, Prilliman KR;
 XX WPI; 2003-863700/80.
 XX
 CC Producing soluble human leukocyte antigen molecules, for testing the
 CC functionality of peptide ligands, comprises utilizing a locus-specific
 CC primer having a stop codon incorporated into a 3' primer, or that
 CC truncates the allelic cDNA.
 XX
 PS Disclosure; Page; 148pp; English.
 XX
 CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules comprising utilising a locus-specific primer
 CC having a stop codon incorporated into a 3' primer, or a locus-specific
 CC primer that truncates the allelic cDNA resulting in a truncated PCR
 CC product having the coding regions encoding cytoplasmic and transmembrane
 CC domains of the allelic cDNA removed so that the truncated PCR product has
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC multimeric HLA complex comprising a substrate, and at least two soluble
 CC HLA molecules attached to the substrate and an apparatus or a bioreactor
 CC unit for producing major histocompatibility complex molecules. The
 CC methods are useful for producing soluble human leukocyte antigen (HLA)
 CC molecules. The multimeric HLA complex is useful for testing the
 CC functionality of peptide ligands bound to the soluble HLA molecules. The
 CC HLA molecules are also useful in vaccine development. This is the amino
 CC acid sequence of a ligand derived from a human leukocyte antigen (HLA)-
 CC B*15 family member. Note: This sequence is shown in table 4 on pages 69-70
 CC of the figures.
 XX
 SQ Sequence 7 AA;

Query Match 38.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FISNHAY 20
 Db 1 FVSNHAY 7
 |:|||||
 |:|||||

RESULT 11
 ADL98370
 ID ADL98370 standard; peptide; 7 AA.
 XX
 AC ADL98370;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human leukocyte antigen-B15 allotype B*1508/B*1501 peptide #4.
 XX
 KW soluble human leukocyte antigen; HLA; locus-specific primer; truncation;
 KW multimeric HLA complex; bioreactor;
 KW major histocompatibility complex molecule; MHC; vaccine; HLA-B*15;
 XX
 OS Homo sapiens.
 XX
 FN US2003166057-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 18-DEC-2001; 2001US-00022066.
 XX
 PR 17-DEC-1999; 99US-00465321.
 PR 18-DEC-2000; 2000US-0256409P.
 PR 18-DEC-2000; 2000US-0256410P.
 PR 24-MAY-2001; 2001US-0293261P.
 PR 09-OCT-2001; 2001US-0327907P.
 PR 10-OCT-2001; 2001US-00974366.
 XX
 PA (HILD//) HILDEBRAND W H.
 PA (PRIL//) PRILLIMAN K R.
 XX

PI Hildebrand WH, Prilliman KR;
 XX WPI; 2003-863700/80.
 XX
 PT Producing soluble human leukocyte antigen molecules, for testing the
 PT functionality of peptide ligands, comprises utilizing a locus-specific
 PT primer having a stop codon incorporated into a 3' primer, or that
 PT truncates the allelic cDNA.
 XX
 PS Disclosure; Fig 26; 148pp; English.
 XX
 CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules comprising utilising a locus-specific primer
 CC having a stop codon incorporated into a 3' primer, or a locus-specific
 CC primer that truncates the allelic cDNA resulting in a truncated PCR
 CC product having the coding regions encoding cytoplasmic and transmembrane
 CC domains of the allelic cDNA removed so that the truncated PCR product has
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC multimeric HLA complex comprising a substrate, and at least two soluble
 CC HLA molecules attached to the substrate and an apparatus or a bioreactor
 CC unit for producing major histocompatibility complex molecules. The
 CC methods are useful for producing soluble human leukocyte antigen (HLA)
 CC molecules. The multimeric HLA complex is useful for testing the
 CC functionality of peptide ligands bound to the soluble HLA molecules. The
 CC HLA molecules are also useful in vaccine development. This is the amino
 CC acid sequence of a human leukocyte antigen (HLA)-B15 peptide found in
 CC allotypes B*1508 and B*1501.
 XX
 SQ Sequence 7 AA;
 Query Match 38.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FISNHAY 20
 Db 1 FVSNHAY 7
 |.|||||
 |.|||||
 1 FVSNHAY 7
 RESULT 12
 ADL98676
 ID ADL98676 standard; peptide; 7 AA.
 XX
 AC ADL98676;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human leukocyte antigen-B15 allotype B*1501 peptide #122.
 XX
 KW soluble human leukocyte antigen; HLA; locus-specific primer; truncation;
 KW multimeric HLA complex; bioreactor;
 KW major histocompatibility complex molecule; MHC; vaccine; HLA-B15;
 KW allotype; B*1501.
 XX
 OS Homo sapiens.
 XX
 PN US2003166057-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 18-DEC-2001; 2001US-00022066.
 XX
 PR 17-DEC-1999; 99US-00465321.
 PR 18-DEC-2000; 2000US-0256409P.
 PR 18-DEC-2000; 2000US-0256410P.
 PR 24-MAY-2001; 2001US-0293261P.
 PR 09-OCT-2001; 2001US-0327907P.
 PR 10-OCT-2001; 2001US-00974366.
 XX
 PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 XX
 PI Hildebrand WH, Prilliman KR;

XX WPI; 2003-863700/80.
 XX
 PT Producing soluble human leukocyte antigen molecules, for testing the
 PT functionality of peptide ligands, comprises utilizing a locus-specific
 PT primer having a stop codon incorporated into a 3' primer, or that
 PT truncates the allelic cDNA.
 XX
 PS Disclosure; Page; 148pp; English.
 XX
 CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules comprising utilising a locus-specific primer
 CC having a stop codon incorporated into a 3' primer, or a locus-specific
 CC primer that truncates the allelic cDNA resulting in a truncated PCR
 CC product having the coding regions encoding cytoplasmic and transmembrane
 CC domains of the allelic cDNA removed so that the truncated PCR product has
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC multimeric HLA complex comprising a substrate, and at least two soluble
 CC HLA molecules attached to the substrate and an apparatus or a bioreactor
 CC unit for producing major histocompatibility complex molecules. The
 CC methods are useful for producing soluble human leukocyte antigen (HLA)
 CC molecules. The multimeric HLA complex is useful for testing the
 CC functionality of peptide ligands bound to the soluble HLA molecules. The
 CC HLA molecules are also useful in vaccine development. This is the amino
 CC acid sequence of a human leukocyte antigen (HLA)-B15 peptide found in
 CC allotypes B*1508 and B*1501.
 XX
 SQ Sequence 7 AA;
 Query Match 38.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FISNHAY 20
 Db 1 FVSNHAY 7
 |.|||||
 |.|||||
 1 FVSNHAY 7
 RESULT 13
 ADL98857
 ID ADL98857 standard; peptide; 7 AA.
 XX
 AC ADL98857;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human leukocyte antigen-B15 allotype B*1508 peptide #11.
 XX
 KW soluble human leukocyte antigen; HLA; locus-specific primer; truncation;
 KW multimeric HLA complex; bioreactor;
 KW major histocompatibility complex molecule; MHC; vaccine; HLA-B15;
 KW allotype; B*1508.
 XX
 OS Homo sapiens.
 XX
 PN US2003166057-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 18-DEC-2001; 2001US-00022066.
 XX
 PR 17-DEC-1999; 99US-00465321.
 PR 18-DEC-2000; 2000US-0256409P.
 PR 18-DEC-2000; 2000US-0256410P.
 PR 24-MAY-2001; 2001US-0293261P.
 PR 09-OCT-2001; 2001US-0327907P.
 PR 10-OCT-2001; 2001US-00974366.
 XX
 PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 XX
 PI Hildebrand WH, Prilliman KR;

XX WPI; 2003-863700/80.
 XX Producing soluble human leukocyte antigen molecules, for testing the
 PT functionality of peptide ligands, comprises utilizing a locus-specific
 PT primer having a stop codon incorporated into a 3' primer, or that
 PT truncates the allelic cDNA.
 XX
 PS Disclosure; Page; 148pp; English.
 XX
 CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules comprising utilising a locus-specific primer
 CC having a stop codon incorporated into a 3' primer, or a locus-specific
 CC primer that truncates the allelic cDNA resulting in a truncated PCR
 CC product having the coding regions encoding cytoplasmic and transmembrane
 CC domains of the allelic cDNA removed so that the truncated PCR product has
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC multimeric HLA complex comprising a substrate, and at least two soluble
 CC HLA molecules attached to the substrate and an apparatus or a bioreactor
 CC unit for producing major histocompatibility complex molecules. The
 CC methods are useful for producing soluble human leukocyte antigen (HLA)
 CC molecules. The multimeric HLA complex is useful for testing the
 CC functionality of peptide ligands bound to the soluble HLA molecules.
 CC HLA molecules are also useful in vaccine development. This is the amino
 CC acid sequence of a human leukocyte antigen (HLA)-B15 allotype B*1508
 CC peptide. Note: This sequence is shown in table C on page 93-94 of the
 CC figures.
 XX
 SQ Sequence 7 AA;
 Query Match 38.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FISNHAY 20
 Db |:|||||
 1 FVSNHAY 7
 RESULT 14
 ADL98439
 ID ADL98439 standard; peptide; 7 AA.
 AC ADL98439;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human leukocyte antigen-B15 ligand #20.
 XX
 KW soluble human leukocyte antigen; HLA; locus-specific primer; truncation;
 KW multimeric HLA complex; bioreactor;
 KW major histocompatibility complex molecule; MHC; vaccine; HLA-B15; ligand.
 XX
 OS Homo sapiens.
 XX
 PN US2003166057-A1.
 PD 04-SEP-2003.
 XX
 PF 18-DEC-2001; 2001US-00022066.
 XX
 PR 17-DEC-1999; 99US-00465321.
 PR 18-DEC-2000; 2000US-0256409P.
 PR 18-DEC-2000; 2000US-0256410P.
 PR 24-MAY-2001; 2001US-0293261P.
 PR 09-OCT-2001; 2001US-0327907P.
 PR 10-OCT-2001; 2001US-00974366.
 XX
 PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLMAN K R.
 XX
 PI Hildebrand WH, Prillman KR;
 ,XX

DR WPI; 2003-863700/80.
 XX Producing soluble human leukocyte antigen molecules, for testing the
 PT functionality of peptide ligands, comprises utilizing a locus-specific
 PT primer having a stop codon incorporated into a 3' primer, or that
 PT truncates the allelic cDNA.
 XX
 PS Disclosure; Page; 148pp; English.
 XX
 CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules comprising utilising a locus-specific primer
 CC having a stop codon incorporated into a 3' primer, or a locus-specific
 CC primer that truncates the allelic cDNA resulting in a truncated PCR
 CC product having the coding regions encoding cytoplasmic and transmembrane
 CC domains of the allelic cDNA removed so that the truncated PCR product has
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC a coding region encoding a soluble HLA molecule. Also described is a
 CC multimeric HLA complex comprising a substrate, and at least two soluble
 CC HLA molecules attached to the substrate and an apparatus or a bioreactor
 CC unit for producing major histocompatibility complex molecules. The
 CC methods are useful for producing soluble human leukocyte antigen (HLA)
 CC molecules. The multimeric HLA complex is useful for testing the
 CC functionality of peptide ligands bound to the soluble HLA molecules.
 CC HLA molecules are also useful in vaccine development. This is the amino
 CC acid sequence of a ligand derived from a human leukocyte antigen (HLA)-
 CC B15 family member. Note: This sequence is shown in table 4 on pages 69-70
 CC of the figures.
 XX
 SQ Sequence 7 AA;
 Query Match 38.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FISNHAY 20
 Db |:|||||
 1 FVSNHAY 7
 RESULT 15
 ABG70560
 ID ABG70560 standard; peptide; 20 AA.
 AC ABG70560;
 XX
 DT 29-AUG-2003 (revised)
 DT 25-NOV-2002 (first entry)
 XX
 DE A. oryzae glutaminase, peptide #1.
 XX
 KW Glutaminase; taste enhancement; soy; miso; EC 3.5.1.2; enzyme.
 XX
 OS Aspergillus oryzae; KBN616.
 XX
 PN JP2002218986-A.
 PD 06-AUG-2002.
 XX
 PF 26-JAN-2001; 2001JP-00019108.
 XX
 PR 26-JAN-2001; 2001JP-00019108.
 XX
 PA (AICH-) AICHI KEN PREFECTURE.
 PA (ICHI-) ICHIBIKI KK.
 XX
 DR WPI; 2002-631625/68.
 XX
 PT A new glutaminase, useful for enhancing the taste of soy and miso.
 XX
 PS Example 2; Page 8; 43pp; Japanese.
 XX
 CC The present invention relates to the isolation of glutaminase (EC
 CC 3.5.1.2) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104, and
 CC the polynucleotide sequences encoding them. The invention also describes

CC a vector containing a polynucleotide sequence encoding glutaminase, a
CC host cell containing such a vector, and a method for the preparation of
CC glutaminase. The glutaminase is useful for enhancing the taste of soy and
CC miso. The present sequence represents a peptide from *A. oryzae* KBN616
CC glutaminase. (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 20 AA;

Query Match 37.0%; Score 37; DB 5; Length 20;
Best Local Similarity 61.5%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GAAASESLFISNH 18

||| ||| |

Db 2 GAVASESAICSRH 14

Search completed: June 20, 2005, 10:42:34
Job time : 65.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:00:54 ; Search time 24 seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	363	1 ADRBA	fructose-bisphosph
2	99	99.0	364	1 ADRHA	fructose-bisphosph
3	97	97.0	364	1 ADMSA	fructose-bisphosph
4	97	97.0	364	1 ADRTA	fructose-bisphosph
5	95	95.0	42	2 I51291	aldolase C - chick
6	77	77.0	364	2 JCA189	fructose-bisphosph
7	69.5	69.5	363	2 JCA188	fructose-bisphosph
8	68	68.0	364	1 ADHUC	fructose-bisphosph
9	61	61.0	365	2 T24514	hypothetical prote
10	60.5	60.5	363	2 I53145	zebrin II - mouse
11	59.5	59.5	363	1 ADRTC	fructose-bisphosph
12	58	58.0	137	2 I51292	aldolase A - chick
13	57	57.0	364	2 S45346	fructose-bisphosph
14	55.5	55.5	361	1 ADFF	fructose-bisphosph
15	55.5	55.5	361	2 C42263	fructose 1,6-bisph
16	52	52.0	366	2 T15951	hypothetical prote
17	50	50.0	364	1 ADRTB	fructose-bisphosph
18	48	48.0	179	2 AF0981	probable exported
19	48	48.0	1772	2 A45532	major merozoite su
20	47	47.0	364	2 S48910	fructose-bisphosph
21	46	46.0	170	2 D95178	conserved domain p
22	46	46.0	170	2 C98045	hypothetical prote
23	46	46.0	293	2 AE1950	cytosine-specific
24	46	46.0	364	1 ADHUB	fructose-bisphosph
25	46	46.0	644	2 AD6277	hypothetical prote
26	45	45.0	357	1 ADSAPC	fructose-bisphosph
27	45	45.0	357	2 T12416	fructose-bisphosph
28	45	45.0	364	1 ADCHB	fructose-bisphosph
29	44	44.0	627	2 T02846	dynein light chain

RESULT 1

ADRBA

fructose-bisphosphate aldolase (EC 4.1.2.13) A - rabbit

N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 24-Apr-1984 #sequence revision 27-Nov-1985 #text_change 09-Jul-2004

C:Accession: A92444; A90059; A90305; A90060; 146474; 146475; A01103

R:Tolan, D.R.; Amsden, A.B.; Putney, S.D.; Urdea, M.S.; Penhoet, E.E.

J. Biol. Chem. 259, 1127-1131, 1984

A:Title: The complete nucleotide sequence for rabbit muscle aldolase A messenger RNA.
A:Reference number: A92444; MUID:84111505; PMID:6546378

A:Accession: A92444

A:Molecule type: mRNA

A:Residues: 1-363 <TOL>

A:Cross-references: P00883; GB:K02300; NID:G164751; PIDN:AAA31156.1; PID:G164752

A:Note: Initiator Met not shown

R:Lai, C.Y.; Nakai, N.; Chang, D.

Science 183, 1204-1206, 1974

A:Title: Amino acid sequence of rabbit muscle aldolase and the structure of the active ce

A:Reference number: A94244; MUID:74094688; PMID:4812352

A:Contents: annotation

A:Note: the sequence reported in this paper has been revised in references A90305 and A90

R:Nakai, N.; Chang, D.; Lai, C.Y.

Arch. Biochem. Biophys. 166, 347-357, 1975

A:Title: Studies on the structure of rabbit muscle aldolase. Ordering of the tryptic pep

A:Reference number: A90059; MUID:75145171; PMID:1122141

A:Accession: A90059

A:Molecule type: protein

A:Residues: 1-33, 'Q', 35-164 <NAK>

R:Benfield, P.A.; Forcina, B.G.; Gibbons, I.; Perham, R.N.

Biochem. J. 183, 429-444, 1979

A:Title: Extended amino acid sequences around the active-site lysine residue of class-I f

A:Reference number: A90305; MUID:80109133; PMID:534504

A:Accession: A90305

A:Molecule type: protein

A:Residues: 173-200 <BEN>

R:Lai, C.Y.

Arch. Biochem. Biophys. 166, 358-368, 1975

A:Title: Studies on the structure of rabbit muscle aldolase. Determination of the primary

A:Reference number: A90060; MUID:75145172; PMID:1122142

A:Accession: A90060

A:Molecule type: protein

A:Residues: 251-272, 'S', 274, 'E', 276-277, 'G', 279-292, 'W', 294, 'K', 296-363 <LAI2>

R:Hartman, F.C.; Brown, J.P.

J. Biol. Chem. 251, 3057-3062, 1976

A:Title: Affinity labeling of a previously undetected essential lysyl residue in class I

A:Reference number: A92191; MUID:76190154; PMID:5453

A:Contents: annotation; active site

R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.

Nature 302, 718-721, 1983

A:Title: A new tropoin T and cDNA clones for 13 different muscle proteins, found by shot

A:Reference number: 146471; MUID:83167564; PMID:6687628

ALIGNMENTS

probable lipoprote
translation initia
thioredoxin-disulf
hypothetical prote
prophage p11 prote
prophage p13 prote
prophage p12 prote
hypothetical prote
thioredoxin reduct
fructose-bisphosph
neuron-derived rec
glutamate synthase
neuron-derived rec
neuron derived orp
D-ribulose-5-phosp
hypothetical prote

30 44 44.0 1005 2 S73711
31 44 44.0 1054 2 T43226
32 43 43.0 310 2 B97777
33 42 42.0 259 2 T13260
34 42 42.0 259 2 D86685
35 42 42.0 259 2 C86797
36 42 42.0 259 2 C86757
37 42 42.0 307 2 G70665
38 42 42.0 310 2 D71703
39 42 42.0 359 2 S58167
40 42 42.0 430 2 S66671
41 42 42.0 489 2 F82085
42 42 42.0 625 2 S71930
43 42 42.0 628 2 JC2493
44 41 41.0 209 2 D64212
45 41 41.0 242 2 A82512

A;Accession: I46474
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 37-55 <PUT>
A;Cross-references: EMBL:V00876; NID:g1444; PIDN:CAA242445.1; PID:g929753
A;Accession: I46475
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 349-352, 'R', 354-363 <PUT>
A;Cross-references: EMBL:V00877; NID:g1446; PIDN:CAA242446.1; PID:g833792
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, a C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe F;2-363/Product: fructose-bisphosphate aldolase A #status predicted <MAT>
F;146,229,363/Active site: Lys, Lys, Tyr #status predicted

Query Match 100.0%; Score 100; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20
|||||
DB 344 PSQAGAAASESLFISNHAY 363

RESULT 2
ADHUA
fructose-bisphosphate aldolase (EC 4.1.2.13) A [validated] - human
N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence revision 10-Sep-1991 #text change 09-Jul-2004
A;Accession: S14084; A27186; S00290; S02338; A05177; S03874; S23919; I39429; I39
R;Mukai, T.; Arai, Y.; Yatsuki, H.; Joh, K.; Hori, K.
Eur. J. Biochem. 195, 781-787, 1991
A;Title: An additional promoter functions in the human aldolase A gene, but not in rat.
A;Reference number: S14084; MUID:91153319; PMID:1999195
A;Accession: S14084
A;Molecule type: DNA
A;Residues: 1-364 <UNK>
A;Cross-references: UNIPROT:P04075
R;Izzo, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Borghese, A.M.; Paolella, G.; Salvatore,
Eur. J. Biochem. 164, 9-13, 1987
A;Title: A new human species of aldolase A mRNA from fibroblasts.
A;Reference number: A27186; MUID:87161904; PMID:3030757
A;Accession: A27186
A;Molecule type: mRNA
A;Residues: 1-364 <IZZ>
A;Cross-references: GB:X05236; NID:g28596; PIDN:CAA28861.1; PID:g28597
A;Experimental source: fibroblast
R;Izzo, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Paolella, G.; Salvatore, F.
Eur. J. Biochem. 174, 569-576, 1988
A;Title: Human aldolase A gene. Structural organization and tissue-specific expression b
A;Reference number: S01014; MUID:88271327; PMID:3391172
A;Accession: S01014
A;Molecule type: DNA
A;Residues: 1-72, 'G', 74-195, 'A', 197-229, 'N', 231-279, 'S', 281-364 <IZZ>
A;Cross-references: GB:X12447; NID:g28613; PIDN:CAA30979.1; PID:g28614
R;Freemont, P.S.; Dunbar, B.; Fothergill-Gilmore, L.A.
Biochem. J. 249, 779-788, 1988
A;Title: The complete amino acid sequence of human skeletal-muscle fructose-bisphosphate
A;Reference number: S00290; MUID:88183272; PMID:3355497
A;Accession: S00290
A;Molecule type: protein
A;Residues: 2-358, 'I', 360-364 <FRE>
R;Maire, P.; Gautron, S.; Hakim, V.; Gregori, C.; Mennecier, F.; Kahn, A.
J. Mol. Biol. 197, 425-438, 1987
A;Title: Characterization of three optional promoters in the 5' region of the human ald
A;Reference number: S02338; MUID:88155643; PMID:3441006
A;Accession: S02338
A;Molecule type: DNA
A;Residues: 1-108 <MAI>
A;Cross-references: EMBL:X06352; NID:g28594; PIDN:CAA29654.1; PID:g28595
R;Freemont, P.S.; Dunbar, B.; Fothergill, L.A.

Arch. Biochem. Biophys. 228, 342-352, 1984
A;Title: Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr- and o-iodo
A;Reference number: A05177; MUID:84126818; PMID:6696436
A;Accession: A05177
A;Molecule type: protein
A;Residues: 2-63;148-358 <R2>
R;Sakakibara, M.; Takahashi, I.; Takasaki, Y.; Mukai, T.; Hori, K.
Biochim. Biophys. Acta 1007, 334-342, 1989
A;Title: Construction and expression of human aldolase A and B expression plasmids in Esc
A;Reference number: S03874; MUID:89194215; PMID:2649152
A;Accession: S03874
A;Molecule type: mRNA
A;Residues: 1-33;357-364 <SAK>
R;Lee, K.N.; Maxwell, M.D.; Patterson Jr., M.K.; Birckbichler, P.J.; Conway, E.
Biochim. Biophys. Acta 1136, 12-16, 1992
A;Title: Identification of transglutaminase substrates in HT29 colon cancer cells: use of
A;Reference number: S23919; MUID:92353128; PMID:1353685
A;Accession: S23919
A;Molecule type: protein
A;Residues: 2-16 <LEE>
R;Gamblin, S.J.; Davies, G.J.; Grimes, J.M.; Jackson, R.M.; Littlechild, J.A.; Watson, H.
J. Mol. Biol. 219, 573-576, 1991
A;Title: Activity and Specificity of Human Aldolases.
A;Reference number: A43787; MUID:91278081; PMID:2056525
A;Contents: annotation; active site
R;Sakakibara, M.; Mukai, T.; Hori, K.
Biochem. Biophys. Res. Commun. 131, 413-420, 1985
A;Title: Nucleotide sequence of a cDNA clone for human aldolase: a messenger RNA in the J
A;Reference number: I39429; MUID:85306986; PMID:3840020
A;Accession: I39429
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-364 <RES>
A;Cross-references: GB:M11560; NID:g178350; PIDN:AAA51690.1; PID:g178351
R;Tolan, D.R.; Niclas, J.; Bruce, B.D.; Lebo, R.V.
Am. J. Hum. Genet. 41, 907-924, 1987
A;Title: Evolutionary implications of the human aldolase-A, -B, -C, and -pseudogene chron
A;Reference number: I39435; MUID:88046782; PMID:3674018
A;Accession: I39435
A;Molecule type: mRNA
A;Residues: 139-364 <POL>
A;Cross-references: GB:M21190; NID:g178403; PIDN:AAA51697.1; PID:g178404
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, a
C;Genetics:
A;Gene: GDB:ALDOA
A;Cross-references: GDB:118993; OMIM:103850
A;Map position: 16q22.2-16q22.2
A;Introns: 38/1
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; per
F;2-364/Product: fructose-bisphosphate aldolase A #status experimental <MAT>
F;147,230,364/Active site: Lys, Lys, Tyr #status experimental

Query Match 99.0%; Score 99; DB 1; Length 364;
Best Local Similarity 95.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20
|||||
DB 345 PSQAGAAASESLFISNHAY 364

RESULT 3
ADMSA
fructose-bisphosphate aldolase (EC 4.1.2.13) A - mouse
N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
A;Accession: S06323; B25388; A37062
R;Mestek, A.; Stauffer, J.; Tolan, D.R.; Ciejek-Baez, E.
Nucleic Acids Res. 15, 10595, 1987
A;Title: Sequence of a mouse brain aldolase A cDNA.
A;Reference number: S06323; MUID:88096598; PMID:3697100

A;Accession: S06323
A;Molecule type: mRNA
A;Residues: 1-364 <MES>
A;Cross-references: UNIPROT:P05064; GB:Y00516; NID:g49914; PIDN:CAA68571.1; PID:g49915
A;Experimental source: brain
R;Paolella, G.; Buono, P.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Eur. J. Biochem. 156, 229-235, 1986
A;Title: Structure and expression of mouse aldolase genes. Brain-specific aldolase C ami
A;Reference number: A91165; MUID:86192445; PMID:3009179
A;Accession: B25388
A;Molecule type: mRNA
A;Residues: 99-280, 'C', 282-355 <PAO>
A;Cross-references: GB:X03797; NID:g49916; PIDN:CAA27423.1; PID:g929677
R;Experimental source: brain
R;Stauffer, J.K.; Colbert, M.C.; Ciejek-Baez, E.
J. Biol. Chem. 265, 11773-11782, 1990
A;Title: Nonconservative utilization of aldolase A alternative promoters.
A;Reference number: A37062; MUID:90307699; PMID:2365699
A;Accession: A37062
A;Molecule type: DNA
A;Residues: 1-266;295-364 <STA>
A;Cross-references: GB:J05517
A;Experimental source: strain RIII S/J
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe
F;2-364/Product: fructose-bisphosphate aldolase A #status Predicted <MAT>
F;147,230,364/Active site: Lys, Lys, Tyr #status Predicted

Query Match 97.08; Score 97; DB 1; Length 364;
Best Local Similarity 95.08; Pred. No. 5.8e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
|||||
DB 345 PSQGAGAAASESLFISNHAY 364
|||||

RESULT 4
ADRTA
fructose-bisphosphate aldolase (EC 4.1.2.13) A - rat
N;Alternate names: aldolase A; fructose1,6-bisphosphate triosephosphate-lyase A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence,revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A24532; A25383; I53307; I56408
R;Joh, K.; Mukai, T.; Yatsuki, H.; Hori, K.
Gene 39, 17-24, 1985
A;Title: Rat aldolase A messenger RNA: the nucleotide sequence and multiple mRNA species
A;Reference number: A24532; MUID:86083186; PMID:2416636
A;Accession: A24532
A;Molecule type: mRNA
A;Residues: 1-364 <JOH>
A;Cross-references: UNIPROT:P05065; UNIPROT:Q63038; GB:M14420; NID:g202836; PIDN:AAA4071
R;Mukai, T.; Joh, K.; Arai, Y.; Yatsuki, H.; Hori, K.
J. Biol. Chem. 261, 3347-3354, 1986
A;Title: Tissue-specific expression of rat aldolase A mRNAs: three molecular species dif
A;Reference number: A25383; MUID:86140113; PMID:3753977
A;Accession: A25383
A;Molecule type: mRNA
A;Residues: 1-144, 'F', 146-164, 'M', 166-364 <WUK>
A;Cross-references: GB:M12919; NID:g202834; PIDN:AAA40714.1; PID:g202835
R;Tsumami, R.; Tsumami, K.
Eur. J. Biochem. 142, 161-164, 1984
A;Title: Two different aldolase A mRNA species in rat tissues.
A;Reference number: I53307; MUID:84261525; PMID:6086339
A;Accession: I53307
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 324-329, 'Q', 331-356 <RES>
A;Cross-references: GB:M28282; NID:g202849; PIDN:AAA40720.1; PID:g202850
R;Joh, K.; Arai, Y.; Mukai, T.; Hori, K.
J. Mol. Biol. 190, 401-410, 1986
A;Title: Expression of three mRNA species from a single rat aldolase A gene, differing i
A;Reference number: I56408; MUID:87060996; PMID:3783705

Dd 345 PAGSGSAASESLFIANHAY 364

RESULT 7

JC4188

fructose-bisphosphate aldolase (EC 4.1.2.13), muscle-type - Pacific lamprey

N:Alternate names: muscle-type aldolase

C:Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)

C:Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000

C:Accession: JC4188

R:Zhang, R.; Yatsuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Inai, T.; Yoshida, M.; Horiuchi, J.; Biochem. 117, 545-553, 1995

A:Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lampetra tridentata

A:Reference number: JC4188; MUID:95355304; PMID:7623020

A:Accession: JC4188

A:Molecule type: mRNA

A:Residues: 1-363 <ZHA>

A:CROSS-references: DBJ:D38620; NID:G1619827; PIDN:BA07608.1; PID:G974732

C:Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructose-1,6-bisphosphate to fructose-1,3-bisphosphate and dihydroxyacetone phosphate

C:Superfamily: fructose-bisphosphate aldolase

C:Keywords: aldehyde-lyase; carbon-carbon lyase; muscle

F:230/Active site: Lys #status predicted

Query Match 69.5%; Score 69.5; DB 2; Length 363;

Best Local Similarity 70.0%; Pred. No. 0.0017;

Matches 14; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 PSGQAGAAASESLFIANHAY 20

Dd 345 PTG-TGAAGSGLFVANHAY 363

RESULT 8

ADHUC

fructose-bisphosphate aldolase (EC 4.1.2.13) C - human

N:Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: A25861; S00863; S13192

R:Rottmann, W.H.; Deselms, K.R.; Niclas, J.; Camerato, T.; Holman, P.S.; Green, C.J.; Tjallingii, E.; Biochem. 117, 137-145, 1997

A:Title: The complete amino acid sequence of the human aldolase C isozyme derived from cDNA

A:Reference number: A25861; MUID:87185595; PMID:3105602

A:Accession: A25861

A:Molecule type: DNA

A:Residues: 1-364 <ROT>

A:CROSS-references: UNIPROT:P09972; GB:X05196; NID:G28598; PIDN:CAA28825.1; PID:G28599

R:Buono, P.; Paoletta, G.; Mancini, F.P.; Izzo, P.; Salvatore, F.

Nucleic Acids Res. 16, 4733, 1988

A:Title: The complete nucleotide sequence of the gene coding for the human aldolase C.

A:Reference number: S00863; MUID:88247784; PMID:3267224

A:Accession: S00863

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-310,'V', 312-364 <BUO1>

A:CROSS-references: GB:X07292; NID:G28600; PIDN:CAA30270.1; PID:G312137

R:Buono, P.; Mancini, F.P.; Izzo, P.; Salvatore, F.

Eur. J. Biochem. 192, 805-811, 1990

A:Title: Characterization of the transcription-initiation site and of the promoter region of the human aldolase C gene

A:Reference number: S13192; MUID:91006178; PMID:2209624

A:Accession: S13192

A:Molecule type: DNA

A:Residues: 1-310,'V', 312-364 <BUO2>

A:CROSS-references: GB:X07292; GB:M84921; NID:G28600; PIDN:CAA30270.1; PID:G312137

C:Genetics:

A:Gene: GDB:ALDOC

A:CROSS-references: GDB:119670; OMIM:103870

A:Map position: 17pter-17qter

A:Introns: 38/1, 108/3, 127/1, 180/3; 208/3; 267/1; 333/3

C:Superfamily: fructose-bisphosphate aldolase

C:Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; per

F:2-364/Product: fructose-bisphosphate aldolase C #status predicted <MAT>

F:147,230,364/Active site: Lys, Lys, Tyr #status predicted

Query Match 68.0%; Score 68; DB 1; Length 364;

Best Local Similarity 63.2%; Pred. No. 0.003;

Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SQQAGAAASESLFIANHAY 20

Dd 346 SGEDGAAQSLYIANHAY 364

RESULT 9

T24514

hypothetical protein T05D4.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24514

R:McMurray, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19902

A:Accession: T24514

A:Molecule type: DNA

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Residues: 1-365 <WIL>

A:CROSS-references: UNIPROT:P54216; EMBL:Z81115; PIDN:CAB03291.1; GSPDB:GN00021; CESP:T05D4

A:Experimental source: clone T05D4

C:Genetics:

A:Gene: CESP:T05D4.1

A:Map position: 3

A:Introns: 32/1; 190/3

C:Superfamily: fructose-bisphosphate aldolase

Query Match 61.0%; Score 61; DB 2; Length 365;

Best Local Similarity 68.8%; Pred. No. 0.041;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGAAASESLFIANHAY 20

Dd 350 ADAAAQSLFVANHAY 365

RESULT 10

I53145

zebrin II - mouse

C:Species: Mus sp. (mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999

C:Accession: I53145

R:Ahn, A.H.; Diemnis, S.; Hawkes, R.; Herrup, K.

Development 120, 2081-2090, 1994

A:Title: The cloning of zebrin II reveals its identity with aldolase C.

A:Reference number: I53145; MUID:95009537; PMID:7925012

A:Accession: I53145

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-363 <RES>

A:CROSS-references: GB:S72537; NID:G619372; PIDN:AAB32064.1; PID:G619373

C:Superfamily: fructose-bisphosphate aldolase

Query Match 60.5%; Score 60.5; DB 2; Length 363;

Best Local Similarity 68.4%; Pred. No. 0.049;

Matches 13; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 SQQAGAAASESLFIANHAY 20

Dd 346 SGDGAQA-QSLYIANHAY 363

RESULT 11

ADRTC

fructose-bisphosphate aldolase (EC 4.1.2.13) C - rat

N:Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C; fructo

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S00326; A38817; JN0127; I53313

R; Kukita, A.; Mukai, T.; Miyata, T.; Hori, K.
Eur. J. Biochem. 171, 471-478, 1988
A: Title: The structure of brain-specific rat aldolase C mRNA and the evolution of aldolase C gene
A: Reference number: S00326; MUID: 88151941; PMID: 2831050
A: Accession: S00326
A: Molecule type: mRNA
A: Residues: 1-363 <KUK>
A: Cross-references: UNIPROT:P09117; UNIPROT:Q63037; EMBL:X06984; NID:g55634; PIDN:CAA30030
A: Accession: A38817
A: Molecule type: protein
A: Residues: 2-21 <KU2>
R; Mukai, T.; Yatsuki, H.; Masuko, S.; Arai, Y.; Joh, K.; Hori, K.
Biochem. Biophys. Res. Commun. 174, 1035-1042, 1991
A: Title: The structure of the brain-specific rat aldolase C gene and its regional expression
A: Reference number: JN0127; MUID: 91128359; PMID: 1993044
A: Accession: JN0127
A: Molecule type: DNA
A: Residues: 1-336, 'LAA', 340-363 <MUK>
A: Cross-references: GB:M63656; NID:g202841; PIDN:AAA0717.1; PID:g202842
R; Skala, H.; Vibert, M.; Lamas, E.; Maire, P.; Schweighoffer, F.; Kahn, A.
Eur. J. Biochem. 163, 513-518, 1987
A: Title: Molecular cloning and expression of rat aldolase C messenger RNA during development
A: Reference number: I53313; MUID: 87161851; PMID: 3830170
A: Accession: I53313
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 251-363 <RES>
A: Cross-references: EMBL:X05277; NID:g55632; PIDN:CAA28889.1; PID:g55633
C: Genetics:
A: Introns: 38/1, 108/3; 127/1, 180/3; 208/3; 267/1; 333/3
C: Superfamily: fructose-bisphosphate aldolase
C: Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; pentose-phosphate shunt
F: 2-363/Product: fructose-bisphosphate aldolase C #status experimental <MAT>
F: 147,230,363/Active site: Lys, Lys, Tyr #status predicted

Query Match 59.5%; Score 59.5; DB 1; Length 363;
Best Local Similarity 63.2%; Pred. No. 0.071; Gaps 1;
Matches 12; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 2 SQGAGAAASELFISNHAY 20
||| ||| :||| :|||
Db 346 SDGGAAA-QSLYVANHAY 363

RESULT 12
I51292
aldolase A - chicken (fragment)
C: Species: Gallus gallus (Chicken)
C: Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C: Accession: I51292
R: Meighan-Mantha, R.L.; Tolani, D.R.
J. Cell. Biochem. 57, 423-431, 1995
A: Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and aldolase B
A: Reference number: I51291; MUID: 95286677; PMID: 7768978
A: Accession: I51292
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 1-137 <MEI>
A: Cross-references: UNIPROT:P53449; GB:S78281; NID:g999391; PIDN:AAB34480.1; PID:g999392
C: Superfamily: fructose-bisphosphate aldolase

Query Match 58.0%; Score 58; DB 2; Length 137;
Best Local Similarity 52.6%; Pred. No. 0.043; Gaps 0;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SQGAGAAASELFISNHAY 20
||| ||| :||| :|||
Db 119 SGDDSGAAGQSLYVANHAY 137

RESULT 13
S45346
fructose-bisphosphate aldolase (EC 4.1.2.13) C, brain-type - African clawed frog

DB 344 AGSAG-AGGSLFVANHAY 361

RESULT 15

C42263

fructose 1,6-bisphosphate aldolase - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: C42263

R:Shaw-Lee, R.; Lissenmore, J.L.; Sullivan, D.T.; Tolan, D.R.

J. Biol. Chem. 267, 3959-3967, 1992

A:Title: Alternative splicing of fructose 1,6-bisphosphate aldolase transcripts in Drosophila

A:Reference number: A42263; MUID:92156139; PMID:174044

A:Accession: C42263

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <SHA>

A:Cross-references: UNIPROT:P07764; GB:M98351; GB:M76409; NID:g157395; PIDN:AAA99428.1;

A:Note: sequence extracted from NCBI backbone (NCBIN:82659, NCBIP:93286)

C:Genetics:

A:Gene: FlyBase:Ald

A:Cross-references: FlyBase:FBgn0000064

C:Superfamily: fructose-bisphosphate aldolase

Query Match 55.5%; Score 55.5; DB 2; Length 361;

Best Local Similarity 63.2%; Pred. No. 0.32;

Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 SQQAGAAASESLFISNHAY 20

DB 344 AGSAG-AGGSLFVANHAY 361

Search completed: June 20, 2005, 10:14:37

Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:49:19 ; Search time 113.5 Seconds
(without alignments)
90.234 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQQAASASLFTSNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	363	1 ALFA RABIT	P00883 oryctolagus
2	99	99.0	260	2 Q9BWD9	Q9bwd9 homo sapien
3	99	99.0	363	1 ALFA HUMAN	P04075 homo sapien
4	99	99.0	364	2 Q6FH76	Q6fh76 homo sapien
5	97	97.0	363	1 ALFA MOUSE	P05064 mus musculus
6	97	97.0	363	1 ALFA RAT	P05065 rattus norv
7	97	97.0	364	2 Q6NY00	Q6ny00 mus musculus
8	95	95.0	42	2 Q92007	Q92007 gallus gall
9	94	94.0	704	2 Q8WNT7	Q8wnt7 macaca fasc
10	89	89.0	331	2 Q76BG8	Q76bg8 ambystoma m
11	88	88.0	364	2 Q9CPQ9	Q9cpq9 m mus muscu
12	88	88.0	364	2 Q9CRC1	Q9cr1 m mus muscu
13	85	85.0	364	2 Q6GL64	Q6gl64 xenopus tro
14	83	83.0	364	2 Q6AY07	Q6ay07 rattus norv
15	83	83.0	364	2 Q12975	Q12975 xenopus lae
16	82	82.0	331	2 Q76BE7	Q76be7 amia calva
17	79	79.0	331	2 Q76YU5	Q76yu5 xenopus lae
18	79	79.0	279	2 Q76BF4	Q76bf4 lepisosteus
19	77	77.0	364	1 ALF2 LAMJA	P53446 lampetra ja
20	76	76.0	331	2 Q76B12	Q76b12 procterus
21	75	75.0	364	2 Q8JH72	Q8jh72 brachydanio
22	75	75.0	364	2 Q803Q7	Q803q7 brachydanio
23	74	74.0	331	2 Q76BB1	Q76bb1 callorhinch
24	73	73.0	331	2 Q76BC5	Q76bc5 cephaloscy
25	72	72.0	331	2 Q76BD2	Q76bd2 polypterus
26	72	72.0	364	2 Q6P043	Q6p043 brachydanio
27	71	71.0	331	2 Q76BD9	Q76bd9 acipenser b
28	71	71.0	331	2 Q9USF9	Q9usf9 eptatretus
29	70	70.0	331	2 Q76BE0	Q76be0 acipenser b
30	69.5	69.5	363	1 ALF1 LAMJA	P53445 lampetra ja
31	69	69.0	331	2 Q76BB8	Q76bb8 potamotrygo

32	69	69.0	364	2 Q7ZW73	Q7zw73 brachydanio
33	68	68.0	363	1 ALFC HUMAN	P09972 homo sapien
34	68	68.0	364	2 Q9GKW3	Q9gkw3 macaca fasc
35	68	68.0	394	2 Q6PUL5	Q6p015 homo sapien
36	65	65.0	331	2 Q76BC3	Q76bc3 cephaloscy
37	64	64.0	40	2 Q6UV41	Q6uv41 sus scrofa
38	64	64.0	330	2 Q76BF9	Q76bf9 oryzias lat
39	64	64.0	331	2 Q76BD7	Q76bd7 acipenser b
40	63	63.0	364	2 Q8JH71	Q8jh71 brachydanio
41	62	62.0	330	2 Q76BG1	Q76bg1 oryzias lat
42	61.5	61.5	363	2 Q57518	Q57518 spheroideus
43	61	61.0	331	2 Q76BF2	Q76bf2 lepisosteus
44	61	61.0	365	2 Q8I875	Q8i875 globodera r
45	61	61.0	366	1 ALF1 CAEEL	P54216 caenorhabdi

ALIGNMENTS

RESULT 1
ALFA_RABIT
ID ALFA_RABIT STANDARD; PRT; 363 AA.
AC P00883; Q28671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).
GN Name=ALDOA;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=74094688; PubMed=4812352;
RA Lai C.-Y., Nakai N., Chang D.;
RT "Amino acid sequence of rabbit muscle aldolase and the structure of
the active center";
RL Science 183:1204-1206 (1974).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84111505; PubMed=6546378;
RA Tolan D.R., Amsden A.B., Putney S.D., Urdea M.S., Penhoet E.E.;
RT "The complete nucleotide sequence for rabbit muscle aldolase A
messenger RNA.";
RL J. Biol. Chem. 259:1127-1131 (1984).
RN [3]
RP SEQUENCE OF 1-164.
RX MEDLINE=75145171; PubMed=1122141;
RA Nakai N., Chang D., Lai C.-Y.;
RT "Studies on the structure of rabbit muscle aldolase. Ordering of the
tryptic peptides; sequence of 164 amino acid residues in the NH2-
terminal BrcN peptide.";
RL Arch. Biochem. Biophys. 166:347-357 (1975).
RN [4]
RP SEQUENCE OF 173-200, AND REVISIONS.
RX MEDLINE=80109133; PubMed=534504;
RA Benfield P.A., Forcina B.G., Gibbons I., Perham R.N.;
RT "Extended amino acid sequences around the active-site lysine residue
of class-I fructose 1,6-bisphosphate aldolases from rabbit muscle,
sturgeon muscle, trout muscle and ox liver.";
RL Biochem. J. 183:429-444 (1979).
RN [5]
RP SEQUENCE OF 251-363, AND REVISION.
RX MEDLINE=75145172; PubMed=1122142;
RA Lai C.-Y.;
RT "Studies on the structure of rabbit muscle aldolase. Determination of
the primary structure of the COOH-terminal BrcN peptide; the complete
sequence of the subunit polypeptide chain.";
RL Arch. Biochem. Biophys. 166:358-368 (1975).
RN [6]
RP SEQUENCE OF 37-55 AND 349-363 FROM N.A.
RX MEDLINE=83167564; PubMed=687628;

RA Putney S.D., Herlihy W.C., Schimmel P.R.;
 RT "A new tropomyosin T and cDNA clones for 13 different muscle proteins,
 RL Nature 302:718-721(1983).
 RN (7)
 RP ACTIVE SITE.
 RX MEDLINE=741631196; PubMed=4857186;
 RA Hartman F.C., Welch M.H.;
 RT "Identification of the histidyl residue of rabbit muscle aldolase
 RL alkylated by N-bromoacetylthanolamine phosphate.";
 RN Biochem. Biophys. Res. Commun. 57:85-92(1974).
 RP ACTIVE SITE.
 RX MEDLINE=76190154; PubMed=5453;
 RA Hartman F.C., Brown J.P.;
 RT "Affinity labeling of a previously undetected essential lysyl residue
 RL in class I fructose biphosphate aldolase.";
 RN J. Biol. Chem. 251:3057-3062(1976).
 RP SUBSTRATE-BINDING SITE.
 RX MEDLINE=80046697; PubMed=499203;
 RA Pathy L., Varadi A., Thesz J., Kovacs K.;
 RT "Identification of the C-1-phosphate-binding arginine residue of
 RL rabbit-muscle aldolase. Isolation of 1,2-cyclohexanedione-labeled
 RL peptide by chemisorption chromatography.";
 RN Eur. J. Biochem. 99:309-313(1979).
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=971143309; PubMed=8989320;
 RA Blom N., Sygusch J.;
 RT "Product binding and role of the C-terminal region in class I D-
 RL fructose 1,6-bisphosphate aldolase.";
 RN Nat. Struct. Biol. 4:36-39(1997).
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 2-344 IN COMPLEX WITH
 RP SUBSTRATE, AND MUTAGENESIS OF GLU-34; ARG-42; LYS-146 AND ARG-303.
 RX PubMed=10504235; DOI=10.1021/bi982837i;
 RA Choi K.H., Mazurkie A.S., Morris A.J., Ucheza D., Tolan D.R.,
 RA Allen K.N.;
 RT "Structure of a fructose-1,6-bis(phosphate) aldolase liganded to its
 RL natural substrate in a cleavage-defective mutant at 2.3 A.";
 RN Biochemistry 38:12655-12664(1999).
 RP X-RAY CRYSTALLOGRAPHY (2.46 ANGSTROMS), AND MUTAGENESIS OF GLU-187;
 RP GLU-189 AND LYS-229.
 RX PubMed=11779856; DOI=10.1074/jbc.M107600200;
 RA Maurady A., Zdanov A., de Moissac D., Beaudry D., Sygusch J.;
 RT "A conserved glutamate residue exhibits multifunctional catalytic
 RL roles in D-fructose-1,6-bisphosphate aldolases.";
 CC J. Biol. Chem. 277:9474-9483(2002).
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- PATHWAY: Glycolysis; sixth step.
 CC -!- SUBUNIT: Tetramer of nearly identical chains, alpha and beta,
 CC which differ at only 1 position.
 CC -!- PTM: Asn-360 in the alpha chain is deaminated in the beta chain.
 CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 CC liver and aldolase C in brain.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 CC family.
 CC -!- DATABASE: NAME=Worthington enzyme manual;
 CC WWW="http://www.worthington-biochem.com/ALD".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; K02300; AAA31156.1; -.

DR EMBL; V00876; CAA24245.1; -.
 DR EMBL; V00877; CAA24246.1; -.
 DR PIR; A92444; ADRAA.
 DR PDB; IADO; X-ray; A/B/C/D=1-363.
 DR PDB; LEWD; X-ray; A/B/C/D=1-363.
 DR PDB; LEWG; X-ray; A/B/C/D=1-363.
 DR PDB; LEW5; X-ray; A/B/C/D=1-363.
 DR PDB; LJ4E; X-ray; A/B/C/D=1-363.
 DR PDB; 6ALD; X-ray; A/B/C/D=1-363.
 DR InterPro; IPR000741; Aldolase I.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW 3D-structure: Direct protein sequencing; Glycolysis; Lyase;
 KW Multigene family; Schiff base.
 FT INIT_MET 0
 FT SITE 72 72 Essential for substrate cleavage.
 FT SITE 107 107 Essential for substrate cleavage.
 FT SITE 146 146 Alkylates inactivates the enzyme.
 FT ACT_SITE 187 187 Proton acceptor.
 FT ACT_SITE 229 229 Schiff-base intermediate with
 FT SITE 361 361 dihydroxyacetone-P.
 FT essential for the subsequent hydrolysis
 FT of the dihydroxyacetone Schiff base.
 FT Necessary for preference for fructose
 FT 1,6-bisphosphate over fructose 1-
 FT phosphate.
 FT BINDING 42 42 C-6-phosphate group of the substrate,
 FT BINDING 303 303 alkylation inactivates the enzyme.
 FT MOD_RES 360 360 C-6-phosphate group of the substrate.
 FT MUTAGEN 34 34 Deamidated asparagine (in beta chain).
 FT MUTAGEN 42 42 E->A: Reduces activity 14-fold.
 FT MUTAGEN 146 146 R->A: Reduces activity 14-fold.
 FT MUTAGEN 187 187 K->A: Loss of activity.
 FT MUTAGEN 189 187 E->A: Reduces activity over 100-fold.
 FT MUTAGEN 229 229 E->Q: Reduces activity over 1000-fold.
 FT MUTAGEN 303 303 E->M: Loss of activity 20-fold.
 FT CONFLICT 34 34 R->A: Reduces activity 400-fold.
 FT CONFLICT 273 275 E -> Q (in Ref. 3).
 FT CONFLICT 275 275 QQS -> SQE (in Ref. 5).
 FT CONFLICT 293 295 S -> E (in Ref. 5).
 FT CONFLICT 353 353 KPW -> WPK (in Ref. 5).
 FT HELIX 9 22 S -> R (in Ref. 6).
 FT TURN 23 23
 FT TURN 25 26
 FT STRAND 28 32
 FT HELIX 36 45
 FT TURN 46 47
 FT TURN 52 63
 FT TURN 64 64
 FT HELIX 67 72
 FT STRAND 73 78
 FT HELIX 80 83
 FT TURN 84 84
 FT STRAND 86 86
 FT TURN 88 89
 FT STRAND 92 92
 FT HELIX 93 99
 FT TURN 100 101
 FT STRAND 103 107
 FT STRAND 112 114
 FT TURN 116 117
 FT STRAND 122 124
 FT TURN 128 129
 FT HELIX 130 139
 FT TURN 140 141
 FT STRAND 144 151
 FT HELIX 160 179
 FT TURN 180 181

KW	Glycolysis; Lyase.
FT	NON TER
SQ	SEQUENCE 260 AA; 27898 MW; 861B9CDE0F1E2784 CRC64;
Query Match	99.0%; Score 99; DB 2; Length 260;
Best Local Similarity	95.0%; Pred. No. 1.le-07;
Matches 19; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
QY	1 PSQGAGAAASESLFISNHAY 20
Db	241 PSQGAGAAASESLFVSNHAY 260
RESULT 3	
ALFA HUMAN	
ID	ALFA HUMAN STANDARD; PRT; 363 AA.
AC	P04075;
DT	01-NOV-1986 (Rel. 03, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Fragment).
DN	Name=ALDOA; Synonyms=ALDA;
OS	Homo sapiens (Human);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Fibroblast;
RX	MEDLINE=87161904; PubMed=3030757;
RA	Izzo P., Costanzo P., Lupo A., Rippa E., Borghese A.M., Paolella G.,
RA	A Salvatore F.;
RT	"A new human species of aldolase A mRNA from fibroblasts.";
RL	Eur. J. Biochem. 164:9-13(1987).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88371327; PubMed=3391172;
RA	Izzo P., Costanzo P., Lupo A., Rippa E., Paolella G., Salvatore F.;
RT	"Human aldolase A gene. Structural organization and tissue-specific expression by multiple promoters and alternate mRNA processing.";
RL	Eur. J. Biochem. 174:569-578(1988).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=85306986; PubMed=3840020;
RA	Sakakibara M., Mukai T., Hori K.;
RT	"Nucleotide sequence of a cDNA clone for human aldolase: a messenger RNA in the liver.";
RL	Biochem. Biophys. Res. Commun. 131:413-420(1985).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91153319; PubMed=1999195;
RA	Mukai T., Araki Y., Yatsuki H., Joh K., Hori K.;
RT	"An additional promoter functions in the human aldolase A gene, but not in rat.";
RL	Eur. J. Biochem. 195:781-787(1991).
RN	[5]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Cervix, Eye, Lung, Testis, and Uterus;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA	Stausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Hong L.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Skalko J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalaka U., Smallick D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RA	Strausberg R.;
RN	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RA	Strausberg R.;
CC	-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase family
DR	EMBL; BC000367; AH003367.2; --
DR	EMBL; BC016170; AAH16170.1; --
DR	HSP; P04075; IALD.
DR	GO; GO:0004332; P:fructose-bisphosphate aldolase activity; IEA.
DR	GO; GO:0006096; P:glycolysis; IEA.
DR	InterPro; IPR000741; Aldolase_1.
DR	Tram; PF00274; Glycolytic; 1.
DR	PRODom; PD001128; Aldolase_I; 1.
DR	PROSITE; PS00158; ALDOLASE CLASS I; UNKNOWN 1.

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE
RX MEDLINE=88183272; PubMed=3355497;
RA Freemon P.S., Dunbar B., Fothergill-Gilmore L.A.;
RT "The complete amino acid sequence of human skeletal-muscle fructose-
RT biphosphate aldolase.";
RL Biochem. J. 249:779-788(1998).
RN [7]
RP SEQUENCE OF 1-62 AND 147-357.
RX MEDLINE=84126818; PubMed=6696436;
RA Freemon P.S., Dunbar B., Fothergill L.A.;
RT "Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr-
RT and o-iodosobenzoic acid-cleavage fragments.";
RL Arch. Biochem. Biophys. 228:342-352(1984).
RN [8]
RP SEQUENCE OF 1-107 FROM N.A.
RX MEDLINE=88155643; PubMed=3441006;
RA Maire P., Gautron S., Hakim V., Gregori C., Mennecier F., Kahn A.;
RT "Characterization of three optional promoters in the 5' region of the
RT human aldolase A gene.";
RL J. Mol. Biol. 197:425-438(1987).
RN [9]
RP SEQUENCE OF 138-363 FROM N.A.
RX MEDLINE=88046782; PubMed=3674018;
RA Tolan D.R., Nicolas J., Bruce B.D., Lebo R.V.;
RT "Evolutionary implications of the human aldolase-A, -B, -C, and -
RT pseudogene chromosome locations.";
RL Am. J. Hum. Genet. 41:907-924(1987).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=90242948; PubMed=2335208; DOI=10.1016/0014-5793(90)80211-Z;
RA Gamblin S.J., Cooper B., Millar J.R., Davies G.J., Littlechild J.A.,
RA Watson H.C.;
RT "The crystal structure of human muscle aldolase at 3.0-A resolution.";
RL FEBS Lett. 262:282-286(1990).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91278081; PubMed=2056525;
RA Gamblin S.J., Davies G.J., Grimes J.M., Jackson R.M.,
RA Littlechild J.A., Watson H.C.;
RT "Activity and specificity of human aldolases.";
RL J. Mol. Biol. 219:573-576(1991).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99156067; PubMed=10048322;
RA Dalby A., Dauter Z., Littlechild J.A.;
RT "Crystal structure of human muscle aldolase complexed with fructose
RT 1,6-bisphosphate: mechanistic implications.";
RL Protein Sci. 8:291-297(1999).
RN [13]
RP VARIANT HEMOLYTIC ANEMIA GLY-128.
RX MEDLINE=88068641; PubMed=2825199;
RA Kishi H., Mukai T., Hirono A., Fujii H., Miwa S., Hori K.;
RT "Human aldolase A deficiency associated with a hemolytic anemia:
RT thermolabile aldolase due to a single base mutation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8623-8627(1987).
RN [14]
RP VARIANT HEMOLYTIC ANEMIA GLY-128.
RX MEDLINE=91035340; PubMed=2229018;
RA Takasaki Y., Takahashi I., Mukai T., Hori K.;
RT "Human aldolase A of a hemolytic anemia patient with Asp-128-->Gly
RT substitution: characteristics of an enzyme generated in E. coli
RT transfected with the expression plasmid pHAAD128G.";
RL J. Biochem. 108:153-157(1990).
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone

phosphate + D-glyceraldehyde 3-phosphate.
-!- PATHWAY: Glycolysis; sixth step.
-!- SUBUNIT: Homotrimer.
-!- DISEASE: Defects in ALDOA are a cause of hemolytic anemia
[MIM:103050].
-!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
glycolytic enzyme are found, aldolase A in muscle, aldolase B in
liver and aldolase C in brain.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
family.

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EMBL; X05236; CAA28861.1; -.
EMBL; M11560; AAA51690.1; -.
EMBL; X06352; CAA29654.1; -.
EMBL; X12447; CAA30379.1; ALT_SEQ.
EMBL; BC004333; AAH04333.1; -.
EMBL; BC010660; AAH10660.1; -.
EMBL; BC012880; AAH12880.1; -.
EMBL; BC013614; AAH13614.1; -.
EMBL; BC015888; AAH15888.1; -.
EMBL; BC016800; AAH16800.1; -.
EMBL; M21190; AAA51697.1; -.
PIR; S14084; ADHUA.
PDB; 1ALD; X-ray; @=1-363.
PDB; 2ALD; X-ray; A=1-363.
PDB; 4ALD; X-ray; @=1-363.
DR SWISS-2DPAGE; P04075; HUMAN.
DR Aathus/Ghent-2DPAGE; 1302; NEPHGE.
DR OGP; P04075; -.
DR Siena-2DPAGE; P04075; -.
DR Genew; HGNC:414; ALDOA.
DR H-INVDB; HIX0012935; -.
DR Reactome; P04075; -.
DR MIM; 103850; -.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; TAS.
DR GO; GO:0006000; P:fructose metabolism; TAS.
DR GO; GO:0006096; P:glycolysis; TAS.
DR GO; GO:0006941; P:striated muscle contraction; TAS.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW 3D-structure; Direct protein sequencing; Disease mutation; Glycolysis;
KW Lyase; Multigene family; Schiff base.
FT INIT MET 0
FT ACT_SITE 187 187 Proton acceptor (By similarity).
FT ACT_SITE 229 229 Schiff-base intermediate with
FT ACT_SITE 229 229 dihydroxyacetone-P.
FT SITE 363 363 Necessary for preference for fructose
FT SITE 363 363 1,6-bisphosphate over fructose 1-
FT BINDING 55 55 phosphate.
FT BINDING 146 146 C-1-phosphate group of the substrate.
FT VARIANT 128 128 D -> G (in hemolytic anemia;
FT VARIANT 128 128 thermolabile).
FT /FTid=VAR_000550.
FT HELIX 9 22
FT TURN 23 23
FT TURN 25 26
FT STRAND 28 32
FT HELIX 36 45
Query Match 99.0%; Score 99; DB 1; Length 363;
Best Local Similarity 95.0%; Pred. No. 1.5e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASLSIFSNHAY 20
 DB 344 PSQAGAAASLSIFSNHAY 363

RESULT 4

Q6FH76 PRELIMINARY; PRT; 364 AA.
 AC Q6FH76;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DE ALDOA protein (Fragment).
 GN Name=ALDOA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., LaBaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 CC family.
 DR EMBL; CR541880; CAG46678.1; --
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000741; Aldolase_1.
 DR Pfam; PF00274; Glycolytic_1.
 DR ProDom; PD001128; Aldolase_1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
 KW Glycolysis; Lyase.
 FT NON_TER 364
 SQ SEQUENCE 364 AA; 39448 MW; 0B7DD9DDA4897BEB CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
 Best Local Similarity 95.0%; Pred. No. 1.5e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASLSIFSNHAY 20
 DB 345 PSQAGAAASLSIFSNHAY 364

RESULT 5

ALFA_MOUSE STANDARD; PRT; 363 AA.
 AC P05064;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
 DE (Aldolase 1).
 GN Name=Aldoa; Synonyms=Aldol1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=129.
 RC MEDLINE=88096598; PubMed=3697100;
 RX Mestek A., Stauffer J., Tolan D.R., Ciejek-Baez E.;
 RA "Sequence of a mouse brain aldolase A cDNA."
 RL Nucleic Acids Res. 15:10595-10595 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE OF 1-265 AND 294-363 FROM N.A.
 RX MEDLINE=90307699; PubMed=2365699;
 RA Stauffer J.K., Colbert M.C., Ciejek-Baez E.;
 RT "Nonconservative utilization of aldolase A alternative promoters."
 RL J. Biol. Chem. 265:11773-11782 (1990).
 RN [4]
 RP SEQUENCE OF 98-354 FROM N.A.
 RX MEDLINE=86192445; PubMed=3009179;
 RA Paoletta G., Buono P., Mancini P., Izzo P., Salvatore F.;
 RT "Structure and expression of mouse aldolase genes. Brain-specific
 RT aldolase C amino acid sequence is closely related to aldolase A."
 RL Eur. J. Biochem. 156:229-235 (1986).
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- PATHWAY: Glycolysis; sixth step.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 CC liver and aldolase C in brain.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 CC family.
 CC -----
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 CC -----
 DR EMBL; X03797; CAA37423.1; --
 DR EMBL; BC043026; AAH43026.1; --
 DR EMBL; BC050896; AAH50896.1; --
 DR EMBL; J05517; AAA37210.2; --
 DR EMBL; Y00516; CAA68571.1; --
 DR FIR; S06323; ADMSA.
 DR HSP; P00883; IADO.
 DR SWISS-2DPAGE; P05064; MOUSE.
 DR MGD; MGI:87994; Aldol.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR InterPro; IPR000741; Aldolase_1.
 DR Pfam; PF00274; Glycolytic_1.
 DR ProDom; PD001128; Aldolase_1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase; Multigene family; Schiff base.
 FT INIT_MET 0
 FT ACT_SITE 187 187 Proton acceptor (By similarity).
 FT ACT_SITE 229 229 Schiff-base intermediate with
 FT dihydroxyacetone-P.
 FT SITE 363 363 Necessary for preference for fructose
 FT 1,6-bisphosphate over fructose 1-

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FT BINDING 55 55 phosphate.
FT BINDING 146 146 C-1-phosphate group of the substrate.
FT CONFLICT 280 280 S -> C (in Ref. 4).
SQ SEQUENCE 363 AA; 39224 MW; 62D27089F284BF74 CRC64;

Query Match 97.0%; Score 97; DB 1; Length 363;
Best Local Similarity 95.0%; Pred. No. 3.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQGAASSESLFISNHAY 20
    ||||:|||||
DB 344 PSGQGAASSESLFISNHAY 363

RESULT 6
ALFA_RAT
ID ALFA_RAT STANDARD; PRT; 363 AA.
AC P05065;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).
GN Name=Aldoa;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86140113; PubMed=3753977;
RA Mukai T., Joh K., Arai Y., Yatsuki H., Hori K.;
RT "Tissue-specific expression of rat aldolase A mRNAs. Three molecular
RT species differing only in the 5'-terminal sequences.";
RL J. Biol. Chem. 261:3347-3354 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86083188; PubMed=2416636; DOI=10.1016/0378-1119(85)90102-7;
RA Joh K., Mukai T., Yatsuki H., Hori K.;
RT "Rat aldolase A messenger RNA: the nucleotide sequence and multiple
RT mRNA species with different 5'-terminal regions.";
RL Gene 39:17-24 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87060996; PubMed=3783705;
RA Joh K., Arai Y., Mukai T., Hori K.;
RT "Expression of three mRNA species from a single rat aldolase A gene,
RT differing in their 5' non-coding regions.";
RL J. Mol. Biol. 190:401-410 (1986).
CC -! CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -! PATHWAY: Glycolysis; sixth step.
CC -! SUBUNIT: Homotetramer.
CC -! MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
CC liver and aldolase C in brain.
CC -! SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC family.

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EMBL; M12919; AAA40714.1; -
DR EMBL; M14420; AAA40715.1; -
DR EMBL; X04261; CAA27815.1; -
DR EMBL; X04262; CAA27815.1; JOINED.
DR EMBL; X04263; CAA27815.1; JOINED.
DR EMBL; X04264; CAA27815.1; JOINED.

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DR PIR; A24532; ADRTA.
DR HSSP; P00883; IADO.
DR Rat-heart-2DPAGE; P05065; -.
DR RGD; 2089; Aldoa.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase; Multigene family; Schiff base.
FT INIT MET 0
FT ACT_SITE 187 187 Proton acceptor (by similarity).
FT ACT_SITE 229 229 Schiff-base intermediate with
FT 363 363 dihydroxyacetone-P.
FT SITE 363 363 Necessary for preference for fructose
FT 1,6-bisphosphate over fructose 1-
FT phosphate.
FT BINDING 55 55 C-1-phosphate group of the substrate.
FT BINDING 146 146 C-1-phosphate group of the substrate.
FT CONFLICT 144 144 F -> S (in Ref. 2).
FT CONFLICT 164 164 M -> V (in Ref. 2).
SQ SEQUENCE 363 AA; 39220 MW; 48A0468B9E3B9DB8 CRC64;

Query Match 97.0%; Score 97; DB 1; Length 363;
Best Local Similarity 95.0%; Pred. No. 3.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQGAASSESLFISNHAY 20
    ||||:|||||
DB 344 PSGQGAASSESLFISNHAY 363

RESULT 7
Q6NY00 PRELIMINARY; PRT; 364 AA.
AC Q6NY00;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Aldolase 1, A isoform.
GN Name=Aldoa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr, and C3H/He;
RC TISSUE=Hematopoietic Stem Cell, and Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;

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RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RA Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 family.
 CC
 DR EMBL; BC066801; AAH66801.1; -.
 DR EMBL; BC066218; AAH66218.1; -.
 DR HSSP; P00883; IADO.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.
 DR InterPro; IPR000741; Aldolase_1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase.
 SQ SEQUENCE 364 AA; 39312 MW; 5BD82BBE3B6D738A CRC64;

Query Match 97.0%; Score 97; DB 2; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.2e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAAGAAASESLFISNHAY 20
 |||||
 DB 345 PSQGAAGAAASESLFISNHAY 364

RESULT 8

Q22007 PRELIMINARY; PRT; 42 AA.
 AC Q92007
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Aldolase C (Aldolase A) (Fragment).
 GN Name=aldolase C;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95286677; PubMed=7768978;
 RA Meighan-Mantha R.L., Tolan D.R.;
 RT "Noncoordinate changes in the steady-state mRNA expressed from
 RT aldolase A and aldolase C genes during differentiation of chicken
 RT myoblasts.";
 RL J. Cell. Biochem. 57:423-431(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Meighan-Mantha R.L., Tolan D.R.;
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Meighan-Mantha R.L., Tolan D.R.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; S78288; AAB34479.1; -.
 DR EMBL; L25374; AAA99864.1; -.
 DR EMBL; L25373; AAA48588.1; -.
 DR PIR; I51291; I51291.
 DR HSSP; P00883; 6ALD.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR Pfam; PF00274; Glycolytic; 1.
 FT NON_TER 42
 FT NON_TER 42
 SQ SEQUENCE 42 AA; 4384 MW; 780E34B8C695DC4B CRC64;

Query Match 95.0%; Score 95; DB 2; Length 42;
 Best Local Similarity 95.0%; Pred. No. 7.1e-08;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAAGAAASESLFISNHAY 20
 |||||
 DB 23 PSQGAAGAAASESLFISNHAY 42

RESULT 9

Q8WNT7 PRELIMINARY; PRT; 704 AA.
 ID Q8WNT7
 AC Q8WNT7
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fructose-1,6-bisphosphate aldolase A.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
 RA Terao K., Sugano S., Hashimoto K.;
 RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
 RT in the human genome sequence.";
 RL BMC Genomics 3:36-36(2002).
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 family.
 CC EMBL; AB066558; BAB84033.1; -.
 DR HSSP; P04075; 2ALD.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
 KW Glycolysis; Lyase.
 SQ SEQUENCE 704 AA; 74686 MW; 02D9A004C37DFF39 CRC64;

Query Match 94.0%; Score 94; DB 2; Length 704;
 Best Local Similarity 90.0%; Pred. No. 2e-06;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAAGAAASESLFISNHAY 20
 |||||
 DB 685 PSQGAAGAAASESLFISNHAY 704

RESULT 10

Q76BG8 PRELIMINARY; PRT; 331 AA.
 ID Q76BG8
 AC Q76BG8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fructose-bisphosphate aldolase A (Fragment).
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tail;
 RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,
 RA Miyata T.;
 RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-

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RT coded genes."
RL BMC Biol. 2:3-3(2004).
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC family.
DR EMBL; AB111374; BAD17888.1; -.
DR HSP; P04075; 1ALD.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
FT NON_TER
SQ SEQUENCE 331 AA; 36170 MW; B7374F829DE6C591 CRC64;

Query Match 89.0%; Score 89; DB 2; Length 331;
Best Local Similarity 85.0%; Pred. No. 5.8e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSNHAY 20
Db 312 PSAQAGAAAGESLFSNHAY 331
||| ||||| ||||| |||||
||| ||||| ||||| |||||

RESULT 11
Q9CPQ9 PRELIMINARY; PRT; 364 AA.
AC Q9CPQ9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933417120 product:FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC
DE 4.1.2.13) (MUSCLE-TYPE ALDOLASE) homolog (Mus musculus adult male
DE testis cDNA, RIKEN full-length enriched library, clone:4921524E03
DE product:FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE
DE ALDOLASE) homolog).
GN Name=Aldoa; Synonyms=Aldol;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC STRAIN=C57BL/6J; Akimura T., Arai A., Aono H.,
RA Adachi J., Aizawa K., Akahira S., Fukuda S., Fukunishi Y., Furuno M.,
RA Arakawa T., Bono H., Carninci P., Hiramoto K., Hiraoka T., Hori F.,
RA Hanagaki T., Hara A., Hayatsu N., Izawa M., Kasukawa T., Kato H.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Koya S., Kurihara C.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Nomura K., Numazaki R., Ohno M.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Sakai K.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC family.
CC EMBL; AK016845; BAB30459.1; -.
DR EMBL; AK014956; BAB29638.1; -.
DR HSP; P04075; 2ALD.
DR MGI; MGI:87994; Aldoa.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39285 MW; 53C8A3919977FF2F CRC64;

Query Match 88.0%; Score 88; DB 2; Length 364;
Best Local Similarity 85.0%; Pred. No. 9.4e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSNHAY 20
Db 345 PSGKTGATASELSLFSNHAY 364
||| ||| ||||| |||||
||| ||||| ||||| |||||

RESULT 12
Q9CRC1 PRELIMINARY; PRT; 364 AA.
AC Q9CRC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933425L11 product:fructose-bisphosphate aldolase (EC
DE 4.1.2.13) A homolog (Mus musculus adult male testis cDNA, RIKEN full-
DE length enriched library, clone:1700027120 product:fructose-
DE bisphosphate aldolase (EC 4.1.2.13) A homolog).
GN Name=4933425L11R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Iehi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Tova T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
family
CC EMBL; AK016920; BAB30498.1; -.
DR EMBL; AK006425; BAB24582.1; -.
DR HSSP; P04075; 2ALD.
DR GO; GO:0004332; P:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39372 MW; 28BE4763348E44F CRC64;

DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39370 MW; 0360CD12B8509A0D CRC64;

Query Match 88.0%; Score 88; DB 2; Length 364;
Best Local Similarity 85.0%; Pred. No. 9.4e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAAGAAASESLFISNHAY 20
||:|||||
Db 345 PSNESGAAGAAASESLFISNHAY 364

RESULT 13
Q6GL64 PRELIMINARY; PRT; 364 AA.
AC Q6GL64;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Aldoa-prov protein.
GN Name=aldoa-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Roshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gehard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
family
CC EMBL; BC074643; AH74643.1; -.
DR GO; GO:0004332; P:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39372 MW; 28BE4763348E44F CRC64;

Query Match 85.0%; Score 85; DB 2; Length 364;
Best Local Similarity 84.2%; Pred. No. 2.9e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2  SQGAGAAASESLFISNHAY 20
      ||:||||| ||||:|||||
Db      346  SGEAGAAAGESLFVFNHAY 364

RESULT 14
Q6AY07
ID      Q6AY07      PRELIMINARY;      PRT;      364 AA.
AC
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Hypothetical protein.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,
RA      Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA      Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RA      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RA      Director MGC Project;
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC      phosphate + D-glyceraldehyde 3-phosphate.
CC      -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC      family.
DR      EMBL; BC079243; AAH79243.1; -.
DR      GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR      GO; GO:0006096; P:glycolysis; IEA.
DR      InterPro; IPR000741; Aldolase_I.
DR      Pfam; PF00274; Glycolytic; 1.
DR      ProDom; PD001128; Aldolase_I; 1.
DR      PROSITE; PS00158; Aldolase_CLASS_I; 1.
KW      Glycolysis; Hypothetical protein; Lyase.
SQ      SEQUENCE 364 AA; 39492 MW; B77BE52EC6672195 CRC64;

Query Match      83.0%; Score 83; DB 2; Length 364;
Best Local Similarity 80.0%; Pred. No. 6.1e-05;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  PSQGAGAAASESLFISNHAY 20
      ||:||||| ||||:|||||
Db      345  PSDEGAVASESLFISNHAY 364

RESULT 15
O12975
ID      O12975      PRELIMINARY;      PRT;      364 AA.

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AC      O12975;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DT      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Aldolase (MGC53030 protein).
OS      Xenopus laevis (African clawed frog).
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=98087400; PubMed=9427528; DOI=10.1016/S0167-4781(97)00086-9;
RA      Hikasa H., Hori K., Shiohawa K.;
RT      "Structure of muscle-type (type-A) aldolase cDNA and its regulated
RT      expression in oocytes, embryos and adult tissue of Xenopus laevis.";
RL      Biochim. Biophys. Acta 1354:189-203(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Yatsuki H.;
RL      Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA      Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA      Richardson P.;
RT      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT      initiative.";
RL      Dev. Dyn. 225:384-391(2002).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Strausberg R.;
RL      Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC      -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC      phosphate + D-glyceraldehyde 3-phosphate.
CC      -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC      family.
DR      EMBL; AB022267; BAA19524.1; -.
DR      EMBL; BC046673; AAH46673.1; -.
DR      HSP; P00883; IADO.
DR      GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR      GO; GO:0006096; P:glycolysis; IEA.
DR      InterPro; IPR000741; Aldolase_I.
DR      Pfam; PF00274; Glycolytic; 1.
DR      ProDom; PD001128; Aldolase_I; 1.
DR      PROSITE; PS00158; Aldolase_CLASS_I; 1.
KW      PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW      Glycolysis; Lyase.

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SQ SEQUENCE 364 AA; 39386 MW; 2F2A5142A4BB3986 CRC64;
Query Match 83.0%; Score 83; DB 2; Length 364;
Best Local Similarity 84.2%; Pred. NO. 6.1e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 SGOAGAAASESLFISNHAY 20
Db 346 SGDAGAAAGESLFVSNHAY 364

Search completed: June 20, 2005, 10:13:44
Job time : 115.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:48:14 ; Search time 119 Seconds
(without alignments)
65.002 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQGAGAAASESLFTSNHAY 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	2	AAR37301 Rabbit Mu
2	99	99.0	153	5	ABP42706 Human ova
3	99	99.0	363	2	AAV071116 Lung canc
4	99	99.0	364	2	AAV06992 Glycolyti
5	99	99.0	364	7	ADP76857 Novel hum
6	99	99.0	364	7	ADP68731 Human hea
7	99	99.0	364	8	ADP771178 Human pro
8	99	99.0	364	8	ADI02918 Human fru
9	99	99.0	364	8	ADQ76754 Human fru
10	99	99.0	364	8	ABW81754 Tumour-as
11	97	97.0	364	7	ADB79827 Rat aldol
12	95	95.0	31	3	AAB44017 Human can
13	68	68.0	364	5	ABP65148 Hypoxia-r
14	68	68.0	364	7	ADJ68292 Human hea
15	68	68.0	364	8	ADL12661 Human ste
16	61	61.0	365	8	ADN23270 Bacterial
17	55.5	55.5	361	4	ABB66969 Drosophil
18	52	52.0	366	8	ADN23082 Bacterial
19	50.5	50.5	215	8	ABO60233 Human gen
20	50.5	50.5	836	7	ABR83671 Human bkl
21	50.5	50.5	836	7	ADM05015 Human pro
22	50.5	50.5	836	8	ADO85827 Different
23	48	48.0	1772	8	ADR12606 Gene vacc
24	47	47.0	1223	4	ABB63399 Drosophil
25	46	46.0	9	8	ADN63558 HLA bindi

26	46	46.0	9	8	ADN64270 HLA bindi
27	46	46.0	132	6	ABP96323 Human AGE
28	46	46.0	170	6	ABU01993 S. pneumo
29	46	46.0	170	8	ADK46838 Streptoco
30	46	46.0	171	8	ADR95229 Novel S.
31	46	46.0	283	4	AAM93735 Human pol
32	46	46.0	283	8	ADL31668 Human pro
33	46	46.0	292	6	AAO19583 Human pho
34	46	46.0	292	6	ABB99461 Protein S
35	46	46.0	295	6	AAO19582 Human pho
36	46	46.0	295	8	ADR10068 Human pro
37	46	46.0	324	5	ABP69378 Human pol
38	46	46.0	324	8	ADP29611 Human sec
39	46	46.0	364	6	ABR47389 Breast ca
40	46	46.0	364	7	ABU64480 Human fru
41	46	46.0	364	8	ABW81063 Tumour-as
42	46	46.0	644	7	ADJ69390 Human hea
43	46	46.0	811	5	ABP43842 DXFp564M
44	46	46.0	896	8	ADO67676 Novel hum
45	46	46.0	902	8	ABO58476 Human gen

ALIGNMENTS

RESULT 1

AAR37301

ID AAR37301 standard; protein; 20 AA.

XX

AC AAR37301;

XX

DT 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX

DE Rabbit Muscle aldolase peptide segment.

XX

KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin; human engineered antibody;
KW variable region; light chain; cell targeting; chimeric antibody; RNA;
KW linker.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT Cleavage-site 1..20

FT FT /note= "contains several potential cathepsin cleavage sites"

XX

PN WO9309130-A1.

XX

PD 13-MAY-1993.

XX

PF 04-NOV-1992; 92MO-US009487.

XX

PR 04-NOV-1991; 91US-00787567.

XX

PR 19-JUN-1992; 92US-00901707.

XX

PA (XOMA) XOMA CORP.

XX

PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX

XX WPI; 1993-167617/20.

DR

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic agents; immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo.

XX

PS Example 10; Page 115; 163pp; English.

XX

CC The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules

CC are antibodies or their fragments, esp. human engineered H65 antibody
CC fragments. Fusion constructs were assembled that included a natural
CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an
CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of
CC the rabbit muscle aldolase was inserted between the gelonin gene and the
CC Ab gene. The resulting immunoconjugates can be used as cytotoxic
CC therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSINHAY 20
|||||
DB 1 PSGQAGAAASLSLFSINHAY 20
|||||

RESULT 2
ID ABP42706 standard; protein; 153 AA.
XX
AC ABP42706;
XX
XX 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HOPKN14, SEQ ID NO:3838.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX
XX N-PSDB; ABQ55783.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 3838; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 153 AA;

Query Match 99.0%; Score 99; DB 5; Length 153;
Best Local Similarity 95.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFSINHAY 20
|||||
DB 134 PSGQAGAAASLSLFSINHAY 153
|||||

RESULT 3
RAY07116
ID AA07116 standard; protein; 363 AA.
XX
AC AA07116;
XX
XX 02-JUL-1999 (first entry)
XX
XX Lung cancer associated antigen precursor sequence.
XX
XX Cancer associated antigen; diagnosis; research; treatment; human;
XX breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX prostate cancer.
XX
XX Homo sapiens.
XX
XX WO9904265-A2.
XX
XX 28-JAN-1999.
XX
XX 15-JUL-1998; 98WO-US014679.
XX
XX 17-JUL-1997; 97US-00896164.
XX
XX 10-OCT-1997; 97US-0061599P.
XX
XX 10-OCT-1997; 97US-0061765P.
XX
XX 10-OCT-1997; 97US-00948705.
XX
XX 11-OCT-1997; 97GB-00021697.
XX
XX 22-JUN-1998; 98US-00102322.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX WPI; 1999-132448/11.
XX
XX New isolated cancer associated nucleic acids and polypeptides - isolated
XX using sera from cancer patients, used to develop products for the
XX diagnosis, monitoring or treatment of cancers.
XX
XX Disclosure; Page 733-734; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer
 XX Sequence 363 AA;
 SQ

Query Match 99.0%; Score 99; DB 2; Length 363;
 Best Local Similarity 95.0%; Pred. No. 3.6e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
 Db 344 PSQAGAAASESLFVSNHAY 363
 |||||

RESULT 4
 AAY06992
 ID AAY06992 standard; protein; 364 AA.
 XX
 AC AAY06992;
 XX
 DT 02-JUL-1999 (first entry)
 DE Glycolytic enzyme aldolase A.
 XX
 KW Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO9904265-A2.
 XX
 PD 28-JAN-1999.
 XX
 PF 15-JUL-1998; 98WO-US014679.
 XX
 PR 17-JUL-1997; 97US-00896164.
 PR 10-OCT-1997; 97US-0061599P.
 PR 10-OCT-1997; 97US-0061765P.
 PR 10-OCT-1997; 97US-00948705.
 PR 11-OCT-1997; 97GB-00021697.
 PR 22-JUN-1998; 98US-00102322.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
 PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
 XX
 DR WPI; 1999-132448/11.
 DR N-PSDB; AAX40193.
 XX
 XX New isolated cancer associated nucleic acids and polypeptides - isolated
 PT using sera from cancer patients, used to develop products for the
 PT diagnosis, monitoring or treatment of cancers.
 XX
 PS Example 8; Page 769-770; 787pp; English.
 XX
 CC The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a

CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer
 XX Sequence 364 AA;
 SQ

Query Match 99.0%; Score 99; DB 2; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
 Db 345 PSQAGAAASESLFVSNHAY 364
 |||||

RESULT 5
 ADF76857
 ID ADF76857 standard; protein; 364 AA.
 XX
 AC ADF76857;
 XX
 DT 26-FEB-2004 (first entry)
 DE Novel human secreted and transmembrane protein SeqID 532.
 XX
 KW human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neuroepithelial; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072035-A2.
 XX
 PD 04-SEP-2003.
 XX
 PF 21-FEB-2003; 2003WO-US005241.
 XX
 PR 22-FEB-2002; 2002US-0359461P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WI, Wu TD;
 XX
 DR WPI; 2003-721702/68.
 DR N-PSDB; ADF76856.
 XX
 XX New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.
 XX
 PS Claim 10; SEQ ID NO 532; 918pp; English.
 XX
 CC This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neuroepithelial and hormones) which are received and interpreted by diverse

CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytosolic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.

XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 7; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQQAAGAAASESLFISNHAY 20
 |||||:|||||:|||||
 Db 345 PSQQAAGAAASESLFVSNHAY 364

RESULT 6

ADJ68731
 ID ADJ68731 standard; protein; 364 AA.

XX AC ADJ68731;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID537.

XX KW mitochondrial; human; screening assay; diabetes mellitus;

XX KW Huntington's disease; osteoarthritis;

XX KW Leber's hereditary optic neuropathy; LHON;

XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;

XX KW osteopathic; ophthalmological; cytosolic.

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

XX PI Warnock DE;

XX DR WPI; 2003-845369/78.

XX CC Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.

XX PS Claim 1; SEQ ID NO 537; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nontropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytosolic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 7; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQQAAGAAASESLFISNHAY 20
 |||||:|||||:|||||
 Db 345 PSQQAAGAAASESLFVSNHAY 364

RESULT 7

ADE77178
 ID ADE77178 standard; protein; 364 AA.

XX AC ADE77178;

XX DT 29-JAN-2004 (first entry)

XX DE Human protein expressed in a liver disorder #87.

XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
 KW tumour; liver; inflammatory disorder; immune response disorder;
 KW high-throughput screening; differential gene expression; gene therapy.

XX OS Homo sapiens.

XX PN US2003108871-A1.

XX PD 12-JUN-2003.

XX PF 30-JUL-2001; 2001US-00919039.

XX PR 28-JUL-2000; 2000US-0222113P.

XX PA (KASE/) KASER M R.

XX PI Kaser MR;

XX DR WPI; 2004-031227/03.

XX DR N-PSDB; ADE77177.

XX CC Composition comprising several cDNAs that are differentially expressed in
 PT treated human C3A liver cell cultures, useful for treating liver
 PT disorders.

XX PS Claim 1; SEQ ID NO 343; 41pp; English.

XX CC The invention relates to a composition comprising several cDNAs that are
 CC differentially expressed in a liver disorder. The composition is useful
 CC for treating liver disorder such as hyperlipidaemia, hypertension, type
 CC II diabetes, tumours of the liver and disorders of the inflammatory and
 CC immune response. The composition is useful for a high-throughput method
 CC of screening several molecules or compounds to identify a ligand which
 CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
 CC high-throughput method for using a protein to screen several molecules or
 CC compounds to identify at least one ligand which specifically binds the
 CC protein which involves combining the protein encoded by the cDNA with
 CC several of molecules or compounds under conditions to allow specific
 CC binding, and detecting specific binding between the protein and a
 CC molecule or compound, therefore identifying a ligand which specifically

CC binds the protein. The composition is useful for detecting and
 CC quantifying differential gene expression, can be used in gene therapy, to
 CC formulate prognosis and to design a treatment regimen and to monitor the
 CC efficacy of treatment. The present sequence represents the amino acid
 CC sequence of a protein encoded by a cDNA differentially expressed in a
 CC liver disorder.
 XX
 SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20
 |||||
 DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 8

AD102918
 ID AD102918 standard; protein; 364 AA.

XX AC AD102918;

XX DT 22-APR-2004 (first entry)

XX DE Human fructose-bisphosphate aldolase.

XX KW gene database preparation; cDNA microarray; human;
 fructose-bisphosphate aldolase; GP2; enzyme.

XX OS Homo sapiens.

XX PN JP2004005319-A.

XX PD 08-JAN-2004.

XX PF 10-JUN-2002; 2002JP-00168894.

XX PR 24-APR-2002; 2002JP-00123176.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX PA (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.

XX DR WPI; 2004-113174/12.

XX DR N-PSDB; AD102917.

XX PT Gene database production method for microarray preparation, comprises
 PT searching homology of a candidate sequence determined by a primer probe
 PT designing unit, for a matching candidate sequence.

XX PS Disclosure; Fig 9; 33pp; Japanese.

XX CC The invention relates to a method for preparing a gene database. The
 CC method comprises a search unit searching homology of a candidate sequence
 CC determined by a primer probe designing unit, for determining homologous
 CC presence or absence of a determined candidate sequence. The method of the
 CC invention is useful for the preparation of a microarray, such as a cDNA
 CC microarray. The present amino acid sequence represents a human fructose-
 CC bisphosphate aldolase.
 XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20
 |||||
 DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 9

ADQ76754

XX ID ADQ76754 standard; protein; 364 AA.

XX AC ADQ76754;

XX DT 07-OCT-2004 (first entry)

XX DE Human fructose bisphosphate aldolase A, target for anti-HIV agent.

XX KW Human; fructose bisphosphate aldolase A; enzyme;
 human immunodeficiency virus; HIV; anti-HIV; virucide.

XX OS Homo sapiens.

XX PN WO2004061088-A2.

XX PD 22-JUL-2004.

XX PF 30-DEC-2003; 2003WO-US041790.

XX PR 30-DEC-2002; 2002US-0436936P.

XX PA (PPDP-) PPD DEV LP.

XX PI Dunn SJ;

XX DR WPI; 2004-534379/51.

XX DR N-PSDB; ADQ76753.

XX PT Use of an inhibitor of a member of a biological pathway for inhibiting,
 PT suppressing, treating, or preventing human immunodeficiency virus (HIV)
 PT infection.

XX PS Claim 1; SEQ ID NO 22; 143pp; English.

XX CC The present sequence is that of human fructose bisphosphate aldolase A
 CC (ALDOA), which has been identified as a cellular target for HIV
 CC inhibition. The invention relates to methods for identifying human
 CC cellular genes that encode products that are necessary for productive HIV
 CC infection for use as targets in the design of therapeutic agents for
 CC suppressing HIV infection. The invention also includes methods for
 CC identifying biological pathways comprising the products of such cellular
 CC genes, as well as substrates and metabolic products of these pathways,
 CC and methods for identifying additional human cellular genes that encode
 CC products comprising other members of such pathways for use as targets in
 CC the design of therapeutic agents for suppressing HIV infection. It also
 CC relates to methods for identifying protective compounds that inhibit HIV
 CC infection and to the use of such compounds in the treatment or prevention
 CC of HIV. The compounds include chemical compounds such as small molecule
 CC inhibitors or substrate compounds such as products of chemical
 CC combinatorial libraries, or biological compounds including peptides,
 CC antisense molecules and antibodies. In one embodiment of the invention,
 CC the target gene encodes a target product that is a member of the
 CC glycolysis pathway of the host cell. Random fragment expression libraries
 CC were constructed from mRNA isolated from HU-60 and Hela cells, and from
 CC phytohemagglutinin-stimulated peripheral blood mononuclear cells (PBMC).
 CC These were used for the isolation and identification of human cell-
 CC derived genetic suppressor elements (GSEs) exhibiting HIV suppressive
 CC activity. The human cellular genes from which these GSEs were derived
 CC were identified, and included the ALDOA gene from a PBMC library.
 XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
 Best Local Similarity 95.0%; Pred. No. 3.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20
 |||||
 DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 10

```
ABM81754
ID  ABM81754 standard; protein; 364 AA.
AC  ABM81754;
XX
XX
XX  18-NOV-2004 (first entry)
DT
DE
DE
XX  Tumour-associated antigenic target (TAT) polypeptide PRO69617, SEQ:4521.
XX
XX  Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW  tumour; diagnosis; cell proliferative disorder; breast cancer;
KW  colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW  central nervous system cancer; bladder cancer; pancreatic cancer;
KW  cervical cancer; melanoma; leukaemia; hybridisation probe;
KW  chromosome identification; chromosome mapping; gene mapping;
XX  gene therapy; cytostatic.
XX
XX  Homo sapiens.
OS
XX
XX  WO2004030615-A2.
FN
XX
XX  15-APR-2004.
PD
XX
XX  29-SEP-2003; 2003WO-US028547.
PF
XX
XX  02-OCT-2002; 2002US-0414971P.
PR
XX
XX  (GETH ) GENENTECH INC.
PA
XX
XX  Wu TD, Zhang Z, Zhou Y;
PI
XX
XX  WPI; 2004-347921/32.
DR
XX
XX  N-PSDB; ACN40010.
DR
XX
XX  New tumor-associated antigenic target polypeptides and nucleic acids,
PT  useful in preparing a medicament for treating or detecting a
PT  proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT  prostate cancer or tumor.
XX
XX  Claim 12; SEQ ID NO 4521; 7273pp; English.
PS
XX
XX  The invention relates to human tumour-associated antigenic target (TAT)
CC  polypeptides, and their related nucleic acids. The TAT polypeptides are
CC  overexpressed in cancer tissues compared to normal tissues, and may thus
CC  serve as effective targets for the diagnosis and treatment of cancer in
CC  mammals. The invention also relates to nucleic acid and polypeptide
CC  sequences at least 80% identical to the TAT nucleic acids and
CC  polypeptides; expression vectors and host cells comprising a TAT nucleic
CC  acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC  molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC  TAT polypeptide; and methods and compositions for the treatment or
CC  diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC  antibodies, antagonists, binding molecules and compositions are useful
CC  for diagnosing or treating a cell proliferative disorder associated with
CC  increased TAT expression, particularly cancers such as breast cancer,
CC  colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC  cancer, pancreatic cancer, cervical cancer, cancers of the central
CC  nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC  used as hybridisation probes, in chromosome and gene mapping, in
CC  chromosome identification and in gene therapy. The present sequence
CC  represents a TAT polypeptide of the invention
XX
XX  Sequence 364 AA;
SQ
Query Match          99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 3.7e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 PSGQAGAAASESLFISNHAY 20
    |||||
DB  345 PSGQAGAAASESLFISNHAY 364

RESULT 12
AAB44017
ID  AAB44017 standard; protein; 31 AA.
XX
XX  AAB44017;
AC
XX
XX  08-FEB-2001 (first entry)
DT
XX
XX  Human cancer associated protein sequence SEQ ID NO:1462.
DE
XX
XX  Human; cancer associated gene; cancer antigen; detection; cancer;
KW  diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
KW  antidiabetic; antiaesthetic; antirheumatic; antithrombotic; antiviral;
KW  antiinflammatory; antihypertensive; antiallergic; antibacterial; cardiac;
KW  dermatological; neuroprotective; thrombolytic; coagulant; nontoxic;
KW  vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW  immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW  allergic reaction; graft versus host disease; organ rejection;
KW  haemostatic; thrombolytic; cardiovascular disorder; infection;
```

neurological disease; drug screening.

Homo sapiens.

WO200055350-A1.

21-SEP-2000.

08-MAR-2000; 2000WO-US005882.

12-MAR-1999; 99US-0124270P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2000-587533/55.

N-PSDB; AAC78226.

Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.

Claim 11; Page 2142; 2352pp; English.

AAC77607 to AAC78448 encode the human cancer associated proteins given in

AAB43398 to AAB44239. The proteins can have activities based on the

tissues and cells the proteins are expressed in. Example of activities

include: cytostatic; proliferative; vulnary; immunomodulator;

antidiabetic; antiallergic; antirheumatic; antiarthritic;

antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;

dermatological; neuroprotective; cardiant; thrombolytic; coagulant;

neotropic; vasotropic; antipsoriatic and angiogenic. The

polynucleotides and polypeptides can be used for preventing, treating or

ameliorating medical conditions and diagnosing pathological conditions.

Polynucleotides, polypeptides, antibodies, agonists and antagonists from

the present invention may be used to treat immune disorders by activating

or inhibiting the proliferation, differentiation or mobilisation of

immune cells; to treat disorders of haematopoietic cells, autoimmune

disorders, allergic reactions, graft versus host disease and organ

rejection, modulate haemostatic or thrombolytic activity, modulate

inflammation, cancers, cardiovascular disorders, neurological disease and

bacterial or viral infections. The peptides, nucleotides, antibodies,

agonists and antagonists may be also be used in drug screens. AAC78449 to

AAC78457 and AAB44240 represent sequences used in the exemplification of

the present invention

Sequence 31 AA;

Query Match 95.0%; Score 95; DB 3; Length 31;

Best Local Similarity 90.0%; Pred. No. 9.8e-09;

Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20

DB 12 PXGAGAAASESLFVSNHAY 31

RESULT 13

ABP65148

ID ABP65148 standard; protein; 364 AA.

XX: ABP65148;

AC ABP65148;

XX 12-NOV-2002 (first entry)

DT

XX Hypoxia-regulated protein #22.

DE

XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;

KW antiinflammatory; vulnary; gynecological; ophthalmological; vaccine;

KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;

KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;

KW presclapmsia; atherosclerosis; inflammatory condition; wound healing;

KW inflammation; erythropoiesis; hair loss; human.

neurological disease; drug screening.

Homo sapiens.

WO200246465-A2.

13-JUN-2002.

10-DEC-2001; 2001WO-GB005458.

08-DEC-2000; 2000GB-00030076.

08-FEB-2001; 2001GB-00003156.

25-OCT-2001; 2001GB-00025666.

(OXFO-) OXFORD BIOMEDICA UK LTD.

White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;

Rayner WN;

WPI; 2002-627238/57.

Identifying a gene involved in disease for treating hypoxia-regulated

conditions, comprises comparing the transcriptome/proteome of two cell

types under different conditions and identifying a differentially

regulated gene.

Claim 35; Page 345; 538pp; English.

The present invention relates to methods for identifying genes and

proteins that are implicated in a specific disease or physiological

condition. The method comprises comparing the transcriptome/proteome of a

specialised cell type implicated in a disease or condition with that of a

second specialised cell type, under two experimental conditions, and

identifying a gene that is differentially regulated in the two

specialised cell types under experimental conditions. ABV7873-ABV78116

and ABP65061-ABP65257 were identified using the methods of the invention.

The coding sequences and proteins are useful for treating a disease in a

patient, for manufacture of a medicament for treating hypoxia-regulated

conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,

biological response to hypoxia conditions, or hypoxic-associated

pathology in a patient. The coding sequences and proteins are also useful

for monitoring the therapeutic treatment of a disease or physiological

condition, such as cancer, ischaemic conditions, reperfusion injury,

retinopathy, neonatal stress, presclapmsia, atherosclerosis, inflammatory

conditions, wound healing, inflammation, erythropoiesis or hair loss

Sequence 364 AA;

Query Match 68.0%; Score 68; DB 5; Length 364;

Best Local Similarity 63.2%; Pred. No. 0.0075;

Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SQGAGAAASESLFISNHAY 20

DB 346 SGEDGAAQAQSLYIANHAY 364

RESULT 14

ADJ68292

ID ADJ68292 standard; protein; 364 AA.

XX ADJ68292;

AC ADJ68292;

XX 06-MAY-2004 (first entry)

DT

XX Human heat mitochondrial protein as a therapeutic target SeqID98.

DE

XX mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; neotropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

```

XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX PI Warnock DE;
XX DR WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX PS Claim 1; SEQ ID NO 98; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, neurotropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytoskeletal activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX SQ Sequence 364 AA;

Query Match 68.0%; Score 68; DB 7; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.0075;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGOAGAAASESLFISNHAY 20
||:||||:||||:||||
Db 346 SGEDGAAQAQSLYIANHAY 364

RESULT 15
ADL12661
ID ADL12661 standard; protein; 364 AA.
XX AC ADL12661;
XX DT 06-MAY-2004 (first entry)
XX DE Human steroid-induced C3A liver cell protein #59.
XX KW Hepatotropic; Gene therapy; Wilson disease; liver disorder;
XX KW steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
XX OS Homo sapiens.
XX PN US6673549-B1.
XX PD 06-JAN-2004.

```

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XX 12-OCT-2001; 2001US-00976594.
XX PF
XX PR 12-OCT-2000; 2000US-0240409P.
XX PA (INCY-) INCYTE CORP.
XX PI Furness LM, Buchbinder JL;
XX DR WPI; 2004-068610/07.
XX PT Combination useful for preparing a composition for treating liver
XX PT disorders associated with steroid therapy, e.g., cirrhosis or hepatitis,
XX PT comprises cDNAs that are differentially expressed in response to steroid
XX PT treatment.
XX PS Disclosure; SEQ ID NO 390; 141pp; English.
XX CC The invention relates to a combination comprising cDNAs that are
XX CC differentially expressed in response to steroid treatment. Also included
XX CC are the following: a high throughput method for using a cDNA to detect
XX CC differential expression of nucleic acids in a sample; and a high
XX CC throughput method of screening molecules or compounds to identify a
XX CC ligand that specifically binds a cDNA. The sample is from a subject with
XX CC Wilson disease and comparison of a standard defines a stage of that
XX CC disease. The high throughput method of screening molecules or compounds
XX CC to identify a ligand that specifically binds a cDNA comprises: combining
XX CC the combination with molecules or compounds under conditions to allow
XX CC specific binding; and detecting specific binding between each cDNA and at
XX CC least one molecule or compound. The molecules or compounds are regulatory
XX CC proteins. The combination is useful for preparing a composition for
XX CC treating liver disorders associated with steroid therapy, e.g., cirrhosis
XX CC or hepatitis. The present sequence represents a human protein which is
XX CC differentially expressed in steroid-induced C3A liver cells. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 364 AA;

Query Match 68.0%; Score 68; DB 8; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.0075;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGOAGAAASESLFISNHAY 20
||:||||:||||:||||
Db 346 SGEDGAAQAQSLYIANHAY 364

Search completed: June 20, 2005, 10:09:53
Job time : 122 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:13:56 ; Search time 108.5 Seconds

(without alignments)
70.780 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQAGAAASLFTSNHAY 20

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	20	14	US-10-127-890-57
2	100	100.0	20	17	US-10-717-243-57
3	99	99.0	153	15	US-10-264-049-3838
4	99	99.0	364	10	US-09-919-039-343
5	99	99.0	364	16	US-10-408-765A-537
6	99	99.0	364	16	US-10-370-715B-532
7	97	97.0	364	14	US-10-205-219-67
8	96	96.0	112	16	US-10-425-115-196160
9	95	95.0	31	9	US-09-925-301-1462
10	68	68.0	364	15	US-10-170-385-259
11	68	68.0	364	16	US-10-408-765A-98

12	61	61.0	365	15	US-10-369-493-5923	Sequence 5923, Ap
13	55.5	55.5	361	13	US-10-108-605-255	Sequence 255, App
14	52	52.0	366	15	US-10-389-493-5735	Sequence 5735, Ap
15	51	51.0	358	16	US-10-767-701-46629	Sequence 46629, A
16	51	51.0	361	16	US-10-425-115-269098	Sequence 269098, A
17	51	51.0	371	15	US-10-425-114-65982	Sequence 65982, A
18	51	51.0	371	16	US-10-425-115-269100	Sequence 269100, A
19	50.5	50.5	215	14	US-10-029-386-33867	Sequence 33867, A
20	50.5	50.5	836	15	US-10-108-260A-3700	Sequence 3700, Ap
21	46	46.0	98	15	US-10-424-599-161041	Sequence 161041, A
22	46	46.0	132	16	US-10-484-364-2	Sequence 2, Appli
23	46	46.0	170	17	US-10-472-928-3140	Sequence 3140, Ap
24	46	46.0	332	15	US-10-425-114-44042	Sequence 44042, A
25	46	46.0	355	15	US-10-425-114-44220	Sequence 44220, A
26	46	46.0	355	15	US-10-425-114-45677	Sequence 45677, A
27	46	46.0	358	15	US-10-424-593-22971	Sequence 22971, A
28	46	46.0	364	14	US-10-177-293-8	Sequence 8, Appli
29	46	46.0	372	15	US-10-425-114-43852	Sequence 43852, A
30	46	46.0	372	15	US-10-425-114-44097	Sequence 44097, A
31	46	46.0	372	15	US-10-425-114-44837	Sequence 44837, A
32	46	46.0	375	15	US-10-425-114-45592	Sequence 45592, A
33	46	46.0	375	15	US-10-425-114-51423	Sequence 51423, A
34	46	46.0	375	15	US-10-425-114-55978	Sequence 55978, A
35	46	46.0	375	15	US-10-425-114-55981	Sequence 55981, A
36	46	46.0	392	16	US-10-437-963-151748	Sequence 151748, A
37	46	46.0	416	16	US-10-437-963-180885	Sequence 180885, A
38	46	46.0	644	16	US-10-408-765A-1196	Sequence 1196, Ap
39	46	46.0	902	14	US-10-029-386-32110	Sequence 32110, A
40	45.5	45.5	404	16	US-10-767-701-46406	Sequence 46406, A
41	45.5	45.5	404	16	US-10-425-115-351374	Sequence 351374, A
42	45.5	45.5	414	15	US-10-425-114-70495	Sequence 70495, A
43	45	45.0	267	14	US-10-314-657-50	Sequence 50, Appl
44	45	45.0	267	17	US-10-473-193-50	Sequence 50, Appl
45	45	45.0	403	16	US-10-437-963-114024	Sequence 114024, A

ALIGNMENTS

RESULT 1

US-10-127-890-57

; Sequence 57, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Heid & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIORITY DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

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; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-127-830-57

Query Match 100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 2
US-10-717-243-57
; Sequence 57, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
```

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; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 110222US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-717-243-57

Query Match 100.0%; Score 100; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 3
US-10-264-049-3838
; Sequence 3838, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3838
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3838

Query Match 99.0%; Score 99; DB 15; Length 153;
Best Local Similarity 95.0%; Pred. No. 7.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
Db 134 PSGQAGAAASESLFVSNHAY 153

RESULT 4
US-09-919-039-343
; Sequence 343, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 343
; LENGTH: 364
; TYPE: PRT
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 2706606CD1
US-09-919-039-343

Query Match 99.0%; Score 99; DB 10; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
|||:|||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 5

US-10-408-765A-537
Sequence 537, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 537
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-537

Query Match 99.0%; Score 99; DB 16; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
|||:|||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 6

US-10-370-715B-532
Sequence 532, Application US/10370715B
Publication No. US20040258678A1
GENERAL INFORMATION:
Patin Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BRISDELL, HUNTE
APPLICANT: JACKMAN, JANET
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 532
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapien

US-10-370-715B-532

Query Match 99.0%; Score 99; DB 16; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
|||:|||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 7

US-10-205-219-67
Sequence 67, Application US/10205219
Publication No. US20030138803A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Pincock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
LENGTH: 364
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Aldolase A
US-10-205-219-67

Query Match 97.0%; Score 97; DB 14; Length 364;
Best Local Similarity 95.0%; Pred. No. 4e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
|||:|||||:|||||:
Db 345 PSGQAGAAASESLFISNHAY 364

RESULT 8

US-10-425-115-196160
Sequence 196160, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 196160
LENGTH: 112
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(112)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_110484C.1.pap
US-10-425-115-196160

Query Match 96.0%; Score 96; DB 16; Length 112;
Best Local Similarity 95.0%; Pred.No. 1.6e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	PSGQGAASESLFISNHAY	20
D _b	93	PSGOXGAAASESLFISNHAY	112

RESULT 9

```

US-09-925-301-1462
; Sequence 1462, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1462
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1462

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Query Match	95.0%	Score 95;	DB 9;	Length 31;
Best Local Similarity	90.0%;	Pred. No. 5.7e-08;		
Matches 18:	Conservative	1: Mismatches	1: Indels	0: Gaps

```

QY      1  PSGQAGAAASESLFISNHAY 20
      | | | | | | | | | | | | | |
Db      12 PXGOAGAAASESLFVSNHAY 31

```

RESULT 10

```

US/10-170-385-259
; Sequence 259, Application US/10170385
; Publication No. US2003020372A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
;
; TITLE OF INVENTION: ANALYSIS METHOD
;
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
;
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
;
; NUMBER OF SEQ ID NOS: 549
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 259
;
; LENGTH: 364
;
; TYPE: PRT
;
; ORGANISM: Homo Sapiens

```

US-10-170-385-259

Query Match 68.0%; Score 68; DB 15; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.019;
Matches 12: Conservative 5; Mismatches 2; Indels

QY 2 SQAGAAASESLFISNHAY 20
 ||: | |:| |:| |:|
Db 346 SGEDGGAASOPLYIANHAY 364

RESULT 11

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US-10-408-765A-98
; Sequence 98, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-98

```

Query Match 68.0%; Score 68; DB 16; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.019;
Matches 12; Conservative 5; Mismatches 2; Indels

Qy 2 SGQGAASESLFISNHAY 20
||:| ||:| ||:| ||:|
Db 346 SGEDGAAQSLYIANHAY 364

RESULT 12

```

US-10-369-493-5923
; Sequence 5923, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5923
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5923

```

Query Match 61.0%; Score 61; DB 15; Length 365;
Best Local Similarity 68.8%; Pred. No. 0.26;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Qy      5 AGAAASESLFISNHAY 20
         | ||| : ||| : ||| :
Db     350 ADAAASQSLEFVANHSY 365
```

RESULT 13

```

US-10-108-605-255
; Sequence 255, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kandari, Kim
; TITLE OF INVENTION: NUCLEOTIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-255

```

Query Match 55.5%; Score 55.5; DB 13; Length 361;
Best Local Similarity 63.2%; Pred. No. 2;
Matches 12; Conservative 3; Mismatches 3; Indels 1

```

Qy      2  SQAGAAASESLFISNHAY 20
          :| | | | | | | | | | | |
Db      344 AGSAG-AGSGSLEFVANHAY 361

```

RESULT 14

```

US-10-369-493-5735
; Sequence 5735, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5735
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5735

```

Query Match 52.0%; Score 52; DB 15; Length 366;
Best Local Similarity 56.2%; Pred. No. 7.4;
Matches 9; Conservative 4; Mismatches 3; Indels

Qy 5 AGAAASESLFISNHAY 20
| : | : | : | : | : |
Db 351 AAGAAAESLFVAKHSY 366

RESULT 15

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US-10-767-701-46629
; Sequence 46629, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCES: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46629
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C104_46.ppep
US-10-767-701-46629

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Query Match 51.0%; Score 51; DB 16; Length 358;
Best Local Similarity 52.6%; Pred. No. 10;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHAY 20
DB 340 SGAGDAAASESLYVKGYK 358

Search completed: June 20, 2005, 10:40:20
Job time : 109.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:36:43 ; Search time 29.5 Seconds
(without alignments)
50.610 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARMASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	20	1 US-07-988-430-58	Sequence 58, Appl
2	114	100.0	20	1 US-08-425-336-56	Sequence 56, Appl
3	114	100.0	20	1 US-08-488-1138-56	Sequence 56, Appl
4	114	100.0	20	1 US-08-477-4848-56	Sequence 56, Appl
5	114	100.0	20	2 US-08-646-360-56	Sequence 56, Appl
6	114	100.0	20	3 US-08-839-765-56	Sequence 56, Appl
7	114	100.0	20	3 US-09-136-389-56	Sequence 56, Appl
8	114	100.0	20	3 US-09-610-838-56	Sequence 56, Appl
9	114	100.0	20	4 US-09-711-485-56	Sequence 56, Appl
10	114	100.0	20	5 PCT-US92-09487-58	Sequence 58, Appl
11	36	31.6	16	1 US-08-109-391A-6	Sequence 6, Appl
12	36	31.6	16	1 US-08-459-019A-6	Sequence 6, Appl
13	36	31.6	16	1 US-08-408-120-14	Sequence 14, Appl
14	36	31.6	16	2 US-08-460-428A-6	Sequence 6, Appl
15	36	31.6	16	3 US-08-482-304-21	Sequence 21, Appl
16	36	31.6	16	3 US-08-483-474-21	Sequence 21, Appl
17	36	31.6	16	3 US-08-458-860A-6	Sequence 6, Appl
18	36	31.6	16	4 US-09-391-270-21	Sequence 21, Appl
19	34	29.8	9	4 US-09-129-192C-51	Sequence 51, Appl
20	34	29.8	18	3 US-09-208-277-8	Sequence 8, Appl
21	34	29.8	18	4 US-09-556-877-8	Sequence 8, Appl
22	34	29.8	18	4 US-09-288-594A-8	Sequence 8, Appl
23	34	29.8	18	4 US-09-620-412C-8	Sequence 8, Appl
24	34	29.8	18	4 US-09-410-568-8	Sequence 8, Appl
25	34	29.8	18	4 US-09-598-419-8	Sequence 8, Appl
26	33	28.9	7	3 US-09-219-849-11	Sequence 11, Appl
27	33	28.9	7	4 US-09-809-517A-12	Sequence 12, Appl

28 33 28.9 12 2 US-08-752-852A-120 Sequence 120, Appl
29 33 28.9 13 3 US-09-331-362-8 Sequence 8, Appl
30 33 28.9 13 4 US-09-823-266-5 Sequence 5, Appl
31 33 28.9 18 4 US-09-395-017B-28 Sequence 28, Appl
32 32 28.1 16 3 US-08-706-945D-145 Sequence 145, Appl
33 32 28.1 19 4 US-09-933-999A-31 Sequence 31, Appl
34 31 27.2 10 1 US-08-687-226-70 Sequence 70, Appl
35 31 27.2 10 3 US-08-556-978B-10 Sequence 10, Appl
36 31 27.2 10 4 US-09-239-043D-2266 Sequence 2266, Appl
37 31 27.2 10 5 PCT-US95-04975-19 Sequence 19, Appl
38 31 27.2 13 3 US-08-556-978B-40 Sequence 40, Appl
39 31 27.2 18 3 US-08-895-707-15 Sequence 15, Appl
40 31 27.2 18 3 US-08-952-127-17 Sequence 17, Appl
41 30 26.3 18 3 US-08-856-841-8 Sequence 8, Appl
42 29 25.4 10 4 US-09-239-043D-2319 Sequence 2319, Appl
43 29 25.4 12 1 US-07-616-910-25 Sequence 25, Appl
44 29 25.4 12 5 PCT-US91-08497-25 Sequence 25, Appl
45 29 25.4 16 1 US-07-906-871-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-07-988-430-58

; Sequence 58, Application US/07988430

; Patent No. 5416202

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Lane, Julie A.

; APPLICANT: Lei, Shau-Ping

; TITLE OF INVENTION: Materials Comprising and Methods of

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/988,430

; FILING DATE: 19921209

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5416202and, Greta E.

; REGISTRATION NUMBER: 35302

; REFERENCE/DOCKET NUMBER: 31133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-07-988-430-58

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 2

US-08-425-336-56
; Sequence 56, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-425-336-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 3

US-08-488-113B-56
; Sequence 56, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-113B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 4

US-08-477-484B-56
; Sequence 56, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-484B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSC 20
DB 1 CHHHSRVARMASDEFPSC 20

RESULT 5
US-08-646-360-56
Sequence 56, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-360-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSC 20
DB 1 CHHHSRVARMASDEFPSC 20

RESULT 6
US-08-839-765-56
Sequence 56, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-839-765-56

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```

Query Match      100.0%; Score 114; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CHHHSRVARVMSDEFFPSMC 20
Db      1 CHHHSRVARVMSDEFFPSMC 20

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RESULT 7
US-09-136-389-56
; Sequence 56, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-389-56

Query Match      100.0%; Score 114; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHHHSRVARVMSDEFFPSMC 20
Db      1 CHHHSRVARVMSDEFFPSMC 20

RESULT 8
US-09-610-838-56
; Sequence 56, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389

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;; FILING DATE: 18-AUG-1998
;; APPLICATION NUMBER: 08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION DATA:
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 56:
;; TYPE: amino acids
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-610-838-56

Query Match 100.0%; Score 114; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARVASDEFPSC 20
DB 1 CHHHSRVARVASDEFPSC 20

RESULT 9
US-09-711-485-56
; Sequence 56, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 56:
;; TYPE: amino acids
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-711-485-56

Query Match 100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARVASDEFPSC 20
DB 1 CHHHSRVARVASDEFPSC 20

RESULT 10
PCT-US92-09487-58
; Sequence 58, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-09487-58

Query Match 100.0%; Score 114; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFFSMC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CHHHSRVARVASDEFFSMC 20

RESULT 11
US-08-109-391A-6
; Sequence 6, Application US/08109391A
; Patent No. 5639876
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grieve, Robert B.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING NOVEL
; TITLE OF INVENTION: PARASITIC HELMINTH PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/109,391A
; FILING DATE: 19-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-109-391A-6

Query Match 31.6%; Score 36; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 MASDEFFSMC 20
| | | | | | | | | | | | | | | | | | | | | |

Db 1 MAQDAFPNAC 10
RESULT 12
US-08-459-019A-6
; Sequence 6, Application US/08459019A
; Patent No. 5686080
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grieve, Robert B.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P4 PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, #3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,019A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 33,020
; REFERENCE/DOCKET NUMBER: 2618-13-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-459-019A-6
Query Match 31.6%; Score 36; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 MASDEFFSMC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 MAQDAFPNAC 10

RESULT 13
US-08-408-120-14
; Sequence 14, Application US/08408120
; Patent No. 5804200
; GENERAL INFORMATION:
; APPLICANT: GRIEVE, ROBERT B.
; APPLICANT: FRANK, GLENN R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFICATION
; TITLE OF INVENTION: OF VACCINES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,120
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,257
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 27010-20006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-408-120-14

Query Match 31.6%; Score 36; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFPMC 20
DB 1 MAQDAFPNAC 10

RESULT 14
US-08-460-428A-6
Sequence 6, Application US/08460428A
Patent No. 5912337
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
TITLE OF INVENTION: P220 PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,428A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-13-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-428A-6

Query Match 31.6%; Score 36; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFPMC 20
DB 1 MAQDAFPNAC 10

RESULT 15
US-08-482-304-21
Sequence 21, Application US/08482304
Patent No. 6060281
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH PLA2 PROTEINS AND
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,304
FILING DATE:
CLASSIFICATION: 254
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-304-21

Query Match 31.6%; Score 36; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFPMC 20
DB 1 MAQDAFPNAC 10

Search completed: June 20, 2005, 10:59:06
Job time : 30.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:27:32 ; Search time 23 Seconds
(without alignments)
83.667 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHASRVARWASDEFPSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	25.4	20	2	H22565
2	26	22.8	20	2	S33001
3	25	21.9	18	2	A61577
4	25	21.9	20	2	S18582
5	24	21.1	9	2	S66635
6	24	21.1	13	2	AB0764
7	24	21.1	15	2	A28965
8	24	21.1	16	1	LFEC
9	24	21.1	16	2	C90981
10	24	21.1	16	2	A85827
11	24	21.1	20	2	I79432
12	24	21.1	20	2	T50757
13	24	21.1	20	2	A61414
14	23	20.2	20	2	I55663
15	22	19.3	18	1	A58589
16	22	19.3	20	2	D4164
17	22	19.3	20	2	S78760
18	21	18.4	15	2	B60763
19	21	18.4	17	2	B86323
20	21	18.4	17	2	JQ2310
21	21	18.4	17	2	JQ2320
22	20	17.5	10	2	S63478
23	20	17.5	11	2	A55149
24	20	17.5	11	2	A14454
25	20	17.5	12	2	PN0663
26	20	17.5	13	2	H85575
27	20	17.5	16	2	PH1637
28	20	17.5	20	2	B48400
29	19	16.7	6	2	S71349

30 19 16.7 10 2 PH1592 Ig H chain V-D-J r
31 19 16.7 10 2 A37268 Ig heavy chain C r
32 19 16.7 12 2 A35585 cytokinin-binding
33 19 16.7 13 2 S15755 actin 7 - soybean
34 19 16.7 15 2 PA0088 protein QF200051 -
35 19 16.7 15 2 S30608 translation elonga
36 19 16.7 16 2 S55307 glutathione transf
37 19 16.7 16 2 S78415 ribosomal protein
38 19 16.7 17 2 A34835 ribosomal protein
39 19 16.7 17 2 S15754 actin 6 - soybean
40 19 16.7 17 2 G83975 hypothetical prote
41 19 16.7 17 2 S77901 methyllitaconate De
42 19 16.7 18 2 F49215 urease (EC 3.5.1.5
43 19 16.7 18 2 S57518 T cell receptor be
44 19 16.7 19 2 PC1323 endopeptidase Clp
45 19 16.7 19 2 S02808 nucleolin - bovine

ALIGNMENTS

RESULT 1

H22565
R-phycoerythrin gamma-C chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
C:Accession: H22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: H22565
A:Molecule type: protein
A:Residues: 1-20 <KLO>

A:Cross-references: UNIPROT:Q7M270

C:Superfamily: Aglaothamnium neglectum R-phycoerythrin gamma chain 33

Query Match 25.4%; Score 29; DB 2; Length 20;

Best Local Similarity 37.5%; Pred. No. 3.2e+02;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CHHHASRV 8

DB 7 CHHETQI 14

RESULT 2

S33001

hypothetical protein - human herpesvirus 4

C:Species: human herpesvirus 4, Epstein-Barr virus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S33001

R:Farrell, P. J.

submitted to the EMBL Data Library, March 1988

A:Reference number: S32973

A:Accession: S33001

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-20 <FAR>

A:Cross-references: UNIPROT:Q9QCF1; EMBL:V01555; NID:g59074; PIDN:CAA24847.1; PID:gl33486

Query Match 22.8%; Score 26; DB 2; Length 20;

Best Local Similarity 38.5%; Pred. No. 9.6e+02;

Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 SRVARNASDEFPS 18

DB 8 SFTSSIGNSDPA 20

RESULT 3

A61577

24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)

C:Species: Streptomyces fradiae
 C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
 C:Accession: A61577
 R:Sinha, U.; Wolz, S.A.; Lad, P.J.
 Int. J. Biochem. 23, 979-984, 1991
 A>Title: Two new extracellular serine proteases from Streptomyces fradiae.
 A:Reference number: A61577; MUID:92155439; PMID:1786859
 A:Accession: A61577
 A:Molecule type: protein
 A:Residues: 1-18 <SIN>
 A:Cross-references: UNIPROT:Q7M198
 C:Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 21.9%; Score 25; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 ASDEFPMS 19
 | : |||||
 Db 7 AAQEFPWM 14

RESULT 4
 S18582
 hypothetical protein K (pufQ 3' region) - Rhodobacter sphaeroides
 C:Species: Rhodobacter sphaeroides
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994
 C:Accession: S18582; S32855
 R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
 Mol. Microbiol. 5, 2649-2661, 1991
 A>Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg
 A:Reference number: S18580; MUID:92140030; PMID:1779756
 A:Accession: S18582
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-20 <HUN>
 A:Cross-references: EMBL:X68795

Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 HHASRVAR 10
 | : | : |
 Db 9 HNFVASVLR 17

RESULT 5
 S66635
 alpha-2-macroglobulin isoform 1 - bovine (fragment)
 C:Species: Bos primigenius indicus (zebu cattle)
 C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S66635
 R:Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup
 FEBS Lett. 372, 93-95, 1995
 A>Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
 A:Reference number: S66634; MUID:96032553; PMID:7556551
 A:Accession: S66635
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <DOL>
 A:Cross-references: UNIPROT:Q7M2N8

Query Match 21.1%; Score 24; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 DEFP 17
 | : |||||
 Db 2 DEFP 5

RESULT 6

AB0764
 his operon leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A>Note: this species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AB0764
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AB0764
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD02432.1; PID:GL6503299; GSPDB:GN00176
 C:Genetics:
 A:Gene: hisL

Query Match 21.1%; Score 24; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHH 4
 | : |||
 Db 8 HHH 10

RESULT 7
 A28965
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach (fragments)
 C:Species: Spinacia oleracea (spinach)
 C>Date: 22-Dec-1988 #sequence_revision 22-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A28965
 R:Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988
 A>Title: Reaction-intermediate analogue binding by ribulose biphosphate carboxylase/oxy
 cetylated proline.
 A:Reference number: A28965; MUID:88144466; PMID:3422748
 A:Accession: A28965
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <MUL>
 A:Cross-references: UNIPROT:P00875
 C:Keywords: carbon-carbon lyase; carboxy-lyase; chloroplast

Query Match 21.1%; Score 24; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EPPSM 19
 | : |||||
 Db 8 EPPAM 12

RESULT 8
 LFECB
 his operon leader peptide - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C>Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
 C:Accession: A03594; I41073; A64967
 R:Verde, P.; Frunzio, R.; di Nocera, P.P.; Blasi, F.; Bruni, C.B.
 Nucleic Acids Res. 9, 2075-2086, 1981
 A>Title: Identification, nucleotide sequence and expression of the regulatory region of t
 A:Reference number: A03594; MUID:82059525; PMID:6170941
 A:Accession: A03594
 A:Molecule type: DNA
 A:Residues: 1-16 <VER>
 A:Cross-references: UNIPROT:P60995; GB:V00284; GB:J01627; GB:J01628; NID:g41692; PIDN:CM
 A>Note: this protein is involved in the attenuation mechanism for the control of the exp
 R:Di Nocera, P.P.; Blasi, F.; Di Lauro, R.; Frunzio, R.; Bruni, C.B.

Proc. Natl. Acad. Sci. U.S.A. 75, 4276-4280, 1978
A>Title: Nucleotide sequence of the attenuator region of the histidine operon of *Escherichia coli*
A:Reference number: I41073; MUID:19033821; PMID:360215
A:Accession: I41073
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: EMBL:Y00285; NID:G41701; PIDN:CAA23550.1; PID:G41702
R:Blattner, P.R.; Mau, B.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.; Rose, D.J.; Mau, B.; Shao, Y.
A>Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A64967
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-16 <BLAT>
A:Cross-references: GB:AE000293; GB:U00096; NID:G2367127; PIDN:AACT5079.1; PID:G1788329;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: hisL
A:Superfamily: his leader peptide
C:Keywords: histidine biosynthesis

Query Match 21.1%; Score 24; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 HHH 4
Db 8 HHH 10

RESULT 9
C90981
his operon leader peptide [imported] - *Escherichia coli* (strain O157:H7, substrain R1MD)
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C90981
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90981
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <HAY>
A:Cross-references: UNIPROT:Q8X8T5; GB:BA000007; PIDN:BAB36242.1; PID:G13362287; GSPDB:G
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs2819

Query Match 21.1%; Score 24; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 HHH 4
Db 9 HHH 11

RESULT 10
A85827
his operon leader peptide [imported] - *Escherichia coli* (strain O157:H7, substrain EDL93)
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85827
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85827
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <STO>
A:Cross-references: UNIPROT:Q8X8T5; GB:AE005174; NID:G12516199; PIDN:AAG57077.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: hisL

Query Match 21.1%; Score 24; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 HHH 4
Db 9 HHH 11

RESULT 11
I79432
MHC class II histocompatibility antigen HLA-DRw6b-beta-6III - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I79432
R:Angelini, G.; de Preval, C.; Gorski, J.; Mach, B.
Proc. Natl. Acad. Sci. U.S.A. 83, 4489-4493, 1986
A>Title: High-resolution analysis of the human HLA-DR polymorphism by hybridization with
A:Reference number: 159073; MUID:86233452; PMID:3012569
A:Accession: I79432
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <ANG>
A:Cross-references: UNIPROT:O19726; GB:M13562; NID:G188312; PIDN:AAAS9797.1; PID:G188313
C:Genetics:
A:Gene: HLA-DRB3
A:Map position: 6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 21.1%; Score 24; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 3 HHASRVARMSD 14
Db 7 HNQEYARFSD 18

RESULT 12
TS0757
pufK protein [imported] - *Rhodobacter sphaeroides*
C:Species: *Rhodobacter sphaeroides*
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: TS0757
R:Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A>Title: DNA sequence analysis of the photosynthesis region of *Rhodobacter sphaeroides* 2.
A:Reference number: 225222; MUID:20115911; PMID:10648776
A:Accession: TS0757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <CHO>
A:Cross-references: UNIPROT:Q53121; EMBL:AF195122; PIDN:AAF24301.1
A:Experimental source: strain 2.4.1
C:Genetics:
A:Gene: pufK

Query Match 21.1%; Score 24; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 HHASRVAR 10
Db 7 HNQEYARFSD 18

Db 9 HOHVASVLR 17

RESULT 13

A61414

chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)

C:Species: Chelydra serpentina (snapping turtle)

C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C:Accession: A61414

R:Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2, 187-198, 1973

A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined

A:Reference number: A61414; MUID:76146602; PMID:4807189

A:Accession: A61414

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <BHA>

A:Cross-references: UNIPROT:Q7LZ34

C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 21.1%; Score 24; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 2e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 SRVARMASDE 15

Db 11 SGLARIVGDE 20

RESULT 14

I55663

MHC HLA-DR gamma chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I55663

R:O'Sullivan, D.M.; Noonan, D.; Quaranta, V.

J. Exp. Med. 166, 444-460, 1987

A:Title: Four Ia invariant chain forms derive from a single gene by alternate splicing

A:Reference number: I55663; MUID:87252940; PMID:3036998

A:Accession: I55663

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-20 <RES>

A:Cross-references: UNIPROT:O19685; NID:3292150; PIDN:AAA58655.1; PID:g292151

C:Genetics:

A:Gene: HLA-DR

Query Match 20.2%; Score 23; DB 2; Length 20;

Best Local Similarity 38.9%; Pred. No. 2.9e+03;

Matches 7; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

QY 2 HHHASRVARMASDEFFPSM 19

Db 2 HRRRSRSCR--EDQKPV 17

RESULT 15

A58589

alpha-conotoxin EI - cone shell (Conus ermineus)

C:Species: Conus ermineus (ermine cone)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A58589

R:Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.; Biochemistry 34, 14519-14526, 1995

A:Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with novel

A:Reference number: A58589; MUID:96062516; PMID:7578057

A:Accession: A58589

A:Molecule type: protein

A:Residues: 1-18 <MAR>

A:Cross-references: UNIPROT:P50982

A>Note: sequence confirmed by chemical synthesis

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; post F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;4-10,5-18/Disulfide bonds: #status experimental

F;18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 19.3%; Score 22; DB 1; Length 18;

Best Local Similarity 20.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

QY 1 CHHHASRVARMASDEFFPSMC 20

Db 5 CYHPTCNMSN-----PQIC 18

Search completed: June 20, 2005, 10:47:10

Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:15:52 ; Search time 110.5 Seconds
(without alignments)
92.684 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARVASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	36	31.6	16 2 Q9TWC5	Q9TWC5 dirofilaria
2	30	26.3	13 2 Q8SL68	Q8SL68 monanthes a
3	29	25.4	20 2 Q7M270	Q7M270 gastrocioni
4	27	23.7	12 2 Q7YKE9	Q7YKE9 ribes divar
5	25	21.9	9 1 BS43 SERPL	P83375 serratia pl
6	25	21.9	15 2 Q26323	Q26323 lymanaea sta
7	25	21.9	16 2 Q26322	Q26322 lymanaea sta
8	25	21.9	17 1 PA2 AUSSU	P59066 austrelaps
9	25	21.9	18 2 Q7M198	Q7M198 streptomyc
10	25	21.9	19 2 Q26321	Q26321 lymanaea sta
11	25	21.9	20 1 NF19 NAEFO	P83899 naegleria f
12	25	21.9	20 2 Q6BDK5	Q6BDK5 tricholoma
13	25	21.9	20 2 Q90X91	Q90X91 gallus gall
14	24.5	21.5	20 2 Q95MK2	Q95MK2 papio cynoc
15	24	21.1	9 2 Q7M2N8	Q7M2N8 bos indicus
16	24	21.1	11 2 Q9BJ761	Q9BJ761 dictyosteli
17	24	21.1	12 1 LOSK LOEMI	P47733 locusta mig
18	24	21.1	13 1 LPHI_SALTI	Q825K2 salmonella
19	24	21.1	13 1 LPHI_SHIFL	Q83R06 shigella fl
20	24	21.1	15 1 LPHI_YERPE	Q8D079 yersinia pe
21	24	21.1	16 1 LPHI_ECO57	Q8X8T5 escherichia
22	24	21.1	16 1 LPHI_ECOL6	P60996 escherichia
23	24	21.1	16 1 LPHI_ECOL1	P60995 escherichia
24	24	21.1	16 1 LPHI_KLEPN	Q48439 klebsiella
25	24	21.1	16 1 LPHI_SALTY	P60997 salmonella
26	24	21.1	16 2 Q810X4	Q810X4 cricetus
27	24	21.1	17 2 P83061	P83061 spinacia ol
28	24	21.1	18 2 Q8WVI6	Q8WVI6 homo sapien
29	24	21.1	18 2 Q6LD66	Q6LD66 gallus gall
30	24	21.1	19 2 Q90635	Q90635 cercopithe
31	24	21.1	20 1 PUFK_RHOSH	Q53121 rhodobacter

32	24	21.1	20 2 Q19726	Q19726 homo sapien
33	24	21.1	20 2 Q7LZ34	Q7LZ34 chelydra se
34	23	20.2	12 2 Q8SL28	Q8SL28 aeonium hol
35	23	20.2	12 2 Q8SL40	Q8SL40 aeonium urb
36	23	20.2	12 2 Q8SL42	Q8SL42 aeonium sim
37	23	20.2	12 2 Q8SL49	Q8SL49 aeonium lan
38	23	20.2	13 2 Q8SL43	Q8SL43 aeonium spa
39	23	20.2	13 2 Q8SL74	Q8SL74 aichryson p
40	23	20.2	15 2 Q8SL26	Q8SL26 aeonium vis
41	23	20.2	16 2 Q8SL27	Q8SL27 aeonium leu
42	23	20.2	16 2 Q8SL38	Q8SL38 aichryson t
43	23	20.2	16 2 Q8SL50	Q8SL50 aeonium mas
44	23	20.2	16 2 Q8SL52	Q8SL52 aeonium kor
45	23	20.2	16 2 Q8SL53	Q8SL53 aeonium hie

ALIGNMENTS

RESULT 1

ID	Q9TWC5	PRELIMINARY;	PRT;	16 AA.
DT	Q1-MAY-2000 (TREMELrel. 13, Created)			
DT	Q1-MAY-2000 (TREMELrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMELrel. 21, Last annotation update)			
DE	220 kDa excretory-secretory protein (Fragment).			
OS	Dirofilaria immitis (Canine heartworm).			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Filarioidea;			
OC	Onchocercidae; Dirofilaria.			
OX	NCBI_TaxID=6287;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=96258562; PubMed=8992320; DOI=10.1016/0166-6851(95)02533-2;			
RA	Frank G.R., Grieve R.B.;			
RT	"Purification and characterization of three larval excretory-secretory			
RT	proteins of Dirofilaria immitis."			
RL	Mol. Biochem. Parasitol. 75:221-229(1996).			
FT	NON_TER 16			
SQ	SEQUENCE 16 AA; 1678 MW; EBA42D9637CDDBE7 CRC64;			

Query Match 31.6%; Score 36; DB 2; Length 16;

Best Local Similarity 60.0%; Pred. No. 70; Mismatches 3; Indels 0; Gaps 0;

Qy 11 MASDEFFSMC 20

Db 1 MAQDAFPNAC 10

RESULT 2

ID	Q8SL68	PRELIMINARY;	PRT;	13 AA.
AC	Q8SL68;			
DT	01-JUN-2002 (TREMELrel. 21, Created)			
DT	01-JUN-2002 (TREMELrel. 21, Last sequence update)			
DE	PsbA (Fragment).			
GN	Name=pabA;			
OS	Monanthes anagensis.			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Saxifragales; Crassulaceae; Monanthes.			
OX	NCBI_TaxID=91110;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mort M.E., Soltis D.E., Soltis P.S., Francisco-Ortega J.,			
RA	Santos-Guerra A.;			
RT	"Phylogenetics and Evolution of the Macaronesian Clade of Crassulaceae			
RT	Inferred from Nuclear and Chloroplast Sequence Data.";			
RL	Syst. Bot. 27:271-288(2002).			
DR	EMBL; AY082189; AAM13933.1; -.			

```

DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 13 AA; 1361 MW; C0FB1B6DAD15CB02 CRC64;

Query Match 26.3%; Score 30; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MASDEFPSM 19
Db 3 LASVEFPSI 11

RESULT 3
Q7M270 PRELIMINARY; PRT; 20 AA.
ID Q7M270
AC Q7M270;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE R-phycoerythrin gamma-C chain (Fragment).
OS Gastroclonium coulteri (Red alga).
OC Eukaryota; Rhodophyta; Florideophyceae; Rhodymeniales; Champiaceae;
OC Gastroclonium.
OC Eukaryota; Rhodophyta; Florideophyceae; Rhodymeniales; Champiaceae;
OX NCBI_TaxID=2773;
RN [1]
RP SEQUENCE.
RX MEDLINE=85182601; PubMed=3886644;
RA Klotz A.V.; Glazer A.N.;
RT "Characterization of the bilin attachment sites in R-phycoerythrin.";
RL J. Biol. Chem. 260:4856-4863(1985).
DR PIR; H22565; H22565. 1
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2353 MW; 166FE7DB5F309DF CRC64;

Query Match 25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CHHNASRV 8
Db 7 CHHEETQI 14

RESULT 4
Q7YKE9 PRELIMINARY; PRT; 12 AA.
ID Q7YKE9
AC Q7YKE9;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Photosystem Q(B) protein (Fragment).
GN Name=pba;
OS Ribes divaricatum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Grossulariaceae; Ribes.
OX NCBI_TaxID=175193;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulteis L.M.; Donoghue M.J.;
RT "Molecular phylogeny and biogeography of Ribes (Grossulariaceae), with
RT an emphasis on gooseberries (subg. Grossularia).";
RL Syst. Bot. 29:77-96(2004).
DR EMBL; AY138064; AAP92219.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1160 MW; 8C210A9DF36DDB1A CRC64;

Query Match 23.7%; Score 27; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MASDEFPS 18
Db 2 LADEAFPS 9

RESULT 5
BS43_SERPL STANDARD; PRT; 9 AA.
ID BS43_SERPL
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Van Beeumen J.; Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against Erwinia amylovora, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
KW Antibiotic; Bacteriocin; Direct protein sequencing.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871E1FB CRC64;

Query Match 21.9%; Score 25; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HHNASRV 8
Db 2 YHGVVRV 8

RESULT 6
Q26323 PRELIMINARY; PRT; 15 AA.
ID Q26323
AC Q26323;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VDI/RPD2 alpha peptide (Fragment).
GN Name=VDI/RPD2 alpha peptide;
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93351194; PubMed=8348590;
RA Bogerd J.; Van Kesteren R.E.; Van Heerikhuizen H.; Geraerts W.P.;
RA Venstra J.; Smit A.B.; Joosse J.;
RT "Alternative splicing generates diversity of VDI/RPD2 alpha peptides
RT in the central nervous system of Lymnaea stagnalis.";
RL Cell. Mol. Neurobiol. 13:123-136(1993).
DR EMBL; S65078; AAB27755.1; -.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1812 MW; 3F7AE460A6713943 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 4.2e+03;

```

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHHH 4
| | |
4 CQHH 7

Db

RESULT 7

Q26322 ID Q26322 PRELIMINARY; PRT; 16 AA.

AC Q26322; DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)

DE VDI/RPD2 alpha peptide (Fragment).

GN Name=VDI/RPD2 alpha peptide;

OS Lymnaea stagnalis (Great pond snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC Lymnaeidae; Lymnaeidae; Lymnaea.

OX NCBI_TaxID=6523;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93351194; PubMed=8348590;

RA Bogard J., Van Keesteren R.E., Van Heerikhuizen H., Geraerts W.P.,

RA Veenstra J., Smit A.B., Joosse J.;

RT "Alternative splicing generates diversity of VDI/RPD2 alpha peptides

RT in the central nervous system of Lymnaea stagnalis.";

RL Cell. Mol. Neurobiol. 13:123-136(1993).

DR EMBL; S65072; AAB27754.1; -.

FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1869 MW; 4EBAA60A679907A CRC64;

Query Match 21.9%; Score 25; DB 2; Length 16;

Best Local Similarity 75.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHHH 4
| | |
5 CQHH 8

Db

RESULT 8

PA2_AUSSU STANDARD; PRT; 17 AA.

AC P59066; DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)

DE (Fragment).

OS Austrelaps superbus (Australian copperhead).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Acanthophiinae; Austrelaps.

OX NCBI_TaxID=29156;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=93369790; PubMed=8362372; DOI=10.1016/0049-3848(93)90089-7;

RA Yuan Y., Jackson S.P., Mitchell C.A., Salem H.H.;

RT "Purification and characterisation of a snake venom phospholipase A2:

RT a potent inhibitor of platelet aggregation."

RL Thromb. Res. 70:471-481(1993).

CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-

CC acyl groups in 3-sn-phosphoglycerides. Inhibits collagen-, ADP-,

CC thrombin-, ionophore-, adrenaline-, ristocetin-, and arachidonic

CC acid-induced platelet aggregation. Inhibits serotonin release.

CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

CC acylglycerophosphocholine + a carboxylate.

CC -!- COFACTOR: Calcium (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group I

CC subfamily.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phospholip_A2_1; 1.

KW Calcium; Direct protein sequencing; Hydrolase; Lipid degradation;

KW Toxin.

FT NON_TER 17 17

SQ SEQUENCE 17 AA; 1846 MW; 03FB7DD7B7D7D1CB CRC64;

Query Match 21.9%; Score 25; DB 1; Length 17;

Best Local Similarity 57.1%; Pred. No. 4.8e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CHHHASR 7
| | | |
11 CANHGSR 17

Db

RESULT 9

Q7M198 PRELIMINARY; PRT; 18 AA.

ID Q7M198; AC Q7M198;

DT 01-MAR-2004 (TREMELrel. 26, Created)

DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)

DE 24k serine proteinase (EC 3.4.21.-) (Fragment).

OS Streptomyces fradiae.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1906;

RN [1]

RP SEQUENCE.

RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;

RA Sinha U., Wolt S.A., Lad P.J.;

RT "Two new extracellular serine proteases from Streptomyces fradiae."

RL Int. J. Biochem. 23:979-984(1991).

DR PIR; A61577; A61577.

FT NON_TER 1 18

SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 18;

Best Local Similarity 62.5%; Pred. No. 5.1e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 ASDPEFPM 19
| : | | | |
7 AAQEFPM 14

Db

RESULT 10

Q26321 PRELIMINARY; PRT; 19 AA.

ID Q26321; AC Q26321;

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)

DE VDI/RPD2 alpha peptide (fragment).

GN Name=VDI/RPD2 alpha peptide;

OS Lymnaea stagnalis (Great pond snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC Lymnaeidae; Lymnaeidae; Lymnaea.

OX NCBI_TaxID=6523;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93351194; PubMed=8348590;

RA Bogard J., Van Keesteren R.E., Van Heerikhuizen H., Geraerts W.P.,

RA Veenstra J., Smit A.B., Joosse J.;

RT "Alternative splicing generates diversity of VDI/RPD2 alpha peptides

RT in the central nervous system of Lymnaea stagnalis.";

RL Cell. Mol. Neurobiol. 13:123-136(1993).

DR EMBL; S65071; AAB27753.1; -.

FT NON_TER 19 19

SQ SEQUENCE 19 AA; 2110 MW; 069874E166799F4C CRC64;

Query Match 21.9%; Score 25; DB 2; Length 19;
 Best Local Similarity 75.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHHH 4
 Db 8 CQHH 11

RESULT 11
 ID NF19_NAEFO STANDARD; PRT; 20 AA.
 AC P83899;
 DT 25-OCT-2004 (Rel. 45; Created)
 DT 25-OCT-2004 (Rel. 45; Last sequence update)
 DT 25-OCT-2004 (Rel. 45; Last annotation update)
 DE Unknown protein NF019 from 2D-PAGE (Fragment).
 OS Naegleria fowleri.
 OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
 OX NCBI_TaxID=5763;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NF 66;
 RA Omura M., Furushima-Shimogawara R., Izumiyama S., Endo T.;
 RT "Comparative study of protein profiles on pathogenic and nonpathogenic
 Naegleria species by 2D-PAGE";
 RL J. Eukaryot. Microbiol. 0:0-0(2004).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
 CC 7.2, its MW is: 92.4 kDa.
 KW Direct protein sequencing.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2392 MW; AFC7B2F54C39DEF9 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 5.7e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 SRVARMASDE 15
 Db 8 SRVVKFSIDE 17

RESULT 12
 ID Q6BDK5 PRELIMINARY; PRT; 20 AA.
 AC Q6BDK5;
 DT 25-OCT-2004 (TReMBLrel. 28; Created)
 DT 25-OCT-2004 (TReMBLrel. 28; Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28; Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Tricholoma matsutake.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Tricholoma.
 OX NCBI_TaxID=40145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murata H.;
 RT "Characterization of the insertion sites of mary1, the gypsy-type
 retrotransposon from the ectomycorrhizal basidiomycete Tricholoma
 matsutake strain Y1, in the genome of the fungus based on the inter-
 RT retrotransposon amplified polymorphism analysis.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB160895; BAD32671.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2213 MW; 84BDB0AB47F6443C CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.7e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 8 VARMASDEFP 17
 Db 9 ILRVFSSDFP 18

RESULT 13
 ID Q90X91 PRELIMINARY; PRT; 20 AA.
 AC Q90X91;
 DT 01-DEC-2001 (TReMBLrel. 19; Created)
 DT 01-DEC-2001 (TReMBLrel. 19; Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19; Last annotation update)
 DE Tyrosinase (Fragment).
 GN Name=TVR;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deng X., Yang Y., Liu W.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF416916; AAL14562.1; -.
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2217 MW; BC677F25FA1BA696 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 33.3%; Pred. No. 5.7e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 12 ASDEFPSMC 20
 Db 4 STGQFPRVC 12

RESULT 14
 ID Q95MK2 PRELIMINARY; PRT; 20 AA.
 AC Q95MK2;
 DT 01-DEC-2001 (TReMBLrel. 19; Created)
 DT 01-DEC-2001 (TReMBLrel. 19; Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26; Last annotation update)
 DE Growth hormone receptor (Fragment).
 OS Papio cynocephalus (Yellow baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21265430; PubMed=11371592;
 RX Liu J.C., Makova K.D., Adkins R.M., Gibson S., Li W.H.;
 RT "Episodic evolution of growth hormone in primates and emergence of the
 RT species specificity of human growth hormone receptor.";
 RL Mol. Biol. Evol. 18:945-953(2001).
 DR EMBL; AF339074; AAK62301.1; -.
 DR HSSP; P10912; IAXI.
 KW GO; GO:0004872; F:receptor activity; IEA.
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2339 MW; 3FC9F94636B38BE7 CRC64;

Query Match 21.5%; Score 24.5; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 6.9e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 CH-----HHAS 6
 Db 10 CHWTDVHHGS 20

```
RESULT 15
Q7M2N8
ID Q7M2N8 PRELIMINARY; PRT; 9 AA.
AC Q7M2N8;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Alpha-2-macroglobulin isoform 1 (Fragment).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE.
RX MEDLINE=96032553; PubMed=7556651; DOI=10.1016/0014-5793(95)00960-H;
RA Dolmer K., Jenner L.B., Jacobsen L., Andersen G.R., Koch T.J.,
RA Thirup S., Sottrup-Jensen L., Nyborg J.;
RT "Crystallisation and preliminary X-ray analysis of the receptor-
RL binding domain of human and bovine alpha(2)-macroglobulin.";
RL FEBS Lett. 372:93-95(1995).
DR PIR; S66635; S66635.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1095 MW; 87502DD9D769CB1A CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 DEFP 17
DB 2 DEFP 5
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Search completed: June 20, 2005, 10:46:18
Job time : 112.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:14:47 ; Search time 62.5 Seconds
(without alignments)
123.763 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARWASDEFPSC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	AAR37300	E.coli sh
2	45	39.5	19	ABR82617	P. aerugi
3	38	33.3	16	ADN61592	Adn61592 Salmonell
4	36	31.6	16	AAY88253	D. immiti
5	36	31.6	16	AAB08745	Peptide d
6	36	31.6	16	ADJ87174	Parasitic
7	36	31.6	19	AD229094	MTN-13/I
8	36	31.6	19	ADK40590	KDR & VEG
9	36	31.6	19	ADR40808	Cyclic KD
10	35	30.7	14	AAY47525	Immunogen
11	35	30.7	20	ABP59407	Self-asse
12	34	29.8	9	ADM78554	Green flu
13	34	29.8	15	AAE08870	Escherich
14	34	29.8	15	AAU77664	His tag p
15	34	29.8	18	AAI33448	Protein e
16	34	29.8	18	AAG83124	Peptide e
17	34	29.8	18	ADK40464	KDR & VEG
18	34	29.8	18	ADR40682	Cyclic KD
19	34	29.8	20	AAY83783	Poly(His)
20	33	28.9	6	AAV28952	Sequence
21	33	28.9	6	AAW88019	Peptide u
22	33	28.9	6	AAW88022	Peptide u
23	33	28.9	6	AAW88020	Peptide u
24	33	28.9	6	AAW88023	Peptide u
25	33	28.9	6	AAW73340	Peptide #

26	33	28.9	7	8	ADR06001	Adr06001 Labelling
27	33	28.9	9	4	AAB20296	Aab20296 Histidine
28	33	28.9	9	7	ABU64370	Abu64370 LI9/HyHEL
29	33	28.9	9	8	ADR90088	Adr90088 Bacteriop
30	33	28.9	10	4	AAB20300	Aab20300 Histidine
31	33	28.9	10	8	ADR90092	Adr90092 Bacteriop
32	33	28.9	11	4	AAB68981	Aab68981 Fluoresce
33	33	28.9	12	2	AAW36319	Aaw36319 Antinicro
34	33	28.9	12	7	ADD49244	Add49244 Biopannin
35	33	28.9	13	2	AAW61548	Aaw61548 Endoprote
36	33	28.9	13	4	AAU09365	Aau09365 N-termina
37	33	28.9	14	5	ABG67084	Abg67084 Streptavi
38	33	28.9	14	6	ABU57606	Abu57606 Streptavi
39	33	28.9	15	8	ADJ34592	Adj34592 AKT subet
40	33	28.9	18	8	ABO59184	Abo59184 Human gen
41	33	28.9	19	2	AAR41773	Aar41773 Specific
42	33	28.9	19	2	AAR41770	Aar41770 Specific
43	33	28.9	20	8	ADR05559	Adr05559 Novel ssd
44	32	28.1	10	7	ADF28734	Adf28734 SUR2-type
45	32	28.1	15	8	ADR90500	Adr90500 H. longic

ALIGNMENTS

RESULT 1

AAR37300
ID AAR37300 standard; protein; 20 AA.

XX AAR37300;

XX 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX E.coli shiga-like toxin segment.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin; human engineered antibody;
KW variable region; light chain; cell targeting; chimeric antibody; SLT.
XX Escherichia coli.

XX Key Location/Qualifiers

FT Disulfide-bond 1..20

FT /note= "intervening loop includes protease sensitive
amino acid sequence"

XX W09309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

XX Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic
PT agents, immuno toxins for treating auto immune diseases, cancer, graft
PT versus host disease and selective cell killing in-vivo.

XX Example 10; Page 114; 163pp; English.

XX The invention covers analogues of the plant type I RIP gelonin which have
CC a non-naturally occurring Cys residue in a position which enables the
CC analogue to be conjugated via a disulphide linkage to a molecule which
CC specifically binds to a target cell. Pref. target-cell binding molecules
CC are antibodies or their fragments, esp. human engineered H65 antibody

CC fragments. Fusion constructs were assembled that included a natural
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an
 CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of
 CC the E.coli shiga-like toxin was inserted between the gelonin gene and the
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 114; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
 |||||
 DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 2

ABR82617
 ID ABR82617 standard; peptide; 19 AA.

XX
 AC ABR82617;

DT 04-DEC-2003 (first entry)

DE P. aeruginosa detecting papal modified peptide substrate papa3.

XX Microorganism detection; antimicrobial therapy; DNA metabolism; protease;
 KW lipase.

OS Pseudomonas aeruginosa.

XX
 FH Key Location/Qualifiers

FT Modified-site 7 /note= "Glu-Edans label"

FT Modified-site 19

FT /note= "Lys-dabsyl label"

XX WO2003063693-A2.

XX
 PN 07-AUG-2003.

XX
 PD 31-JAN-2003; 2003WO-US003172.

XX
 PF 31-JAN-2002; 2002US-0354001P.

XX
 PR 28-MAY-2002; 2002US-0383847P.

XX
 PA (EXPR-) EXPRESSIVE CONSTRUCTS INC.

XX
 PI Sanders MC, Lowe AM, Hamilton MA, Colpas GJ;

XX
 DR WPI; 2003-636762/60.

XX
 PT Detection of microorganism in sample e.g. wound and body fluid, by
 PT contacting sample with detectably labeled substrate for enzyme produced
 PT and/or secreted by microorganism, and detecting modification or absence
 PT of substrate.

XX
 PS Example 15; Page 48; 84pp; English.

XX The invention relates to a method for detecting the presence or absence
 CC of microorganism in a sample. The method involves contacting the sample
 CC with a detectably labeled substrate for an enzyme produced and/or
 CC secreted by microorganism, which results in modification of substrate by
 CC enzyme and detecting the modification or the absence of the modification
 CC of substrate. The method is useful for detecting the presence or absence
 CC of microorganism in a sample e.g. wound-specific bacteria selected from
 CC S. aureus, S. epidermidis, Streptococcus pyogenes, P. aeruginosa,
 CC Enterococcus faecalis, Proteus mirabilis, S. marcescens, Enterobacter
 CC cloacae, Acetivibacter aniratus, Klebsiella pneumoniae and E. coli in wound
 CC or body fluid. The system detects the early stages of infection before
 CC the symptoms develop. Therefore appropriate antimicrobial therapy can be

CC initiated early enough to prevent more serious infection. Sequences
 CC ABR82616-17 represent fluorescently labelled peptide substrates used to
 CC detect the presence of P. aeruginosa using a protease assay
 XX
 SQ Sequence 19 AA;

Query Match 39.5%; Score 45; DB 7; Length 19;
 Best Local Similarity 53.8%; Pred. No. 2.1;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CHHHSRVARMAS 13
 |||||
 DB 1 CHHHSXAAHKSA 13

RESULT 3

ADN61592
 ID ADN61592 standard; peptide; 16 AA.

XX
 AC ADN61592;

XX
 DT 29-JUL-2004 (first entry)

XX
 DE Salmonella typhosa LSP-1 peptide.

XX
 KW Crystal structure;

XX Mitogen activated protein kinase activated protein kinase 2;

XX MAP kinase activated protein kinase 2; MK2; drug design; crytallography;

XX inflammatory disease; antiinflammatory; LSP-1 peptide.

XX Salmonella sp.

XX
 PN US2004091872-A1.

XX
 PD 13-MAY-2004.

XX
 PF 13-NOV-2002; 2002US-00294027.

XX
 PR 13-NOV-2002; 2002US-00294027.

XX
 PA (PARR/) PARRIS K D.

XX
 PA (UNDE/) UNDERWOOD K W.

XX
 PA (STA/) STAHL M L.

XX
 PA (MOS/) MOSYAK L.

XX
 PA (SVEN/) SVENSON K.

XX
 PA (SHAN/) SHANE T.

XX
 PA (TAYL/) TAYLOR M L.

XX
 PI Parris KD, Underwood KW, Stahl ML, Mosyak L, Svenson K, Shane T;
 PI Taylor ML;

XX
 DR WPI; 2004-410434/38.

XX
 PT Novel isolated mitogen activated protein kinase activated protein kinase
 PT polypeptides, useful as therapeutic agents in treating inflammatory based
 PT diseases.

XX
 PS Example 1; SEQ ID NO 10; 272pp; English.

XX The present invention relates to the crystal structures of human mitogen
 CC activated protein (MAP) kinase activated protein kinase 2 (MK2), and the
 CC use of these structures in drug design. Also disclosed are the
 CC polynucleotide sequence encoding MK2, a vector comprising the
 CC polynucleotide, a transformed host cell transfected or infected with the
 CC vector, and a method of producing crystallised MK2. The crystallised MK2
 CC is useful as a therapeutic agent in treating inflammatory based diseases.
 CC The present sequence represents Salmonella typhosa LSP-1 peptide. The
 CC peptide is used in the kinetic analysis of MK2.

XX
 SQ Sequence 16 AA;

Query Match 33.3%; Score 38; DB 8; Length 16;
 Best Local Similarity 61.5%; Pred. No. 27;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 RVARWASDEFFSM 19
DB :||| ||| |||
4 KLARQASIELPSM 16

RESULT 4
RAY88253
ID AAY88253 standard; protein; 16 AA.

XX AC AAY88253;

DT 06-OCT-2000 (first entry)

XX DE D. immitis P22U tryptic fragment #1.

XX PLA2; parasitic helminth; phospholipase A2; antihelminthic; detection;
KW onchocerciasis; heartworm; filariasis; mosquito; diagnostic; vaccine.

XX Dirofilaria immitis.

XX US6060281-A.

XX 09-MAY-2000.

PF 07-JUN-1995; 95US-00482304.

PR 12-FEB-1991; 91US-00654226.

PR 12-JAN-1993; 93US-00003257.

PR 03-AUG-1993; 93US-00101283.

PR 12-JAN-1994; 94WO-US000679.

PR 08-APR-1994; 94US-00225479.

PR 20-MAR-1995; 95US-00408120.

XX (HESK-) HESKA CORP.

PA (COLS) UNIV COLORADO STATE RES FOUND.

XX PI Wisniewski N, Frank GR, Grieve RB;

XX WPI; 2000-364419/31.

DR New parasitic helminth phospholipase A2-like nucleic acid molecule for

PT protecting animals from diseases caused by parasitic helminth, preventing

PT the spread of onchocerciasis, heartworm and/or filariasis.

XX Example 4; Col 75-76; 62pp; English.

XX This invention describes a novel isolated parasitic helminth nucleic acid

CC (NA) molecule (NAM) (I). (I) is selected from: (a) a NAM comprising a

CC sequence selected from cDNA sequences of Dirofilaria immitis: nDiPLA2-

CC 586, nDiPLA2-450, nDiPLA2-387, nDiPLA2-63 and nDiPLA2-557; Onchocerca

CC volvulus: nOVPLA2-420, nOVPLA2-354, and nOVPLA2-66 and Brugia malayi:

CC nBmPLA2(19)-242, nBmPLA2(19)-163, nBmPLA2(25)-255 and nBmPLA2(25)-163;

CC (b) a NAM comprising a homolog that has at least 15 contiguous NAs

CC identical to the sequence selected from nDiPLA2-450, nDiPLA2-387, nDiPLA-

CC 263 and nOVPLA2-557 encoding a protein comprising at least one epitope

CC that has at least 5 contiguous amino acids (aa) that elicits an immune

CC response against a protein comprising aa sequence selected from the PLA2

CC proteins (c) a NAM that is complementary to (a) or (b). The products of

CC the invention have antihelminthic activity and can be used in vaccines.

CC (I) is useful for protecting the animals from diseases caused by

CC parasitic helminth; for preventing the spread of onchocerciasis,

CC heartworm and/or filariasis by administering it to vectors such as

CC mosquitoes, in which the parasitic helminth develops; as diagnostic

CC reagents for detecting parasitic helminth infections. This sequence

CC represents a Dirofilaria immitis P22U protein tryptic fragment

XX Sequence 16 AA;

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

Query Match 31.6%; Score 36; DB 3; Length 16;

Best Local Similarity 60.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 MASDEFFSMC 20

DB 1 MAQDAFPNAC 10

RESULT 6

ADJ87174

ID ADJ87174 standard; peptide; 16 AA.
 XX AC ADJ87174;
 XX XX
 DT 06-MAY-2004 (first entry)
 XX XX
 DE Parasitic helminth PLA-2 related peptide #1.
 XX XX
 KW Parasitic helminth; phospholipase A2; PLA2; parasitic infection;
 KW antiparasitic; enzyme.
 XX XX
 OS Unidentified.
 XX OS
 PN US6673916-B1.
 XX PN
 PD 06-JAN-2004.
 XX PD
 XX 07-SEP-1999; 99US-00391270.
 PF XX
 PR 12-FEB-1991; 91US-00654226.
 PR 12-JAN-1993; 93US-00003257.
 PR 03-AUG-1993; 93US-00101283.
 PR 20-MAR-1995; 95US-00408120.
 PR 07-JUN-1995; 95US-00482304.
 XX PR
 XX (COLS) UNIV COLORADO STATE RES FOUND.
 PA (HESK-) HESKA CORP.
 XX PA
 XX Grieve RB, Frank GR, Wisniewski N;
 PI Grieve RB, Frank GR, Wisniewski N;
 XX PI
 DR WPI; 2004-068618/07.
 XX DR
 XX Composition useful for preventing parasitic helminth infection, comprises
 PT an excipient and a nucleic acid encoding a protein that binds to immune
 PT serum isolated from an animal that is immune to infection by *Dirofilaria*
 PT immitis.
 XX PT
 XX Example 4; SEQ ID NO 21; 59pp; English.
 PS Example 4; SEQ ID NO 21; 59pp; English.
 XX PS
 CC The invention relates to parasitic helminth phospholipase A2-like (PLA2)
 CC proteins and the nucleic acids encoding them. The invention includes a
 CC method for identifying a compound that is capable of inhibiting
 CC phospholipase A2 activity of a parasitic helminth, comprising contacting
 CC an isolated parasitic helminth PLA2 protein with a putative inhibitory
 CC compound under conditions in which, in the absence of the compound, the
 CC protein has phospholipase A2 activity and determining if the putative
 CC inhibitory compound inhibits the phospholipase A2 activity. The
 CC composition is useful for protecting an animal from infection caused by a
 CC parasitic helminth such as *Dirofilaria immitis*. This sequence represents
 CC a PLA2 related peptide of the invention.
 XX CC
 SQ Sequence 16 AA;
 Query Match 31.6%; Score 36; DB 8; Length 16;
 Best Local Similarity 60.0%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 11 MASDEFPSMC 20
 DB 1 MAQDAFPNAC 10
 XX DB
 XX
 RESULT 7
 ADD29094
 ID ADD29094 standard; peptide; 19 AA.
 XX ID
 XX ADD29094;
 AC ADD29094;
 XX AC
 DT 15-JAN-2004 (first entry)
 XX DT
 DE MTN-13/1 KDR binding peptide SEQ ID NO:29.
 XX DE
 KW display vector library; binding peptide; modular phage display library;
 XX KW

KW recombinatorial phage display library.
 XX KW
 OS Synthetic.
 XX OS
 PN WO2003074678-A2.
 XX PN
 PD 12-SEP-2003.
 XX PD
 XX 03-MAR-2003; 2003WO-US006582.
 PF 03-MAR-2003; 2003WO-US006582.
 XX PF
 PR 01-MAR-2002; 2002US-0361121P.
 XX PR
 XX (DYAX-) DYAX CORP.
 PA (DYAX-) DYAX CORP.
 XX PA
 PI Ladner RC;
 XX PI
 XX WPI; 2003-779023/73.
 DR WPI; 2003-779023/73.
 XX DR
 XX New modular recombinatorial display libraries comprising a plurality of
 PT DNA molecules, useful for isolating binding polypeptides for a target
 PT molecule.
 XX PT
 XX Example 2; SEQ ID NO 29; 53pp; English.
 PS Example 2; SEQ ID NO 29; 53pp; English.
 XX PS
 CC The present invention describes a library of display vectors comprising a
 CC plurality of DNA molecules that comprise a general structure: R1-Z-R2,
 CC where R1 and R2 are independently variable regions; and Z is a constant
 CC region that includes a cleavage site for a restriction endonuclease. Also
 CC described: (1) obtaining a binding peptide, comprising: (a) selecting for
 CC phage in the above library, where a displayed peptide binds to a target
 CC of interest; (b) obtaining RF DNA for the selected phage; (c) cleaving
 CC the library RF DNA at the first and second restriction sites; (d) mixing
 CC the selected RF DNA fragments and the library RF DNA fragments; (e)
 CC ligating the mixed fragments; (f) introducing the ligated fragments into
 CC cells, such that phage displaying a new library are produced; and (g)
 CC selecting and sequencing binding phage from the new library, and so
 CC obtaining the binding peptide; (2) producing a modular phage display
 CC library; and (3) producing a recombinatorial phage display library. The
 CC phage display library, and producing a binding peptide, producing a modular
 CC phage display library, and producing a recombinatorial phage display
 CC library. The library of display vectors is useful in isolating binding
 CC polypeptides for a target molecule. The present sequence is used in the
 XX exemplification of the present invention.
 XX
 SQ Sequence 19 AA;
 Query Match 31.6%; Score 36; DB 7; Length 19;
 Best Local Similarity 83.3%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CHHHAS 6
 DB 4 CHHHIS 9
 XX DB
 XX
 RESULT 8
 ADK40590
 ID ADK40590 standard; peptide; 19 AA.
 XX ID
 XX ADK40590;
 AC ADK40590;
 XX AC
 XX 06-MAY-2004 (first entry)
 DT 06-MAY-2004 (first entry)
 XX DT
 DE KDR & VEGF/KDR complex binding peptide of an MTN13 peptide library ID241.
 XX DE
 XX endothelial cell; vacular endothelial growth factor; VEGF;
 KW receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;
 KW foetal liver kinase-1; flk-1; VEGF/KDR complex; angiogenesis;
 KW neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;
 KW simian haemorrhagic fever virus;
 KW enterohaemorrhagic *Escherichia coli* infection; protozoacidal; anti-HIV;
 KW virucidal; antibacterial; cytostatic.
 XX KW

```

OS Synthetic.
XX WO2003074005-A2.
PN
XX
XX 12-SEP-2003.
PD
XX
XX 03-MAR-2003; 2003WO-US006731.
PF
XX
XX 01-MAR-2002; 2002US-0360851P.
PR
XX 15-JAN-2003; 2003US-0440411P.
XX
XX (DYAX-) DYAX CORP.
PA (BRAC ) BRACCO INT BV.
XX
XX Sato AK, Sexton DJ, Ladner RC, Dransfield DT, Swenson RE;
PI Marinelli ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;
PI Pochon S, Bussat P, Arbogast C, Pillai R, Fan H, Linder KE, Song B;
PI Nanjappan P;
XX
XX WPI; 2003-779009/73.
DR
XX New polypeptide that binds to vascular endothelial growth factor receptor
PT -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates
PT with therapeutic or imaging agents.
PT
XX
XX Claim 79; SEQ ID NO 241; 350pp; English.
PS
XX This invention relates to novel peptides useful for detecting and
CC targeting primary receptors on endothelial cells that bind vascular
CC endothelial growth factor (VEGF). Specifically, it refers to detecting
CC the receptor tyrosine kinase identified as VEGF-2, which is also known as
CC kinase domain region (KDR) and foetal liver kinase-1 (flk-1). The present
CC invention describes the involvement of the VEGF/KDR complex as important
CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding
CC polypeptides can be used for imaging neoplastic tumours. Furthermore,
CC these compositions are useful for targeting radiotherapeutics to specific
CC sites for treating diseases associated with KDR activation, which include
CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and
CC enterohaemorrhagic Escherichia coli infection. Accordingly, these
CC compositions exhibit various activities including protozoacidal, anti-
CC HIV, virucidal, antibacterial and cytostatic. This peptide sequence is a
CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of
CC the MTN13 peptide library of the invention.
XX
XX Sequence 19 AA;
SQ
Query Match 31.6%; Score 36; DB 7; Length 19;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHHHAS 6
Db |||||
4 CHHHIS 9
RESULT 9
ADR40808
ID ADR40808 standard; peptide; 19 AA.
XX
XX ADR40808;
AC
XX 21-OCT-2004 (first entry)
DT
XX Cyclic KDR/ VEGF binding peptide of the secondary MTN13 library Seq 241.
DE
XX kinase domain region; KDR: vascular endothelial growth factor; VEGF;
KW VEGF receptor 2; VEGFR2; foetal liver kinase 1; flk-1; angiogenesis;
KW neoplastic tumour; malaria; HIV infection; SIV infection;
KW simian haemorrhagic fever virus infection;
KW enterohaemorrhagic Escherichia coli infection; cytostatic;
KW antiangiogenic; antimalarial; anti-HIV; virucidal; antibacterial;
KW MTN13 library; cyclic.
XX
OS Synthetic.
XX Key Location/Qualifiers
FT Disulfide-bond 4..16
XX
XX WO2004065621-A1.
PN
XX
XX 05-AUG-2004.
PD
XX
XX 11-SEP-2003; 2003WO-US028787.
PF
XX
XX 15-JAN-2003; 2003US-0440411P.
PR
XX 03-MAR-2003; 2003US-00382082.
PR
XX 03-MAR-2003; 2003WO-US006731.
XX
XX (DYAX-) DYAX CORP.
PA (BRAC ) BRACCO INT BV.
XX
XX Sato AK, Sexton DJ, Dransfield DT, Ladner RC, Arbogast C;
PI Bussat P, Fan H, Khurana S, Linder KE, Marinelli ER, Nanjappan P;
PI Nunn A, Pillai R, Pochon S, Ramalingam K, Shrivastava A, Song B;
PI Swenson RE, Von Wronski MA;
XX
XX WPI; 2004-580734/56.
DR
XX Novel isolated polypeptide having ability to bind to kinase domain region
PT or vascular endothelial growth factor/kinase domain region complex,
PT useful in inhibiting vascular endothelial growth factor activation of
PT kinase domain region.
PT
XX Claim 11; SEQ ID NO 241; 470pp; English.
PS
XX This invention relates to novel isolated peptides that can bind to a
CC kinase domain region (KDR) or vascular endothelial growth factor
CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide
CC dimers and multimeric complexes that bind with high affinity to KDR (also
CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (flk-1))
CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and
CC KDR in angiogenesis these binding peptides can be used for imaging
CC important sites of angiogenesis, as well as in targeting therapeutics to
CC such sites. The present invention describes these peptides as useful for
CC promoting or inhibiting angiogenesis and pathogenic conditions associated
CC thereof such as neoplastic tumours. Furthermore, these binding peptides
CC are useful for treating malaria, HIV infection, SIV infection, simian
CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia
CC coli infection. Accordingly, they exhibit cytostatic, antiangiogenic,
CC antimalarial, anti-HIV, virucidal and antibacterial activities. In
CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and
CC enable efficient detection, imaging and localisation of activated
CC endothelial cells exhibiting upregulated KDR expression. This peptide
CC sequence is a high affinity KDR and VEGF/KDR cyclic binding peptide
CC belonging to the secondary MTN13 library of the invention.
XX
XX Sequence 19 AA;
SQ
Query Match 31.6%; Score 36; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHHHAS 6
Db |||||
4 CHHHIS 9
RESULT 10
AA47525
ID AA47525 standard; peptide; 14 AA.
XX
XX AA47525;
AC
XX 01-DEC-1999 (first entry)
DT
XX Immunogenic peptide having a human leukocyte antigen binding motif #2136.
DE

```

XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9945954-A1.
 FN 16-SEP-1999.
 XX 13-MAR-1998; 98WO-US005039.
 PF 13-MAR-1998; 98WO-US005039.
 XX (EPIM-) EPIMMUNE INC.
 PA Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 DR New immunogenic peptides with HLA binding motif, useful in treatment and
 XX diagnosis of cancers and viral diseases.
 XX Claim 1; Page 113; 150pp; English.
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX Sequence 14 AA;
 SQ
 Query Match 30.7%; Score 35; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 75;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 11 MASDEFPSMC 20
 DB : || ||||:|
 2 LPSPFFPSVC 11
 RESULT 11
 ABP59407
 ID ABP59407 standard; peptide; 20 AA.
 AC ABP59407;
 XX 09-JUN-2003 (first entry)
 DT Self-assembling di-block oligopeptide AH20.
 DE Self-assembling oligopeptide; dipolar; nanotube; nanostructure;
 KW drug delivery; carrier.
 KW

XX Synthetic.
 OS WO2003006043-A1.
 FN 23-JAN-2003.
 PD 10-JUL-2002; 2002WO-US021757.
 PF 10-JUL-2001; 2001US-0304256P.
 PR (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Zhang S, Vauthey S;
 PI WPI; 2003-267944/26.
 DR New dipolar oligopeptides in a self-assembled nanostructure useful for
 XX drug delivery.
 XX Claim 17; Page 21; 52pp; English.
 XX The present invention relates to self-assembling dipolar oligopeptides
 CC and di- and tri-block peptide copolymers. The dipolar oligopeptides have
 CC ability to self assemble to form stable nanotubes. The self-assembled
 CC nanostructure have the ability to entrap and deliver molecules with high
 CC degree of efficacy. The copolymers are amenable for molecular systematic
 CC design, modification and synthesis; can be subjected to extensive
 CC molecular modelling and simulations before synthesis; can be highly
 CC purified to be mono-dispersed materials; combinatorial approach can be
 CC employed to systematically characterize these co-polymers at various
 CC ratios; and can be synthesized in vitro or in vivo. The nanotubes fuse
 CC with the lipid bilayers and do not deform the cells as liposomes do. The
 CC oligopeptides can be used in a self-assembled nanostructure (e.g. the
 CC nanotube) for delivering drug into a cell and as a carrier for
 CC biologically active materials. The present sequence is one such di-block
 CC oligopeptide
 XX Sequence 20 AA;
 SQ
 Query Match 30.7%; Score 35; DB 6; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 HHHASRVARMAS 13
 DB ||||:| |:
 8 HHHAAAAAAAAA 19
 RESULT 12
 ADM78554
 ID ADM78554 standard; peptide; 9 AA.
 XX ADM78554;
 AC 03-JUN-2004 (first entry)
 DT Green fluorescent protein phosphorylation motif #36.
 XX fluorescence; Aequorea green fluorescent protein; GFP.
 KW Synthetic.
 OS US2003170767-A1.
 XX 11-SEP-2003.
 PD 12-NOV-2002; 2002US-00293580.
 PF 24-JUL-1998; 98US-00129192.
 XX (AURO-) AURORA BIOSCIENCES CORP.
 PA

PI Cubitt AB;
 XX WPI; 2003-863757/80.
 XX
 XX A fluorescent compound comprising a fluorescent protein moiety and a
 PT substrate recognition motif for an activity, which exhibits a change in
 PT fluorescence in response to the activity, used to detect enzyme activity
 PT in biological samples.
 XX
 XX Disclosure; SEQ ID NO 51; 52pp; English.
 XX
 XX The invention relates to a fluorescent compound for detecting an
 CC activity, comprising a fluorescent protein moiety and at least one
 CC exogenous substrate recognition motif for an activity, where the
 CC fluorescent protein moiety can be converted from a first to a second
 CC state in response to the activity, and where the fluorescent compound
 CC exhibits a different fluorescent property in the two states under
 CC quenching conditions. The activity is an enzymatic activity, preferably a
 CC kinase, phosphatase, protease, glycosylation or farnesyl transferase
 CC activity. The fluorescent protein moiety comprises an Aequorea-related
 CC fluorescent protein preferably comprising the mutations in GFP mutant K8,
 CC where at least one substrate recognition motif for an activity is within
 CC the first 20, more preferably the first 10 amino acids of the amino
 CC terminus. The Aequorea-related moiety comprises a poly-Lys region and a
 CC protein-protein interaction domain and is membrane bound. The quenching
 CC condition is acid quenching. The moiety preferably comprises a
 CC phosphorylation recognition motif for a serine/threonine specific protein
 CC kinase, protein kinase A, protein kinase C, a cAMP-dependent kinase,
 CC Ca2+/calmodulin-dependent protein kinase I or II or MAP kinase activated
 CC protein kinase. The compound is used to detect enzymatic activities in
 CC biological samples. The present sequence represents a phosphorylation
 CC motif used in the fluorescent compound of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 29.8%; Score 34; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 HHHSRVAR 10
 DB 1 HHHSRPKR 9
 |||||
 RESULT 13
 AAE08870
 ID AAE08870 standard; peptide; 15 AA.
 XX
 XX AAE08870;
 AC
 XX 15-NOV-2001 (first entry)
 DT
 XX Escherichia coli cold shock protein (CspA) N-terminal His-tag peptide.
 DE
 XX Chimeric folded protein; vaccine; therapeutic; enzyme inhibitor;
 KW washing powder; cold shock protein; CspA.
 KW
 XX Escherichia coli.
 OS
 XX Synthetic.
 OS
 XX WO200157065-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 02-FEB-2001; 2001WO-GB000445.
 PF
 XX 03-FEB-2000; 2000GB-00002492.
 PR 04-FEB-2000; 2000US-0180326P.
 PR 03-JUL-2000; 2000GB-00016346.
 PR 07-AUG-2000; 2000GB-00019362.
 PA (DIVE-) DIVERSYS LTD.
 XX

PI Riechmann L, Winter G;
 XX WPI; 2001-529779/58.
 XX
 XX Chimeric folded protein domain derived from repertoire of chimeric
 PT proteins useful therapeutically, comprises two or more sequence segments
 PT derived from parent amino acid sequence that are non-homologous.
 XX
 XX Example 16; Page 49; 75pp; English.
 XX
 XX The invention relates to a chimeric folded protein domain derived from a
 CC repertoire of chimeric proteins. The chimeric protein comprises two or
 CC more sequence segments derived from parent amino acid sequence that are
 CC non-homologous. The chimeric protein is useful in vaccination against one
 CC or more of the amino acid sequences from which the chimera is derived,
 CC for administration to a human for therapeutic purposes, and for use in a
 CC commercial product to which humans are exposed. The chimeric protein is
 CC useful as improved enzyme inhibitors, and to avoid sensitisation in
 CC humans (for e.g. enzymes and washing powders). The present sequence is N-
 CC terminal His-tag peptide sequence of Escherichia coli cold shock protein
 CC (CspA) used in the exemplification of the invention
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 29.8%; Score 34; DB 4; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HHHSRVAR 8
 DB 8 HHHSRRL 14
 |||||
 RESULT 14
 AAU77664
 ID AAU77664 standard; peptide; 15 AA.
 XX
 XX AAU77664;
 AC
 XX 05-JUN-2002 (first entry)
 DT
 XX His tag peptide.
 DE
 XX CspA; chimeric folded protein domain; His tag; cold shock protein;
 KW vaccine; asthma; proteolysis resistance.
 KW
 XX Synthetic.
 OS
 XX WO200212277-A2.
 PN
 XX 14-FEB-2002.
 PD
 XX 03-AUG-2001; 2001WO-GB003508.
 PF
 XX 07-AUG-2000; 2000GB-00019362.
 PR 02-FEB-2001; 2001GB-00002678.
 PR
 XX (DIVE-) DIVERSYS LTD.
 PA
 XX Riechmann L, Winter G;
 PI
 XX WPI; 2002-257461/30.
 DR
 XX Novel chimeric folded protein domain, useful in vaccination, is derived
 PT from a repertoire of chimeric proteins and comprises two or more sequence
 PT segments derived from parent non-homologous sequences.
 PT
 XX Example 14; Page 63; 94pp; English.
 PS
 XX The invention relates to a chimeric folded protein domain, when derived
 CC from a repertoire of chimeric proteins comprises two or more sequence
 CC segments derived from parent amino acid sequences that are non-
 CC homologous. Also included are nucleic acids encoding the chimeric

CC protein domains and a method of producing the protein domains. Chimaeric
 CC proteins His-2f3 and His-1c2 were used for immunisation of a rabbit to
 CC analyse, if resulting antisera from the immunised animals are
 CC crossreactive with CspA. The animals were then challenged with an
 CC injection of folded cold shock protein (CspA) to see if a specific anti-
 CC CspA immune response involving T cell mediated help was established
 CC during immunisation. The analyses of the rabbit immune response showed,
 CC that immunisation with both 2f3 and 1c2 raised antisera highly reactive
 CC with their respective antigen as they bound phage displaying the
 CC chimaeric proteins strongly after the second, third and fourth
 CC vaccination. Crossreactivity with CspA was observed. The protein domain
 CC is useful in vaccination against parent proteins from which the chimaera
 CC is derived, for administration to a human for therapeutic purposes and
 CC for use in commercial product to which humans are exposed. The protein
 CC domains are useful for treating asthma and in immunisation. The chimaeric
 CC folded protein domain is resistant to in vivo or in vitro proteolysis by
 CC protease enzymes and is not immunogenic or weakly immunogenic, and hence
 CC suitable for therapeutic purposes and to avoid sensitisation in humans.
 CC The present sequence is a His tag which is added to chimaeric proteins of
 CC the invention to aid protein purification

XX Sequence 15 AA;

Query Match 29.8%; Score 34; DB 5; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHASRV 8
 Db 8 HHGSRL 14

RESULT 15

AAB13448
 ID AAB13448 standard; peptide; 18 AA.

AC AAB13448;

DT 02-FEB-2001 (first entry)

DE Protein encoded by C. trachomatis clone 3-G3-10.

XX Chlamydial infection; sexually transmitted disease;
 KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
 KW trachoma; blindness; acute respiratory tract infection; atherosclerosis;
 KW coronary heart disease; antibacterial.

OS Chlamydia trachomatis.

XX WO200034483-A2.

XX 15-JUN-2000.

PF 08-DEC-1999; 99WO-US029012.

XX 08-DEC-1998; 98US-00208277.

PR 08-APR-1999; 99US-00288594.

PR 01-OCT-1999; 99US-00410568.

PR 22-OCT-1999; 99US-00426571.

XX (CORI-) CORIXA CORP.

XX Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;

XX WPI; 2000-431303/37.

XX Isolated polypeptide for diagnosis and treatment of Chlamydia infection

PT comprises immunogenic portion of Chlamydia antigen, which comprises amino

PT acid sequence encoded by polynucleotide sequence.

XX Example 1; Page 114; 256pp; English.

XX The present invention relates to new nucleic acid sequences and the

CC proteins encoded by the nucleic acid sequences. The encoded proteins
 CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
 CC proteins are useful for the serodiagnosis and treatment of Chlamydia
 CC infection. Chlamydiae are intracellular bacterial pathogens that are
 CC responsible for a wide variety of human infections. C. trachomatis
 CC infection is one of the most common sexually transmitted diseases and can
 CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
 CC and infertility. Trachoma due to ocular infection with C. trachomatis is
 CC the leading cause of preventable blindness worldwide. C. pneumoniae is a
 CC major cause of acute respiratory tract infections in humans and is also
 CC thought to play a role in the pathogenesis of atherosclerosis and
 CC coronary heart disease. The present sequence is a protein isolated in the
 CC present invention

XX Sequence 18 AA;

Query Match 29.8%; Score 34; DB 3; Length 18;
 Best Local Similarity 46.7%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 HHASRVARMASDEPP 17
 Db 3 HHASLQTNMDISNPP 17

Search completed: June 20, 2005, 10:42:31
 Job time : 64.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:46:29 ; Search time 104 Seconds

(without alignments)
73.842 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARWASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 332641

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	20	14	US-10-127-890-56
2	114	100.0	20	17	US-10-717-243-56
3	38	33.3	16	15	US-10-294-027-10
4	36	31.6	19	14	US-10-378-557-29
5	36	31.6	19	17	US-10-661-156-241
6	35	30.7	20	14	US-10-192-832-53
7	34	29.8	9	14	US-10-293-580-51
8	34	29.8	18	9	US-09-841-132-8
9	34	29.8	18	16	US-10-872-155-8
10	34	29.8	18	17	US-10-661-156-115
11	33	28.9	7	9	US-09-809-517A-12
					Sequence 56, Appl
					Sequence 10, Appl
					Sequence 29, Appl
					Sequence 241, Appl
					Sequence 53, Appl
					Sequence 51, Appl
					Sequence 8, Appl
					Sequence 8, Appl
					Sequence 115, Appl
					Sequence 12, Appl

33 28.9 7 15 US-10-342-331-11
33 28.9 7 17 US-10-658-752-12
33 28.9 9 16 US-10-743-649-4
33 28.9 9 16 US-10-743-639-4
33 28.9 10 16 US-10-743-649-8
33 28.9 10 16 US-10-743-639-8
33 28.9 13 9 US-09-823-266-5
33 28.9 13 14 US-10-155-419-5
33 28.9 14 13 US-10-004-381-32
33 28.9 15 14 US-10-174-105A-147
33 28.9 18 14 US-10-029-386-32818
33 28.9 16 10 US-09-405-032-168
32 28.1 19 9 US-09-864-761-48928
32 28.1 19 10 US-09-933-999A-31
32 28.1 19 14 US-10-219-700-32
32 28.1 19 17 US-10-968-317-31
32 28.1 20 16 US-10-776-013-254
32 28.1 10 16 US-10-808-681-6
31 27.2 10 17 US-10-654-601-2266
31 27.2 15 9 US-09-952-432A-8
30 26.3 12 16 US-10-654-623-21
30 26.3 13 17 US-10-808-187-2407
30 26.3 14 16 US-10-608-540-49
30 26.3 16 14 US-10-133-172-16
30 26.3 17 16 US-10-442-506-17
30 26.3 17 17 US-10-839-515-17
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30 26.3 18 10 US-09-804-980-233
30 26.3 18 14 US-10-106-698-7192
30 26.3 18 17 US-10-874-923-14
30 26.3 18 17 US-10-874-923-133
30 26.3 19 17 US-10-630-070-26
30 26.3 19 17 US-10-630-074-26
30 26.3 20 14 US-10-195-730-377

ALIGNMENTS

RESULT 1

US-10-127-890-56

; Sequence 56, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

PROTEINS

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSER: McAndrews, Heid & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

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; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-127-890-56

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Query Match      100.0%; Score 114; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CHHHSRVARWASDEFFSMC 20
Db 1 CHHHSRVARWASDEFFSMC 20

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RESULT 2

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US-10-717-243-56
; Sequence 56, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 110222US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-717-243-56

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Query Match      100.0%; Score 114; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CHHHSRVARWASDEFFSMC 20
Db 1 CHHHSRVARWASDEFFSMC 20

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RESULT 3

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US-10-294-027-10
; Sequence 10, Application US/10294027
; Publication No. US20040091872A1
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin D.
; APPLICANT: Underwood, Kathryn W.
; APPLICANT: Stahl, Mark L.
; APPLICANT: Mosyak, Lidia
; APPLICANT: Svenson, Kristine
; APPLICANT: Shane, Tania
; APPLICANT: Taylor, Meggin L.
; TITLE OF INVENTION: CRYSTAL STRUCTURES OF MK2 AND USES THEREOF
; FILE REFERENCE: 2368/77
; CURRENT APPLICATION NUMBER: US/10/294,027
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Salmonella typhosa
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: LSP-1 peptide
US-10-294-027-10

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```

Query Match      33.3%; Score 38; DB 15; Length 16;
Best Local Similarity 61.5%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 7 RVARWASDEFFSM 19
Db 4 KLARQASIELPSM 16

```

RESULT 4

```

US-10-378-557-29
; Sequence 29, Application US/10378557
; Publication No. US20030186223A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: MODULAR RECOMBINATORIAL DISPLAY
; LIBRARIES
; FILE REFERENCE: 3421.1013-001
; CURRENT APPLICATION NUMBER: US/10/378,557
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,121

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;; PRIOR FILING DATE: 2002-03-01
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 29
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Selected library sequence
US-10-378-557-29

Query Match 31.6%; Score 36; DB 14; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHHHAS 6
|||||
DB 4 CHHHIS 9

RESULT 5
US-10-661-156-241
;; Sequence 241, Application US/10661156
;; Publication No. US20050100963A1
;; GENERAL INFORMATION:
;; APPLICANT: Sato, Aaron K.
;; APPLICANT: Sexton, Daniel J.
;; APPLICANT: Dransfield, Daniel T.
;; APPLICANT: Ladner, Robert C.
;; APPLICANT: Arbogast, Christophe
;; APPLICANT: Bussat, Philippe
;; APPLICANT: Fan, Hong
;; APPLICANT: Khurana, Sudha
;; APPLICANT: Linder, Karen E.
;; APPLICANT: Marinelli, Edmund R.
;; APPLICANT: Nanjappa, Palanappa
;; APPLICANT: Nunn, Adrian
;; APPLICANT: Pillai, Radhakrishna
;; APPLICANT: Pochon, Sibylle
;; APPLICANT: Ramalingam, Kondareddiar
;; APPLICANT: Shrivastava, Ajay
;; APPLICANT: Song, Bo
;; APPLICANT: Swenson, Rolf E.
;; APPLICANT: Von Wronski, Mathew A.

;; TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
;; TITLE OF INVENTION: Their Use in Diagnosis and Therapy
;; FILE REFERENCE: D0617.70012US00
;; CURRENT APPLICATION NUMBER: US/10/661,156
;; CURRENT FILING DATE: 2003-09-11
;; PRIOR APPLICATION NUMBER: US 10/382,082
;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: PCT/US03/06731
;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: US 60/440,411
;; PRIOR FILING DATE: 2003-01-15
;; PRIOR APPLICATION NUMBER: US 60/360,851
;; PRIOR FILING DATE: 2002-03-01
;; NUMBER OF SEQ ID NOS: 617
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 241
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Library Isolate
US-10-661-156-241

Query Match 31.6%; Score 36; DB 17; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHHHAS 6
|||||

Db 4 CHHHIS 9

RESULT 6

US-10-192-832-53
;; Sequence 53, Application US/10192832
;; Publication No. US20030176335A1
;; GENERAL INFORMATION:
;; APPLICANT: ZHANG, SHUGUANG
;; APPLICANT: VAUTHEY, SYLVAIN
;; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
;; FILE REFERENCE: MTV-043.01
;; CURRENT APPLICATION NUMBER: US/10/192,832
;; CURRENT FILING DATE: 2002-07-10
;; PRIOR APPLICATION NUMBER: 60/304,256
;; PRIOR FILING DATE: 2001-07-10
;; NUMBER OF SEQ ID NOS: 76
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 53
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-10-192-832-53

Query Match 30.7%; Score 35; DB 14; Length 20;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HHHSRVARMAS 13
|||||
DB 8 HHHAASAAAAA 19

RESULT 7

US-10-293-580-51
;; Sequence 51, Application US/10293580
;; Publication No. US20030170767A1
;; GENERAL INFORMATION:
;; APPLICANT: Aurora Biosciences Corporation
;; APPLICANT: Cubitt, Andrew B.
;; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
;; FILE REFERENCE: AU01270 (08366/031001)
;; CURRENT APPLICATION NUMBER: US/10/293,580
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US/09/129,192
;; PRIOR FILING DATE: 1998-07-24
;; NUMBER OF SEQ ID NOS: 74
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 51
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: cyclin A-CDK2
US-10-293-580-51

Query Match 29.8%; Score 34; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 HHHSRVAR 10
|||||
DB 1 HHHSRPRK 9

RESULT 8

US-09-841-132-8
;; Sequence 8, Application US/09841132
;; Patent No. US20020061849A1
;; GENERAL INFORMATION:

```
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yaeir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-8
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Query Match 29.8%; Score 34; DB 9; Length 18;
Best Local Similarity 46.7%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Qy 3 HHASRVARMASDEFP 17
Db 3 HHASLQTNWDISNFP 17
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RESULT 9
US-10-872-155-8
; Sequence 8, Application US/10872155
; Publication No. US20040234536A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yaeir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C10
; CURRENT APPLICATION NUMBER: US/10/872,155
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 09/620,412
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/598,419
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/556,877
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/454,684
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/426,571
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 09/410,568
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/288,594
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 09/208,277
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-872-155-8
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Query Match 29.8%; Score 34; DB 16; Length 18;
Best Local Similarity 46.7%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Qy 3 HHASRVARMASDEFP 17
Db 3 HHASLQTNWDISNFP 17
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RESULT 10
US-10-661-156-115
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; Sequence 115, Application US/106611156
; Publication No. US20050100963A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Poehon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
; TITLE OF INVENTION: Their Use in Diagnosis and Therapy
; FILE REFERENCE: D0617.70012US00
; CURRENT APPLICATION NUMBER: US/10/661,156
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 617
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-661-156-115

Query Match 29.8%; Score 34; DB 17; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CHHHASRVAR 10
Db 4 CHEHSDSVTR 13

RESULT 11
US-09-809-517A-12
; Sequence 12, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. US20020034733A1 methods for displaying (poly)peptides/proteins
; TITLE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 7
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; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-12

Query Match 28.9%; Score 33; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHH 4
Db 1 CHHH 4

RESULT 12

US-10-342-331-11
; Sequence 11, Application US/10342331
; Publication No. US20030229205A1
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOUMSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOEBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHEL D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; TITLE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/10/342,331
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US/09/219,849
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Example amino
; OTHER INFORMATION: acid sequence
US-10-342-331-11

Query Match 28.9%; Score 33; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHH 4
Db 2 CHHH 5

RESULT 13

US-10-658-752-12
; Sequence 12, Application US/10658752
; Publication No. US2005005894A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: Novel methods for displaying (poly)peptides/proteins on bacterioph
; TITLE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/10/658,752
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/809,517A
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-10-658-752-12

Query Match 28.9%; Score 33; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHH 4
Db 1 CHHH 4

RESULT 14

US-10-743-649-4
; Sequence 4, Application US/10743649
; Publication No. US20040170607A1
; GENERAL INFORMATION:
; APPLICANT: PRO-VIRUS, INC.
; TITLE OF INVENTION: ONCOLYTIC VIRUS
; FILE REFERENCE: 2370-63
; CURRENT APPLICATION NUMBER: US/10/743,649
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US/09/664,444
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/397,873
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-743-649-4

Query Match 28.9%; Score 33; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHH 4
Db 1 CHHH 4

RESULT 15

US-10-743-639-4
; Sequence 4, Application US/10743639
; Publication No. US20040208849A1
; GENERAL INFORMATION:
; APPLICANT: PRO-VIRUS, INC.
; TITLE OF INVENTION: ONCOLYTIC VIRUS
; FILE REFERENCE: 2370-63
; CURRENT APPLICATION NUMBER: US/10/743,639
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US/09/664,444
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/397,873
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-743-639-4

Query Match 28.9%; Score 33; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHH 4
|||
Db 1 CHHH 4

Search completed: June 20, 2005, 11:15:08
Job time : 105 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 07:01:48 ; Search time 41 Seconds
(without alignments)
36.414 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1. CHHHASRVARMASDEFPSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	114	100.0	20	1 US-07-988-430-58	Sequence 58, Appl
2	114	100.0	20	1 US-08-425-336-56	Sequence 56, Appl
3	114	100.0	20	1 US-08-488-113B-56	Sequence 56, Appl
4	114	100.0	20	1 US-08-477-484B-56	Sequence 56, Appl
5	114	100.0	20	2 US-08-646-360-56	Sequence 56, Appl
6	114	100.0	20	3 US-08-839-765-56	Sequence 56, Appl
7	114	100.0	20	3 US-09-136-389-56	Sequence 56, Appl
8	114	100.0	20	3 US-09-610-838-56	Sequence 56, Appl
9	114	100.0	20	4 US-09-711-485-56	Sequence 56, Appl
10	114	100.0	20	5 PCT-US22-09487-58	Sequence 58, Appl
11	114	100.0	315	1 US-08-378-761A-73	Sequence 73, Appl
12	114	100.0	315	1 US-08-485-286-73	Sequence 73, Appl
13	114	100.0	315	3 US-08-816-977-2	Sequence 2, Appl
14	114	100.0	315	4 US-09-334-477-2	Sequence 2, Appl
15	114	100.0	323	3 US-08-816-977-21	Sequence 21, Appl
16	114	100.0	323	4 US-09-334-477-21	Sequence 21, Appl
17	114	100.0	326	3 US-08-816-977-37	Sequence 37, Appl
18	114	100.0	326	4 US-09-334-477-37	Sequence 37, Appl
19	114	100.0	332	2 US-08-621-803-251	Sequence 251, Appl
20	114	100.0	332	3 US-09-217-352-251	Sequence 251, Appl
21	114	100.0	690	3 US-08-816-977-47	Sequence 47, Appl
22	114	100.0	690	4 US-09-334-477-47	Sequence 47, Appl
23	114	100.0	708	3 US-08-816-977-33	Sequence 33, Appl
24	114	100.0	708	4 US-09-334-477-33	Sequence 33, Appl
25	47	41.2	135	2 US-08-757-036-3	Sequence 3, Appl
26	46	40.4	204	4 US-09-252-991A-18665	Sequence 18665, A
27	45	39.5	413	4 US-09-328-352-5860	Sequence 5860, Ap

28 45 39.5 525 4 US-09-252-991A-28266 Sequence 28266, A
29 44 38.6 138 2 US-08-757-036-1 Sequence 1, Appl
30 44 38.6 297 1 US-08-180-761B-2 Sequence 2, Appl
31 44 38.6 318 3 US-08-816-977-6 Sequence 6, Appl
32 44 38.6 318 4 US-09-334-477-6 Sequence 6, Appl
33 44 38.6 319 1 US-08-180-761B-1 Sequence 1, Appl
34 44 38.6 326 3 US-08-816-977-25 Sequence 25, Appl
35 44 38.6 326 4 US-09-334-477-25 Sequence 25, Appl
36 44 38.6 329 3 US-08-816-977-39 Sequence 39, Appl
37 44 38.6 329 4 US-09-334-477-39 Sequence 39, Appl
38 44 38.6 360 4 US-09-252-991A-28104 Sequence 28104, A
39 44 38.6 433 4 US-09-344-882-26 Sequence 26, Appl
40 44 38.6 450 4 US-09-252-991A-24440 Sequence 24440, A
41 44 38.6 575 4 US-09-107-532A-3910 Sequence 3910, Ap
42 44 38.6 694 3 US-08-816-977-49 Sequence 49, Appl
43 44 38.6 694 4 US-09-334-477-49 Sequence 49, Appl
44 44 38.6 711 3 US-08-816-977-35 Sequence 35, Appl
45 44 38.6 711 4 US-09-334-477-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-07-988-430-58

; Sequence 58, Application US/07988430

; Patent No. 5416202

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Lane, Julie A.

; APPLICANT: Lei, Shau-Ping

; TITLE OF INVENTION: Materials Comprising and Methods of

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/988,430

; FILING DATE: 19921209

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5416202and, Greta E.

; REGISTRATION NUMBER: 35302

; REFERENCE/DOCKET NUMBER: 31133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-07-988-430-58

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFPSMC 20
|||||
Db 1 CHHHSRVARMASDEFFPSMC 20

RESULT 2

US-08-425-336-56
; Sequence 56, Application US/08425336
; Patent No. 5621083

; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-425-336-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFPSMC 20
|||||
Db 1 CHHHSRVARMASDEFFPSMC 20

RESULT 3

US-08-488-113B-56
; Sequence 56, Application US/08488113B
; Patent No. 5744580

; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-488-113B-56
Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFPSMC 20
|||||
Db 1 CHHHSRVARMASDEFFPSMC 20

RESULT 4
US-08-477-484B-56
; Sequence 56, Application US/08477484B
; Patent No. 5756699

; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESS: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-484B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEPPSMC 20
Db 1 CHHHSRVARMASDEPPSMC 20

RESULT 5
US-08-646-360-56
Sequence 56, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-360-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEPPSMC 20
Db 1 CHHHSRVARMASDEPPSMC 20

RESULT 6
US-08-839-765-56
Sequence 56, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/839,765
/ FILING DATE: 15-APR-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70. P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-839-765-56

Query Match 100.0%; Score 114; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFFPSMC 20
Db 1 CHHHSRVARVASDEFFPSMC 20

RESULT 7

/ US-09-136-389-56
/ Sequence 56, Application US/09136389
/ Patent No. 6146850
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389

/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-136-389-56

Query Match 100.0%; Score 114; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFFPSMC 20
Db 1 CHHHSRVARVASDEFFPSMC 20

RESULT 8

/ US-09-610-938-56
/ Sequence 56, Application US/09610838
/ Patent No. 6376217
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/610,838
/ FILING DATE: 06-JUL-2000
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389

;; FILING DATE: 18-AUG-1998
;; APPLICATION NUMBER: 08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-610-838-56

Query Match 100.0%; Score 114; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
DB 1 CHHHASRVARMASDEFPSSMC 20

RESULT 9

US-09-711-485-56
; Sequence 56, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-711-485-56
Query Match 100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
DB 1 CHHHASRVARMASDEFPSSMC 20

RESULT 10

PCT-US92-09487-58
; Sequence 58, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09487-58

Query Match 100.0%; Score 114; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 11
US-08-378-761A-73
Sequence 73, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
TITLE OF INVENTION: USING
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20

Db 264 CHHHSRVARMASDEFFPSMC 283

RESULT 12
US-08-485-286-73
Sequence 73, Application US/08485286
Patent No. 5646026
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
DB 264 CHHHSRVARMASDEFFPSMC 283

RESULT 13
US-08-816-977-2
Sequence 2, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200

Query Match	Score	DB 3	Length	DB 4	Length	DB 5	Length
Best Local Similarity	100.0%	114	315	114	315	114	315
Matches	20	Conservative	0	Mismatches	0	Indels	0
<p>TELEFAX: (415) 397-8338</p> <p>INFORMATION FOR SEQ ID NO: 2:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 315 amino acids</p> <p>TYPE: amino acid</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>SEQUENCE DESCRIPTION: SEQ ID NO: 2:</p>							
QY	1	CHHHSRVARMSDEFFPSMC	20				
Db	264	CHHHSRVARMSDEFFPSMC	283				
<p>RESULT 15</p> <p>US-08-816-977-21</p> <p>Sequence 21, Application US/08816977</p> <p>Patent No. 6080400</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Williams, James A.</p> <p>APPLICANT: Byrne, Lisa M.</p> <p>APPLICANT: Pugh, Charles S.G.</p> <p>TITLE OF INVENTION: Prevention And Treatment Of</p> <p>TITLE OF INVENTION: Verotoxin-Induced Disease</p> <p>NUMBER OF SEQUENCES: 49</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Medlen & Carroll, LLP</p> <p>STREET: 220 Montgomery Street, Suite 2200</p> <p>CITY: San Francisco</p> <p>STATE: California</p> <p>COUNTRY: United States of America</p> <p>ZIP: 94104</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/816,977</p> <p>FILING DATE: 13-MAR-1997</p> <p>CLASSIFICATION: 424</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: MacKnight, Kamrin T.</p> <p>REGISTRATION NUMBER: 38,230</p> <p>REFERENCE/DOCKET NUMBER: OPD-02450</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (415) 705-8410</p> <p>TELEFAX: (415) 397-8338</p> <p>INFORMATION FOR SEQ ID NO: 21:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 323 amino acids</p> <p>TYPE: amino acid</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p>							
QY	1	CHHHSRVARMSDEFFPSMC	20				
Db	264	CHHHSRVARMSDEFFPSMC	283				
<p>RESULT 16</p> <p>US-09-334-477-21</p> <p>Sequence 21, Application US/09334477</p>							

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; Patent No. 6652857
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
;
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-334-477-21

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Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
Db 264 CHHHSRVARMSDEFFPSMC 283

RESULT 17
US-08-816-977-37
; Sequence 37, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-334-477-21

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Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
Db 264 CHHHSRVARMSDEFFPSMC 283

RESULT 18
US-09-334-477-37
; Sequence 37, Application US/09334477
; Patent No. 6652857
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-816-977-37

Query Match 100.0%; Score 114; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
Db 275 CHHHSRVARMSDEFFPSMC 294
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US-09-334-477-37
SEQUENCE DESCRIPTION: SEQ ID NO: 37;
Query Match      100.0%; Score 114; DB 4; Length 326;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHHHASRVARMASDEFFPSMC 20
Db      275 CHHHASRVARMASDEFFPSMC 294

RESULT 19
US-08-621-803-251
Sequence 251, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 22-MAR-1996
APPLICATION NUMBER: US/08/621,803
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-334-477-37

Query Match      100.0%; Score 114; DB 4; Length 326;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHHHASRVARMASDEFFPSMC 20
Db      275 CHHHASRVARMASDEFFPSMC 294

RESULT 19
US-08-621-803-251
Sequence 251, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 22-MAR-1996
APPLICATION NUMBER: US/08/621,803
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-334-477-37

Query Match      100.0%; Score 114; DB 4; Length 326;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHHHASRVARMASDEFFPSMC 20
Db      277 CHHHASRVARMASDEFFPSMC 296

RESULT 20
US-09-217-352-251
Sequence 251, Application US/09217352
Patent No. 6274344
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPD-02450
TELEPHONE: (415) 705-8410
TELEFAX: (415) 705-8410
TELEX: (415) 705-8410
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; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-977-47

Query Match          100.0%; Score 114; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFSMC 20
DB 639 CHHHSRVARMASDEFFSMC 658

RESULT 22
US-09-334-477-47
; Sequence 47, Application US/09334477
; Patent No. 6652857
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-977-33

Query Match          100.0%; Score 114; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFSMC 20
DB 657 CHHHSRVARMASDEFFSMC 676

RESULT 24
US-09-334-477-33
; Sequence 33, Application US/09334477
; Patent No. 6652857
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-334-477-47

Query Match          100.0%; Score 114; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFSMC 20
DB 639 CHHHSRVARMASDEFFSMC 658
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;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/334,477
;; APPLICATION NUMBER: US/09/334,477
;; FILING DATE: 16-Jun-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/816,977
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MacKnight, Kamrin T.
;; REGISTRATION NUMBER: 38,230
;; REFERENCE/DOCKET NUMBER: OPHD-02450
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 708 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-334-477-33

Query Match : 100.0%; Score 114; DB 4; Length 708;
Best Local Similarity 100.0%; Pred. NO. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFFPSMC 20
Db 657 CHHHASRVARMASDEFFPSMC 676

Search completed: June 22, 2005, 07:12:06
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-717-243-56

Perfect score: 114

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	114	100.0	20	17	US-10-717-243-56 Sequence 56, Appl
3	114	100.0	293	9	US-09-792-793A-37 Sequence 37, Appl
4	114	100.0	293	15	US-10-375-209A-37 Sequence 37, Appl
5	114	100.0	315	9	US-09-334-477-2 Sequence 2, Appl
6	114	100.0	323	9	US-09-334-477-21 Sequence 21, Appl
7	114	100.0	326	9	US-09-334-477-37 Sequence 37, Appl
8	114	100.0	332	9	US-09-765-527-251 Sequence 251, Appl
9	114	100.0	690	9	US-09-334-477-47 Sequence 47, Appl
10	114	100.0	708	9	US-09-334-477-33 Sequence 33, Appl
11	48	42.1	96	16	US-10-425-115-237717 Sequence 237717,

12	48	42.1	162	16	US-10-767-701-40168 Sequence 40168, A
13	47	41.2	74	15	US-10-424-599-224605 Sequence 224605,
14	47	41.2	135	9	US-09-962-021-3 Sequence 3, Appl
15	47	41.2	135	16	US-10-408-765A-20 Sequence 20, Appl
16	47	41.2	293	17	US-10-732-923-4254 Sequence 4254, Ap
17	47	41.2	294	16	US-10-437-963-194718 Sequence 194718,
18	46.5	40.8	345	15	US-10-424-599-200140 Sequence 200140,
19	46	40.4	196	15	US-10-282-122A-66424 Sequence 66424, A
20	45	39.5	380	16	US-10-437-963-116579 Sequence 116579, A
21	44.5	39.0	250	15	US-10-369-493-10325 Sequence 10325, A
22	44.5	39.0	275	16	US-10-425-114-52863 Sequence 220907,
23	44.5	39.0	280	15	US-10-425-114-52863 Sequence 52863, A
24	44.5	39.0	544	9	US-09-925-299-1004 Sequence 1004, Ap
25	44.5	39.0	544	10	US-09-925-299-1004 Sequence 216625,
26	44	38.6	82	15	US-10-424-599-216625 Sequence 1100, Ap
27	44	38.6	137	16	US-10-408-765A-1100 Sequence 1, Appl
28	44	38.6	138	9	US-09-962-021-1 Sequence 13851, A
29	44	38.6	249	14	US-10-156-761-13851 Sequence 14451, A
30	44	38.6	286	17	US-10-732-923-14451 Sequence 223435,
31	44	38.6	293	15	US-10-424-599-223435 Sequence 6, Appl
32	44	38.6	318	9	US-09-334-477-6 Sequence 38, Appl
33	44	38.6	319	9	US-09-792-793A-38 Sequence 28, Appl
34	44	38.6	319	9	US-09-870-759-28 Sequence 28, Appl
35	44	38.6	319	10	US-09-751-708A-28 Sequence 38, Appl
36	44	38.6	319	15	US-10-375-209A-38 Sequence 24, Appl
37	44	38.6	319	16	US-10-438-817A-24 Sequence 28, Appl
38	44	38.6	319	17	US-10-937-758A-28 Sequence 25, Appl
39	44	38.6	326	9	US-09-334-477-25 Sequence 39, Appl
40	44	38.6	329	9	US-09-334-477-39 Sequence 106648,
41	44	38.6	427	16	US-10-437-963-106648 Sequence 26, Appl
42	44	38.6	433	9	US-09-344-882-26 Sequence 26, Appl
43	44	38.6	433	14	US-10-293-855-26 Sequence 106650,
44	44	38.6	514	16	US-10-437-963-106650 Sequence 49, Appl
45	44	38.6	694	9	US-09-334-477-49

ALIGNMENTS

RESULT 1

US-10-127-890-56

; Sequence 56, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Heid & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

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/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70-P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-127-890-56

Query Match      100.0%; Score 114; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 2
US-10-717-243-56
/ Sequence 56, Application US/10717243
/ Publication No. US20050054835A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Carroll, Stephen F.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/717,243
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
```

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/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-717-243-56

Query Match      100.0%; Score 114; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
DB 1 CHHHSRVARMASDEFFPSMC 20

RESULT 3
US-09-792-793A-37
/ Sequence 37, Application US/09792793A
/ Patent No. US20020168370A1
/ GENERAL INFORMATION:
/ APPLICANT: McDonald, John R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
/ DISORDERS
/ FILE REFERENCE: 25020-601D
/ CURRENT APPLICATION NUMBER: US/09/792,793A
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 37
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Shigella dysenteriae
US-09-792-793A-37

Query Match      100.0%; Score 114; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
DB 242 CHHHSRVARMASDEFFPSMC 261

RESULT 4
US-10-375-209A-37
/ Sequence 37, Application US/10375209A
/ Publication No. US20030215421A1
/ GENERAL INFORMATION:
/ APPLICANT: McDonald, John R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
/ DISORDERS
/ FILE REFERENCE: 25020-601E
/ CURRENT APPLICATION NUMBER: US/10/375,209A
/ CURRENT FILING DATE: 2003-02-24
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 37
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Shigella dysenteriae
US-10-375-209A-37
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Query Match      100.0%; Score 114; DB 15; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSSMC 20
Db 242 CHHHSRVARMASDEFPSSMC 261

RESULT 5
US-09-334-477-2
; Sequence 2, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-334-477-2

Query Match      100.0%; Score 114; DB 9; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSSMC 20
Db 264 CHHHSRVARMASDEFPSSMC 283

RESULT 6
US-09-334-477-21
; Sequence 21, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-334-477-21

Query Match      100.0%; Score 114; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSSMC 20
Db 264 CHHHSRVARMASDEFPSSMC 283

RESULT 7
US-09-334-477-37
; Sequence 37, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-334-477-21

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-334-477-37

Query Match      100.0%; Score 114; DB 9; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHHHSRVARVASDEFFPSMC 20
Db      275 CHHHSRVARVASDEFFPSMC 294

RESULT 8
US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US2002000638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251
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Query Match      100.0%; Score 114; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHHHSRVARVASDEFFPSMC 20
Db      277 CHHHSRVARVASDEFFPSMC 296

RESULT 9
US-09-334-477-47
; Sequence 47, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; PRIOR APPLICATION DATA:
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-334-477-47

Query Match      100.0%; Score 114; DB 9; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHHHSRVARVASDEFFPSMC 20
Db      639 CHHHSRVARVASDEFFPSMC 658

RESULT 10
US-09-334-477-33
; Sequence 33, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
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Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-334-477-33

Query Match 100.0%; Score 114; DB 9; Length 708;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEPPSMC 20
DB 657 CHHHASRVARMASDEPPSMC 676

RESULT 11
US-10-425-115-237717
; Sequence 237717; Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237717
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_148383C.1.pap
US-10-425-115-237717

Query Match 42.1%; Score 48; DB 16; Length 96;
Best Local Similarity 50.0%; Pred. No. 9.9;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASD 14
DB 82 CHHLARLUGSATD 95

RESULT 12
US-10-767-701-40168
; Sequence 40168; Application US/107677701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40168
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C46914_1.pap
US-10-767-701-40168

Query Match 42.1%; Score 48; DB 16; Length 162;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEPPS 18
DB 44 CYHHHDNYAATVSTDPPS 61

RESULT 13
US-10-424-599-224605
; Sequence 224605; Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 224605
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_44849C.1.pap
US-10-424-599-224605

Query Match 41.2%; Score 47; DB 15; Length 74;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 HHHASRVARMASDEPP 17
DB 58 HCHGSKVSTLASSNEP 73

RESULT 14
US-09-962-021-3
; Sequence 3; Application US/09962021
; Patent No. US20020106737A1
; GENERAL INFORMATION:

```
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: HUMAN SOM1 PROTEIN HOMOLOG
; FILE REFERENCE: PF-0170-2 CON
; CURRENT APPLICATION NUMBER: US/09/962,021
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020106737A1 g180233
US-09-962-021-3
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Query Match 41.2%; Score 47; DB 9; Length 135;
Best Local Similarity 44.4%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
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QY 1 CHHHSRVARMASDEFP 18
DB 58 CAHLIRLLCKKRSFPS 75
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RESULT 15
US-10-408-765A-20
; Sequence 20, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-20
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Query Match 41.2%; Score 47; DB 16; Length 135;
Best Local Similarity 44.4%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
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QY 1 CHHHSRVARMASDEFP 18
DB 58 CAHLIRLLCKKRSFPS 75
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Search completed: June 20, 2005, 10:40:19
Job time : 109.5 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 10:00:54 ; Search time 24 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARMASDEPPSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	315	1	Shigella toxin cha
2	114	100.0	315	1	Shiga-like toxin c
3	114	100.0	315	2	Shiga-like toxin I
4	114	100.0	315	2	Shiga toxin I subu
5	114	100.0	315	2	Shiga toxin I subu
6	114	100.0	315	2	Shiga-like toxin I
7	50.5	44.3	365	2	hypothetical prote
8	50	43.9	451	2	hypothetical prote
9	49	43.0	2152	2	hypothetical prote
10	47	41.2	135	2	cell adhesion prot
11	47	41.2	252	2	conserved hypothet
12	46	40.4	196	2	probable transcript
13	46	40.4	319	2	Shiga-like cytotox
14	46	40.4	507	2	pyridoxine 4-oxida
15	45	39.5	254	2	hypothetical prote
16	45	39.5	278	2	hypothetical prote
17	45	39.5	466	2	nicotinic acetylch
18	44	38.6	252	2	probable DNA-bindi
19	44	38.6	308	2	D-ribose-binding p
20	44	38.6	318	2	Shiga-like toxin I
21	44	38.6	319	2	variant shiga-like
22	44	38.6	319	2	shiga-like toxin I
23	44	38.6	319	2	Shiga-like toxin I
24	44	38.6	319	2	hypothetical prote
25	44	38.6	319	2	Shiga toxin 2 subu
26	44	38.6	319	2	Shiga toxin 2 subu
27	44	38.6	319	2	shiga-like toxin I
28	44	38.6	319	2	verocytotoxin A ch
29	44	38.6	320	2	shiga-like toxin -

30 44 38.6 433 2 T04594
31 44 38.6 475 2 S45116
32 44 38.6 535 2 A54155
33 43 37.7 536 2 S71332
34 43 37.7 540 1 OYHUCR
35 43 37.7 1149 2 T20891
36 43 37.7 2437 2 S53611
37 43 37.7 2500 1 WHHUE2
38 42 36.8 161 2 S76282
39 42 36.8 285 2 B82842
40 42 36.8 381 2 S58663
41 42 36.8 387 2 T13147
42 42 36.8 398 2 AD2944
43 42 36.8 398 2 F98338
44 42 36.8 404 2 AB0376
45 42 36.8 406 1 JCS041

aldehyde dehydroge
natriuretic peptid
natriuretic peptid
natriuretic peptid
hypothetical prote
MIBP1 protein - ra
HIV-EP2 enhancer-b
hypothetical prote
spermidine synthas
isocitrate dehydro
isocitrate dehydro
fosmidomycin resis
fosmidomycin resis
probable membrane
fosmidomycin resis

ALIGNMENTS

RESULT 1

A28626

Shigella toxin chain A precursor - Shigella dysenteriae

N:Alternate names: shiga toxin chain A

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)

C:Species: Shigella dysenteriae

C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C:Accession: A28626; S04021

R:Strockbine, N.A.; Jackson, M.P.; Sung, L.M.; Holmes, R.K.; O'Brien, A.D.

J: Bacteriol. 170, 1116-1122, 1988

A:Title: Cloning and sequencing of the genes for Shiga toxin from Shigella dysenteriae ty

A:Reference number: A91864; MUID:88139166; PMID:2830229

A:Contents: Type 1 3818T

A:Accession: A28626

A:Molecule type: DNA

A:Residues: 1-315 <STR>

A:Cross-references: UNIPROT:Q8X696; GB:M19437; NID:G152784; PIDN:AAA98347.1; PID:G152785

R:Kozlov, Y.V.; Kabishev, A.A.; Fedchenko, V.I.; Baev, A.A.

Dokl. Biochem. 295, 216-220, 1987

A:Title: Cloning and primary structure of Shigella toxin genes.

A:Reference number: S04021

A:Accession: S04021

A:Molecule type: DNA

A:Residues: 1-315 <KOZ>

A:Cross-references: EMBL:X07903; NID:G46946

C:Genetics:

A:Gene: stxA

C:Complex: heterohexamer of one A chain and five B chains (see PIR:XVEBBD)

C:Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific adenine in 28S rRNA

C:Superfamily: Shigella toxin chain A

C:Keywords: cytotoxin; glycosidase; hexamer; hydrolase; RNA binding

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-315/Product: Shigella toxin chain A #status predicted <MAT>

Query Match 100.0%; Score 114; DB 1; Length 315;

Best Local Similarity 100.0%; Pred. NO. 1.2e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEPPSMC 20

DB 264 CHHHSRVARMASDEPPSMC 283

RESULT 2

XUBPH9

Shiga-like toxin chain A precursor - phage H19B

C:Species: phage H19B

A:Note: host Escherichia coli

C>Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C:Accession: A27052

R:Calderwood, S.B.; Auclair, F.; Donohue-Rolfe, A.; Keusch, G.T.; Mekalanos, J.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4364-4368, 1987
A:Title: Nucleotide sequence of the Shiga-like toxin genes of *Escherichia coli*.
A:Reference number: A27052; MUID:87260808; PMID:3299365
A:Accession: A27052
A:Molecule type: DNA
A:Residues: 1-315 <CAL>
A:Cross-references: UNIPROT:P08026; GB:M16625; NID:G215043; PIDN:AAA98099.1; PID:G215044
C:Genetics:
A:Gene: sltA
C:Superfamily: Shigella toxin chain A
C:Keywords: toxin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-315/Product: Shiga-like toxin chain A #status predicted <MAT>
Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHSRVARWASDEFFSMC 20
DB 264 CHHHSRVARWASDEFFSMC 283
RESULT 3
JN0725
Shiga-like toxin I chain A precursor [validated] - *Escherichia coli*
C:Species: *Escherichia coli*
C:Date: 14-Jul-1994 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JN0725; I53932; I68041; I68043; C61473; A61473; S47254; S47256; S47258
R:Paton, A.W.; Paton, J.C.; Goldwater, P.N.; Heuzenroeder, M.W.; Manning, P.A.
Gene 129, 87-92, 1993
A:Title: Sequence of a variant Shiga-like toxin type-I operon of *Escherichia coli* O111:H
A:Reference number: JN0725; MUID:93328129; PMID:8335264
A:Accession: JN0725
A:Molecule type: DNA
A:Residues: 1-315 <PAT>
A:Cross-references: UNIPROT:Q47647; GB:I04539; NID:G147832; PIDN:AAA71893.1; PID:G147833
A:Experimental source: serotype O111:H(-)
R:Paton, A.W.; Beutin, L.; Paton, J.C.
Gene 153, 71-74, 1995
A:Title: Heterogeneity of the amino-acid sequences of *Escherichia coli* Shiga-like toxin
A:Reference number: I53932; MUID:95189106; PMID:7883188
A:Accession: I53932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-170, 'S', 172-248, 'E', 250-315 <PAT1>
A:Cross-references: EMBL:Z36899; NID:G534987; PIDN:CAA85366.1; PID:G534988
A:Experimental source: serotype O48:H21
A:Note: submitted to the EMBL Data Library, August 1994
A:Accession: I68041
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-131, 'S', 133-170, 'S', 172-315 <PAT2>
A:Cross-references: EMBL:Z36900; NID:G535054; PIDN:CAA85368.1; PID:G535055
A:Experimental source: serotype O111:H(-)
A:Note: submitted to the EMBL Data Library, August 1994
A:Accession: I68043
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-170, 'S', 172-250, 'V', 252-273, 'IVPN', 278-284, 'V', 286-308, 'I', 310-311, 'A', 313
A:Cross-references: EMBL:Z36901; NID:G535088; PIDN:CAA85370.1; PID:G535089
A:Experimental source: serotype OX3:H8
R:Takao, T.; Tanabe, T.; Hong, Y.M.; Shimonishi, Y.; Kurazono, H.; Yutsudo, T.; Sasakawa
Microb. Pathog. 5, 357-369, 1988
A:Title: Identity of molecular structure of Shiga-like toxin I (VT1) from *Escherichia coli*
A:Reference number: A61473
A:Accession: C61473
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170, 'S', 172-315 <TA1>
A:Experimental source: strain O157:H7
A:Accession: A61473
A:Status: preliminary

A:Molecule type: protein
A:Residues: 23-51, 62-76; 107-132, 'XX', 135-136; 183-192; 202-224, 'XX', 227-241; 276-282, 291-294
A:Experimental source: strain O157:H7
C:Genetics:
A:Gene: SLT-1A
C:Superfamily: Shigella toxin chain A
C:Keywords: disulfide bond; toxin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-315/Product: Shiga-like toxin I chain A #status experimental <MAT>
Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHSRVARWASDEFFSMC 20
DB 264 CHHHSRVARWASDEFFSMC 283
RESULT 4
F91000
Shiga toxin I subunit A precursor [imported] - *Escherichia coli* (strain O157:H7, substra
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F91000
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Sasawara, N.; Yaginaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <HAY>
A:Cross-references: UNIPROT:Q8X696; GB:BA000007; PIDN:BAB36397.1; PID:G13362443; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS2974
C:Superfamily: Shigella toxin chain A
Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHSRVARWASDEFFSMC 20
DB 264 CHHHSRVARWASDEFFSMC 283
RESULT 5
H85845
Shiga toxin I subunit A precursor [imported] - *Escherichia coli* (strain O157:H7, substra
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85845
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85845
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <STO>
A:Cross-references: UNIPROT:Q8X696; GB:AE005174; NID:G12516395; PIDN:AAG57228.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: stx1A
C:Superfamily: Shigella toxin chain A
Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEPPSMC 20
Db |||||
264 CHHHSRVARMASDEPPSMC 283

RESULT 6
A:Residues: 1-451 <ANT>
A:Cross-references: UNIPROT:Q9TYW1; EMBL:AF100675; PIDN:AAAG9004.1; GSPDB:GN00022; CESP:
A:Experimental source: strain Bristol NZ; clone Y55H10A
C:Genetics:
A:Gene: CESP:Y55H10A.1
A:Map position: 4
A:Introns: 29/2; 57/1; 95/3; 233/1; 319/3
C:Superfamily: Caenorhabditis elegans hypothetical protein Y55H10A.1

Query Match 43.9%; Score 50; DB 2; Length 451;
Best Local Similarity 58.8%; Pred. No. 3.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 HHHSRVARMASDEPPS 18
Db |||||:|:|:|:|
151 HEKSRVRKRVATDFNS 167

RESULT 9
T45583
hypothetical protein F11C1.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45583
R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Maye
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2152 <BAR>
A:Cross-references: UNIPROT:Q9SND1; EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone F11C1
C:Genetics:
A:Map position: 3
A:Introns: 53/3; 411/2; 1479/3; 1543/2; 1592/3; 1659/1; 1750/1; 1965/3
A:Note: F11C1.210

Query Match 43.0%; Score 49; DB 2; Length 2152;
Best Local Similarity 41.2%; Pred. No. 23;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 HHASRVARMASDEPPSM 19
Db |||||:|:|:|:|
131 HHVKVATLRGDEPPSL 147

RESULT 10
A34653
cell adhesion protein SQM1 - human
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34653
R:Wong, Y.C.; Tsao, S.W.; Kakefuda, M.; Bernal, S.D.
Biochem. Biophys. Res. Commun. 166, 984-992, 1990
A:Title: cDNA cloning of a novel cell adhesion protein expressed in human squamous carc
A:Reference number: A34653; MUID:90147818; PMID:2302251
A:Accession: A34653
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <WON>
A:Cross-references: UNIPROT:P17568; GB:M33374; NID:g180232; PIDN:AAA35675.1; PID:g180233
C:Keywords: cell adhesion

Query Match 41.2%; Score 47; DB 2; Length 135;
Best Local Similarity 44.4%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEPPS 18
Db |||||:|:|:|:|
58 CAHLIRLLKCKRDSFPS 75

QY 1 CHHHSRVARMASDEPPSMC 20
Db |||||
264 CHHHSRVARMASDEPPSMC 283

RESULT 6
A:Residues: 1-315 <JAC>
A:Cross-references: UNIPROT:P08026; GB:M19473; NID:g215072; PIDN:AAA98151.1; PID:g215073
C:Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEPPSMC 20
Db |||||
264 CHHHSRVARMASDEPPSMC 283

RESULT 7
T08577
hypothetical protein T22F8.190 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08577
R:Bevan, M.; Zimmermann, W.; Gruenewald, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16442
A:Accession: T08577
A:Molecule type: DNA
A:Residues: 1-365 <BEV>
A:Cross-references: UNIPROT:Q9T035; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.190
A:Experimental source: cultivar Columbia; BAC clone T22F8
C:Genetics:
A:Gene: ATSP:T22F8.190
A:Map position: 4
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 44.3%; Score 50.5; DB 2; Length 365;
Best Local Similarity 47.8%; Pred. No. 2.2;
Matches 11; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 CHHHSRVA---RMASDEPPSMC 20
Db |||||:|:|:|:|
140 CRSHTWREAPSRVARDPPSTC 162

RESULT 8
T33763
hypothetical protein Y55H10A.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33763
R:Antoniou, B.; Smith, A.; Gibson, A.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid Y55H10A.
A:Reference number: Z21402
A:Accession: T33763
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA

```

RESULT 11
D95853
conserved hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magapla
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95853
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95853
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <KUR>
A;Cross-references: UNIPROT:Q92X70; GB:AL591985; PIDN:CAC48492.1; PID:gi5139964; GSPDB:C
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB20092
A;Genome: plasmid

Query Match 41.2%; Score 47; DB 2; Length 252;
Best Local Similarity 52.9%; Pred. No. 5.4;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFP 17
DB 224 CRVHGSTLARSASDHL 240

RESULT 12
D83279
probable transcription regulator PA2931 [imported] - Pseudomonas aeruginosa (strain PA01
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83279
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: UNIPROT:Q9HZR6; GB:AE004719; GB:AE004091; NID:g9949021; PIDN:AAG0631
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2931

Query Match 40.4%; Score 46; DB 2; Length 196;
Best Local Similarity 69.2%; Pred. No. 6;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 VARMSDEFPSMC 20
DB 95 VARFCSEFPFGC 107

RESULT 13
I60446
Shiga-like cytotoxin subunit A - Escherichia coli
N;Alternate names: shiga-like toxin II variant chain A
C;Species: Escherichia coli

```

```

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I60446; I57048; S31420
R;Paton, A.W.; Paton, J.C.; Heuzenroeder, M.W.; Goldwater, P.N.; Manning, P.A.
Microb. Pathog. 13, 225-236, 1992
A;Title: Cloning and nucleotide sequence of a variant Shiga-like toxin II gene from Esche
A;Reference number: I60446; MUID:93180660; PMID:1291844
A;Accession: I60446
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-319 <RES>
A;Cross-references: UNIPROT:Q03037; EMBL:X6S949; NID:g49089; PIDN:C4A46767.1; PID:g49090
R;Paton, A.W.; Paton, J.C.; Manning, P.A.
Microb. Pathog. 15, 77-82, 1993
A;Title: Polymerase chain reaction amplification, cloning and sequencing of variant Esche
A;Reference number: I57048; MUID:94018566; PMID:8412629
A;Accession: I57048
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-197,'G',199-319 <RE2>
A;Cross-references: GB:L11078; NID:g304950; PIDN:AAA16360.1; PID:g304951
C;Superfamily: Shigella toxin chain A
C;Keywords: cytotoxin

Query Match 40.4%; Score 46; DB 2; Length 319;
Best Local Similarity 35.0%; Pred. No. 9.9;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFP 20
DB 263 CHHQARSVRVAVNEEQPEC 282

RESULT 14
JC7855
pyridoxine 4-oxidase (EC 1.1.3.12) - Microbacterium luteolum YK-1
N;Alternate names: PN 4-oxidase; pyridoxin 4-oxidase
C;Species: Microbacterium luteolum YK-1
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 21-Apr-2003
C;Accession: JC7855; PC7192
R;Kaneda, Y.; Ohnishi, K.; Yagi, T.
Biosci. Biotechnol. Biochem. 66, 1022-1031, 2002
A;Title: Purification, Molecular cloning, and characterization of pyridoxine 4-oxidase fr
A;Reference number: JC7855; MUID:22087109; PMID:12092811
A;Accession: JC7855
A;Molecule type: DNA
A;Residues: 1-507 <KAN>
A;Cross-references: DDBJ:AB049341
A;Experimental source: strain YK-1
A;Accession: PC7192
A;Molecule type: protein
A;Residues: 2-20,348-364 <KA2>
C;Comment: This enzyme that is an FAD-dependent enzyme and a monomeric protein belongs to
ors to form pyridoxal and hydrogen peroxide or reduced forms of the acceptors. This enzym
C;Genetics:
A;Gene: pno
C;Keywords: oxidoreductase

Query Match 40.4%; Score 46; DB 2; Length 507;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 HHHSRVARMASDE 15
DB 446 HHHSFGTCRMGKDE 459

RESULT 15
S72759
hypothetical protein B1496_C2_188 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72759; T11014
R;Smith, D.R.; Robison, K.

```

submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B1496.
A:Reference number: S72695
A:Accession: S72759
A:Molecule type: DNA
A:Residues: 1-254 <SMI>
A:Cross-references: UNIPROT:O49688; EMBL:U00013; NID:G466868; PIDN:AAA17126.1; PID:G4668
R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z16918
A:Accession: T11014
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-254 <PAR>
A:Cross-references: EMBL:Z99125; NID:G2398683; PIDN:CAB16173.1; PID:G2398708
C:Genetics:
A:Gene: MLC1536.29c
A:Start codon: GTG

Query Match 39.5%; Score 45; DB 2; Length 254;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 2;

QY 1 CHHH--ASRVARMASDEFFPSMC 20
Db 196 CQHHCPSHVA---EEFFELC 213

Search completed: June 20, 2005, 10:14:36
Job time : 25 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:52:43 ; Search time 174 Seconds
(without alignments)
58.860 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARMASDEFFPSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	313	2 Q7WZ18	Q7WZ18 escherichia
2	114	100.0	315	1 SLTA_BPH19	P08026 bacterioph
3	114	100.0	315	1 SLTA_BPH30	P10149 bacterioph
4	114	100.0	315	2 Q6LDT4	Q6LDT4 coliphage 9
5	114	100.0	315	2 Q776E8	Q776E8 stx1 conver
6	114	100.0	315	2 Q777W4	Q777W4 bacterioph
7	114	100.0	315	2 Q779K4	Q779K4 shigella so
8	114	100.0	315	2 Q7AY18	Q7AY18 bacterioph
9	114	100.0	315	2 Q8L170	Q8L170 escherichia
10	114	100.0	315	2 Q47638	Q47638 escherichia
11	114	100.0	315	2 Q47639	Q47639 escherichia
12	114	100.0	315	2 Q47647	Q47647 escherichia
13	114	100.0	315	2 Q7B2T8	Q7B2T8 shigella so
14	114	100.0	315	2 Q7BQ99	Q7BQ99 shigella dy
15	114	100.0	315	2 Q7WZ17	Q7WZ17 escherichia
16	114	100.0	315	2 Q9FB12	Q9FB12 shigella dy
17	114	100.0	315	2 Q8X696	Q8X696 escherichia
18	114	100.0	315	2 Q7AK38	Q7AK38 escherichia
19	114	100.0	315	2 Q777M7	Q777M7 phage phi 4
20	105	92.1	315	2 Q83XK3	Q83XK3 escherichia
21	96	84.2	315	2 Q94M00	Q94M00 bacterioph
22	96	84.2	315	2 Q8VV67	Q8VV67 escherichia
23	96	84.2	315	2 Q47640	Q47640 escherichia
24	90	78.9	315	2 Q8VV64	Q8VV64 escherichia
25	86	75.4	315	2 Q8L168	Q8L168 escherichia
26	52	45.6	427	2 Q8P7A8	Q8P7A8 xanthomonas
27	50.5	44.3	365	2 Q9T035	Q9T035 arabidopsis
28	50	43.9	451	2 Q9TYW1	Q9TYW1 caenorhabdi
29	49	43.0	460	2 Q6XOV9	Q6XOV9 paracalichth
30	49	43.0	2152	2 Q9SND1	Q9SND1 arabidopsis
31	48	42.1	264	2 Q6W281	Q6W281 rhizobium s

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32 47 41.2 252 2 Q92X70 Q92X70 rhizobium m
33 47 41.2 319 2 Q8VV70 Q8VV70 escherichia
34 47 41.2 353 2 Q9EZ08 Q9EZ08 serratia ma
35 47 41.2 571 2 Q6CAD0 Q6CAD0 yarrowia li
36 46.5 40.8 466 1 ZIC3_MOUSE Q62521 mus musculu
37 46 40.4 85 2 Q7UHI1 Q7UHI1 rhodopirell
38 46 40.4 196 2 Q9HZR6 Q9HZR6 pseudomonas
39 46 40.4 319 2 Q03037 Q03037 escherichia
40 46 40.4 319 2 Q8VLD2 Q8VLD2 escherichia
41 46 40.4 319 2 Q8VLK6 Q8VLK6 escherichia
42 46 40.4 319 2 Q8VV62 Q8VV62 escherichia
43 46 40.4 319 2 Q8VV65 Q8VV65 escherichia
44 46 40.4 319 2 Q8VV71 Q8VV71 escherichia
45 46 40.4 319 2 Q8VV72 Q8VV72 escherichia

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ALIGNMENTS

```

RESULT 1
QWZ18
ID Q7WZ18 PRELIMINARY; PRT; 313 AA.
AC Q7WZ18;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Shiga toxin 1 variant A subunit.
GN Name=stx1;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AI2000/182;
RA Suzuki M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083043; BAC78637.1; -.
DR HSSP; Q9FB12; IDMO.
DR GO; GO:0030598; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 313 AA; 34639 MW; DDF7ABF58F30BD19 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CHHHSRVARMASDEFFPSMC 20
Db 264 CHHHSRVARMASDEFFPSMC 283

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RESULT 2
SLTA_BPH19
ID SLTA_BPH19 STANDARD; PRT; 315 AA.
AC P08026;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Shiga-like toxin I subunit A precursor (EC 3.2.2.22) (Verotoxin 1
DE subunit A) (SLT-I) (rRNA N-glycosidase).
GN Name=SLTA;
OS Bacteriophage H19B.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=69932;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87260808; PubMed=3299365;
RA Calderwood S.B., Auclair F., Donohue-Rolfe A., Keusch G.T.,
RA Mekalanos J.J.;

```

RT "Nucleotide sequence of the Shiga-like toxin genes of *Escherichia coli*.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4364-4368(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87308020; PubMed=3040689;
RA de Grandis S., Ginsberg J., Toone M., Climie S., Friesen J.,
Brunton J.;
RT "Nucleotide sequence and promoter mapping of the *Escherichia coli*
Shiga-like toxin operon of bacteriophage H-19B.";
RL J. Bacteriol. 169:4313-4319(1987).
RN [3]
RP ACTIVE SITE.
RX MEDLINE=88190113; PubMed=3357883;
RA Hovde C.J., Calderwood S.B., Mekalanos J.J., Collier R.J.;
RT "Evidence that glutamic acid 167 is an active-site residue of Shiga-
like toxin I.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2568-2572(1988).
CC -!- FUNCTION: The A subunit is responsible for inhibiting protein
synthesis through the catalytic inactivation of 60S ribosomal
subunits.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: The Shiga-like toxins contain a single A subunit and
multiple copies of B subunit.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M16625; AAA98099.1; -;
DR EMBL; M17358; AAA32229.1; -;
DR PIR; A27052; XUBPH9.
DR PIR; A53887; A53887.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
FT CHAIN 23 315 Shiga-like toxin I subunit A.
FT SIGNAL 1 22
FT ACT_SITE 189 189
FT SEQUENCE 315 AA; 34799 MW; 8B993DF7A8E58F30 CRC64;
Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHASRVARMASDEFPSSMC 20
Db 264 CHHHASRVARMASDEFPSSMC 283
RESULT 3
SLTA_BPH30
ID SLTA_BPH30 STANDARD; PRT; 315 AA.
AC P10149;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Shiga toxin A-chain precursor (EC 3.2.2.22) (rRNA N-glycosidase).
GN Name=STXA;
OS Bacteriophage H30.
OC Viruses.
OX NCBI_TaxID=12371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88139166; PubMed=2830229;
RA Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D.;

RT "Cloning and sequencing of the genes for Shiga toxin from *Shigella dysenteriae* type 1.";
RL J. Bacteriol. 170:1116-1122(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8906281; PubMed=3049254; DOI=10.1016/0378-1119(88)90398-8;
RA Kozlov Y.V., Kabishev A.A., Fedchenko V.I., Bayev A.A.;
RT "The primary structure of the operons coding for *Shigella dysenteriae*
toxin and temperature phage H30 shiga-like toxin.";
RL Gene 67:213-221(1989).
CC -!- FUNCTION: The A chain is responsible for inhibiting protein
synthesis through the catalytic inactivation of 60S ribosomal
subunits.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: Shiga toxin contains a single A-chain and five copies of
B-chain.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M19437; AAA98347.1; -;
DR EMBL; X07903; CAA30741.1; -;
DR EMBL; M24352; AAA26538.1; -;
DR EMBL; M23980; AAA72732.1; -;
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 22
FT CHAIN 23 315 Shiga toxin A-chain.
FT ACT_SITE 189 189 By similarity.
FT CONFLICT 67 67 T -> S (in Ref. 3).
FT CONFLICT 190 190 A -> P (in Ref. 2).
FT SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHASRVARMASDEFPSSMC 20
Db 264 CHHHASRVARMASDEFPSSMC 283
RESULT 4
Q6LDT4
ID Q6LDT4 PRELIMINARY; PRT; 315 AA.
AC Q6LDT4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Shiga toxin-like subunit A precursor.
OS Coliphage 933U.
OC Viruses.
OX NCBI_TaxID=12340;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89180929; PubMed=3333796; DOI=10.1016/0882-4010(87)90106-9;
RA Jackson M.P., Newland J.W., Holmes R.K., O'Brien A.D.;
RT "Nucleotide sequence analysis of the structural genes for Shiga-like
toxin I encoded by bacteriophage 933U from *Escherichia coli*.";

Microb. Pathog. 2:147-153(1987).

[2]

RL RN
RN
RP
SEQUENCE FROM N.A.
MEDLINE=88139166; PubMed=28303229;
RA Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D.;
RT "Cloning and sequencing of the genes for Shiga toxin from Shigella
RT dysenteriae type 1.";
RL J. Bacteriol. 170:1116-1122(1988).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein-family.
CC ENBL; M19473; AAA98151.1; -
DR GO: 0016787; F:hydrolase activity; IEA.
DR GO: 0030598; F:rRNA N-glycosylase activity; IEA.
DR GO: 0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 315 Shiga toxin-like subunit A.
SQ SEQUENCE 315 AA; 34799 MW; 8B993DF7A8E58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 CHHHASRVARMASDEFPSSMC 20
|||||
DB 264 CHHHASRVARMASDEFPSSMC 283
|||||

RESULT 5

ID Q776E8 PRELIMINARY; PRT; 315 AA.

AC Q776E8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Shiga toxin1 subunit A.
GN Name:stx1a;
OS Stx1 converting bacteriophage.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=194948;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Stx1 phage;
RX MEDLINE=22697399; PubMed=12813092;
RY DOI=10.1128/J.B.185.13.3966-3971.2003;
RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA Takeda Y., Yamasaki S.;
RT "genome analysis of a novel Shiga toxin 1 (Stx1)-converting phage
RT which is closely related to Stx2-converting phages but not to other
RT Stx1-converting phages.";
RL J. Bacteriol. 185:3966-3971(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR ENBL; AP005153; BAC77958.1; -
DR GO: 0016787; F:hydrolase activity; IEA.
DR GO: 0030598; F:rRNA N-glycosylase activity; IEA.
DR GO: 0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Protein synthesis inhibitor; Toxin.
SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RX MEDLINE=21562619; PubMed=11705937;
 RA DOI=10.1128/IAI.69.12.7588-7595.2001;
 RA Strauch E., Lurz R., Beutin L.;
 RT "Characterization of a Shiga toxin-encoding temperate bacteriophage of
 RT Shigella sonnei.";
 RL Infect. Immun. 69:7588-7595(2001).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AJ279086; CAC12887.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; F:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolyase; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0;

QY 1 CHHHSRVARVASDEFFPSMC 20
 |||||
 Db 264 CHHHSRVARVASDEFFPSMC 283

RESULT 8

Q7AY18 PRELIMINARY; PRT; 315 AA.
 AC Q7AY18;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Shiga toxin 1 Stx1, A-subunit.
 GN Name=stx1A; ORFNames=EC_CP1639_35;
 OS Bacteriophage CP-1639.
 OC Viruses.
 OX NCBI_TaxID=291401;
 RN SEQUENCE FROM N.A.
 RP Creuzburg K.; Koehler B., Hempel H., Schreiber P. Jacobs E.,
 RA Schmidt H.;
 RT "Genetic structure and chromosomal integration site of the cryptic
 RT Shiga toxin 1-converting prophage CP-1639.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA Creuzburg K.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AJ304858; CAC83149.1; -.
 DR HSP; O9FB12; 1DM0.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0;

QY 1 CHHHSRVARVASDEFFPSMC 20
 |||||
 Db 264 CHHHSRVARVASDEFFPSMC 283

RESULT 9

Q8L170 PRELIMINARY; PRT; 315 AA.
 ID Q8L170;
 AC Q8L170;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Shiga toxin 1 A subunit.
 GN Name=stx1A;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN SEQUENCE FROM N.A.
 RP STRAIN=HI-A;
 EX MEDLINE=99074174; PubMed=9858463;
 RA Asakura H., Makino S., Shirahata T., Tsukamoto T., Kurazono H.,
 RA Ikeda T., Takeshi K.;
 RT "Detection and long-term existence of Shiga toxin (Stx)-producing
 RT Escherichia coli in sheep.";
 RL Microbiol. Immunol. 42:683-688(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HI-A;
 RA Asakura H., Makino S., Kim S., Allano M.R., Kuri A., Watarai M.,
 RA Shirahata T.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB071619; BAC10987.1; -.
 DR HSP; O9FB12; 1DM0.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 SQ SEQUENCE 315 AA; 34756 MW; 1E1F9146E3421149 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0;

QY 1 CHHHSRVARVASDEFFPSMC 20
 |||||
 Db 264 CHHHSRVARVASDEFFPSMC 283

RESULT 10

Q47638 PRELIMINARY; PRT; 315 AA.
 ID Q47638;
 AC Q47638;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE SLT-I A subunit coding region.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN SEQUENCE FROM N.A.
 RP STRAIN=serotype O48:H21;
 EX MEDLINE=95189106; PubMed=7883188; DOI=10.1016/0378-1119(94)00777-P;
 RA Paton A.W., Beutin L., Paton J.C.;
 RT "Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-
 RT like toxin type-I operons.";
 RL Gene 153:71-74(1995).

```

DR EMBL; Z36899; CAA85366.1; -.
DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 315 AA; 3485 MW; 8A423E94CBF6EC50 CRC64;

Query Match      100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
Db 264 CHHHSRVARMASDEFFPSMC 283

RESULT 11
Q47639 PRELIMINARY; PRT; 315 AA.
AC Q47639;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SLT-I alpha subunit coding region.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serotype O111:H-;
RX MEDLINE=95189106; PubMed=7883188; DOI=10.1016/0378-1119(94)00777-P;
RA Paton A.W., Beutin L., Paton J.C.;
RT "Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-
RT like toxin type-I operons.";
RL Gene 153:71-74(1995).
DR EMBL; Z36900; CAA85368.1; -.
DR HSP; Q9FB12; 1DM0.
DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 315 AA; 34843 MW; CE4BE03E7FF59B3F CRC64;

Query Match      100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
Db 264 CHHHSRVARMASDEFFPSMC 283

RESULT 12
Q47647 PRELIMINARY; PRT; 315 AA.
AC Q47647;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Shiga-like toxin type-I alpha subunit precursor.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93328129; PubMed=8335264; DOI=10.1016/0378-1119(93)90700-D;
RA Paton A.W., Paton J.C., Goldwater P.N., Heuzenroeder M.W.,
RA Manning P.A.;

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RT "Sequence of a variant Shiga-like toxin type-I operon of Escherichia
RT coli O111:H-";
RL Gene 129:87-92(1993).
DR EMBL; L04539; AAA71893.1; -.
DR PIR; JN0725; JN0725.
DR HSP; Q9FB12; 1DM0.
DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 315 Shiga-like toxin type-I subunit alpha.
SQ SEQUENCE 315 AA; 34839 MW; 2DBF149B7BF5995C CRC64;

Query Match      100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
Db 264 CHHHSRVARMASDEFFPSMC 283

RESULT 13
Q7B2T8 PRELIMINARY; PRT; 315 AA.
AC Q7B2T8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE StxA protein.
GN Name=stxA;
OS Shigella sonnei.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=624;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB7888;
RX MEDLINE=99247285; PubMed=1023325; DOI=10.1016/S0140-6736(99)00961-7;
RA Beutin L., Strauch E., Fischer I.;
RT "Isolation of Shigella sonnei lysogenic for bacteriophage encoding
RT gene for production of Shiga toxin.";
RL Lancet 353:1498-1498(1999).
DR EMBL; AJ132761; CAA10763.1; -.
DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF59F30 CRC64;

Query Match      100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFFPSMC 20
Db 264 CHHHSRVARMASDEFFPSMC 283

RESULT 14
Q7BQ99 PRELIMINARY; PRT; 315 AA.
AC Q7BQ99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE StxA.
GN Name=stxA;
OS Shigella dysenteriae.

```

CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=622;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=type 1;
 RX MEDLINE=20063152; PubMed=10594830;
 RA McDonough M.A., Butters J.R.;
 RT "Spontaneous tandem amplification and deletion of the shiga toxin
 operon in Shigella dysenteriae 1.";
 RL Mol. Microbiol. 34:1058-1069(1999).
 DR EMBL; AF153317; AAF28121.1; -;
 DR PDB; 1DM0; X-ray; A/L=-;
 DR PDB; 1R4Q; X-ray; A/L=-;
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CHHHSRVARMASDEFFSMC 20
 |||||
 DB 264 CHHHSRVARMASDEFFSMC 283

 RESULT 15
 Q7WZ17
 ID Q7WZ17 PRELIMINARY; PRT; 315 AA.
 AC Q7WZ17;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Shiga toxin 1 variant A subunit.
 GN Name=stx1;
 OS Escherichia coli O157:H7.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AI2001/52;
 RA Suzuki M.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB083044; BAC78639.1; -;
 DR HSSP; Q9FBI2; 1DM0.
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 SQ SEQUENCE 315 AA; 34844 MW; 91588DF7ABF58F31 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CHHHSRVARMASDEFFSMC 20
 |||||
 DB 264 CHHHSRVARMASDEFFSMC 283

 RESULT 16
 Q9FBI2
 ID Q9FBI2 PRELIMINARY; PRT; 315 AA.
 AC Q9FBI2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Shiga toxin A protein.
 GN Name=shiga toxin A;
 OS Shigella dysenteriae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=622;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H2765-39/81;
 RX MEDLINE=20407286; PubMed=10948097;
 RX DOI=10.1128/IAI.68.9.4856-4864.2000;
 RA Unkmeir A., Schmidt H.;
 RT "Structural analysis of phage-borne stx genes and their flanking
 sequences in shiga toxin-producing Escherichia coli and Shigella
 dysenteriae type 1 strains.";
 RL Infect. Immun. 68:4856-4864(2000).
 DR EMBL; AJ271153; CAC05622.1; -;
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 SQ SEQUENCE 315 AA; 34822 MW; 897E3DF7ACB58F30 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CHHHSRVARMASDEFFSMC 20
 |||||
 DB 264 CHHHSRVARMASDEFFSMC 283

 RESULT 17
 Q8X696
 ID Q8X696 PRELIMINARY; PRT; 315 AA.
 AC Q8X696;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Shiga toxin 1 A-subunit (Shiga-like toxin 1 A-subunit) (Stx1A
 protein).
 GN Name=stx1 A-subunit; Synonyms=stx-1 A subunit, stx1, stx1A;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HI-2;
 RX MEDLINE=99074174; PubMed=9858463;
 RA Asakura H., Makino S., Shirahata T., Tsukamoto T., Kurazono H.,
 RA Ikeda T., Takeshi K.;
 RT "Detection and long-term existence of Shiga toxin (Stx)-producing
 Escherichia coli in sheep.";
 RL Microbiol. Immunol. 42:683-688(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HI-2;
 RX MEDLINE=21445868; PubMed=11561972;
 RA Asakura H., Makino S., Kobori H., Watarai M., Shirahata T., Ikeda T.,
 RA Takeshi K.;
 RT "Phylogenetic diversity and similarity of Active sites of Shiga toxin
 (Stx) in Shiga toxin-producing Escherichia coli (STEC) isolates from
 human and animals.";
 RL Epidemiol. Infect. 127:27-36(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99170895; PubMed=10071501;
 RA Iwasa M., Makino S., Asakura H., Kobori H., Morimoto Y.;
 RT "Detection of Escherichia coli O157:H7 from Musca domestica (Diptera:
 Muscidae) at a cattle farm in Japan.";
 RL J. Med. Entomol. 36:108-112(1999).

RA SEQUENCE FROM N.A.
 RT Sou-ichi M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CPU96MW;
 RA Yokoyama S., Suzuki T., Kawai K., Ohishi N., Yagi K., Itoh S.,
 RA Mori H.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EK201, EK921, and FD930;
 RA Yu J.Y., Jeon H.G., Kang Y.H., Kim E.C., Sohn C.K., Lee B.K.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1639/97;
 RX MEDLINE=20407286; PubMed=10948097;
 RX DOI=10.1128/IAI.68.9.4856-4864.2000;
 RA Unkneir A., Schmidt H.;
 RT "Structural analysis of phage-borne stx genes and their flanking
 RT sequences in shiga toxin-producing Escherichia coli and Shigella
 RT dysenteriae type 1 strains."
 RL Infect. Immun. 68:4856-4864 (2000).
 DR EMBL; AB048232; BAB83012.1; -;
 DR EMBL; AB015056; BAA88123.1; -;
 DR EMBL; AB030485; BAB20382.1; -;
 DR EMBL; AB035142; BAA86997.1; -;
 DR EMBL; AF461166; AAM70031.1; -;
 DR EMBL; AF461168; AAM70035.1; -;
 DR EMBL; AF461169; AAM70037.1; -;
 DR EMBL; AF461172; AAM70043.1; -;
 DR EMBL; AJ251325; CAC05535.1; -;
 DR PIR; A28626; A28626.
 DR PIR; F91000; F91000.
 DR PIR; H85845; H85845.
 DR HSSP; Q9FBI2; 1DM0.
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR Pfan; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHSRVARWASDEFFPSMC 20
 DB 264 CHHHSRVARWASDEFFPSMC 283
 RESULT 18
 Q7AK38
 ID Q7AK38 PRELIMINARY; PRT; 315 AA.
 AC Q7AK38; Q7DBC9;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Shiga toxin 1 subunit A (Shiga-like toxin 1 subunit A encoded within
 DE prophage CP-933V) (Shiga toxin 1 subunit A).
 GN Name=stx1A; OrderedLocNameNames=ECs2974, Z3344;
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20564182; PubMed=11111050; DOI=10.1016/S0378-1119(00)00416-9;
 RA Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
 RA Yutamoto C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
 RA Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,

RA Shinagawa H.;
 RT "Complete nucleotide sequence of the defective Sakai-VT1 prophage
 RT carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia
 RT coli O157:H7 derived from the Sakai outbreak."
 RL Gene 258:127-139 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=21074935; PubMed=11208551; DOI=10.1038/35054089;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RMD 0509952 / EHEC;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:111-22 (2001).
 DR EMBL; AF000400; BAB19590.1; -;
 DR EMBL; AE005442; AAG57228.1; -;
 DR EMBL; AP002560; BAB36397.1; -;
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfan; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHSRVARWASDEFFPSMC 20
 DB 264 CHHHSRVARWASDEFFPSMC 283
 RESULT 19
 Q777M7
 ID Q777M7 PRELIMINARY; PRT; 315 AA.
 AC Q777M7;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Stx1 protein.
 GN Name=stx1;
 OS Phage phi 4795.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses.
 OX NCBI_TaxID=196242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reckenwald J., Schmidt H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Reckenwald J., Schmidt H.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AJ487680; CAD32216.1; -

Search completed: June 22, 2005, 07:08:29
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:53:33 ; Search time 163 Seconds
(without alignments)
47.455 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHARSRVARVASDEFPSC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: Genesecp1980s:*
2: Genesecp1990s:*
3: Genesecp2000s:*
4: Genesecp2001s:*
5: Genesecp2002s:*
6: Genesecp2003as:*
7: Genesecp2003bs:*
8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	2 AAR37300	Aar37300 E. coli sh
2	114	100.0	293	2 AAW58827	Aaw58827 Shiga tox
3	114	100.0	293	2 AAY39393	Aay39393 Shiga-lik
4	114	100.0	293	3 AAY69046	Aay69046 Amino aci
5	114	100.0	315	2 AAW06403	Aaw06403 Verotoxig
6	114	100.0	315	2 AAW21702	Aaw21702 Shiga-lik
7	114	100.0	315	2 AAW25139	Aaw25139 SLT-1 (a
8	114	100.0	315	3 AAY96681	Aay96681 E. coli v
9	114	100.0	315	5 AAW77817	Aaw77817 E. coli v
10	114	100.0	315	7 ADC00545	Adc00545 Enterohae
11	114	100.0	315	7 ADH34319	Adh34319 Verotoxin
12	114	100.0	316	2 AAW25786	Aaw25786 Phage H19
13	114	100.0	323	2 AAW06407	Aaw06407 Histidine
14	114	100.0	323	3 AAY96686	Aay96686 Recombina
15	114	100.0	323	5 AAW77822	Aaw77822 H1S-tagge
16	114	100.0	326	2 AAW06413	Aaw06413 Flag tag/
17	114	100.0	326	3 AAY96692	Aay96692 FLAG tag/
18	114	100.0	326	5 AAW77828	Aaw77828 Flag tag/
19	114	100.0	332	2 AAW29294	Aaw29294 BPI pepti
20	114	100.0	409	2 AAR13118	Aar13118 Shiga-lik
21	114	100.0	409	3 AAY55891	Aay55891 E. coli ba
22	114	100.0	409	3 AAY78591	Aay78591 E. coli b
23	114	100.0	690	3 AAY96694	Aay96694 MBP-VT-1
24	114	100.0	690	5 AAW77830	Aaw77830 MBPNT1-A
25	114	100.0	708	2 AAW06411	Aaw06411 Maltose b

26	114	100.0	708	3 AAY96690	Aay96690 MBP-VT-1
27	114	100.0	708	5 AAU77826	Aau77826 MBPNT1-A
28	47	41.2	135	7 ADJ68214	Adj68214 Human hea
29	46	40.4	35	7 ADE95989	Ade95989 Human uri
30	46	40.4	35	7 ADK14898	Adk14898 Urinary s
31	46	40.4	196	6 ABU38500	Abu38500 Protein e
32	46	40.4	204	7 ABO69919	Abog69919 Pseudomon
33	45	39.5	19	7 ABR82617	Abr82617 P. aerugi
34	45	39.5	386	3 AAG59236	Aag59236 Arabidops
35	45	39.5	413	6 ADA34573	Ada34573 Acinetoba
36	45	39.5	525	7 ABO79520	Abog79520 Pseudomon
37	44.5	39.0	250	8 ADS21292	Ads21292 Bacterial
38	44.5	39.0	544	3 AAB53464	Aab53464 Human col
39	44	38.6	137	4 AAM79060	Aam79060 Human pro
40	44	38.6	137	7 ADJ69294	Adj69294 Human hea
41	44	38.6	138	2 AAW60837	Aaw60837 Human SQM
42	44	38.6	138	5 ABG72567	Abg72567 Human cel
43	44	38.6	296	2 AAW58829	Aaw58829 Shiga tox
44	44	38.6	297	2 AAW07643	Aaw07643 Mutant Sh
45	44	38.6	297	2 AAW07641	Aaw07641 Mutant Sh

ALIGNMENTS

RESULT 1

AAR37300

ID AAR37300 standard; protein; 20 AA.

XX AAR37300;

AC

25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX

DE E.coli shiga-like toxin segment.

XX

KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin; human engineered antibody;
KW variable region; light chain; cell targeting; chimeric antibody; SLT.

OS Escherichia coli.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..20

FT /note= "intervening loop includes protease sensitive amino acid sequence"

XX

PN W09309130-A1.

XX

PD 13-MAY-1993.

XX

PF 04-NOV-1992; 92WO-US009487.

XX

PR 04-NOV-1991; 91US-00787567.

PR

19-JUN-1992; 92US-00901707.

XX

(XOMA) XOMA CORP.

XX

PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX

DR WPI; 1993-167617/20.

XX

PT Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo.

PT

XX Example 10; Page 114; 163pp; English.

XX

CC The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules are antibodies or their fragments, esp. human engineered H65 antibody

CC fragments. Fusion constructs were assembled that included a natural
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an
 CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of
 CC the E.coli shiga-like toxin was inserted between the gelonin gene and the
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 20 AA;

Query Match 100.0%; Score 114; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
 |||||
 DB 1 CHHHASRVARMASDEFPSSMC 20

RESULT 2
 AAW58827
 ID AAW58827 standard; peptide; 293 AA.
 XX
 AC AAW58827;

DT 18-AUG-1998 (first entry)
 XX
 DE Shiga toxin type 1 mature A subunit.

XX Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;
 KW haemorrhagic colitis; haemolytic uremic syndrome.
 XX

OS Shigella dysenteriae.

PN WO9811229-A2.

XX 19-MAR-1998.

PF 09-SEP-1997; 97WO-US015836.

PR 10-SEP-1996; 96US-0025637P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI O'Brien AD, Schmitt CK;

XX WPI; 1998-207390/18.

DR N-PSDB; AAV11400.

XX Purification and isolation of histidine-tagged Shiga toxins - useful in
 PT vaccines against haemorrhagic colitis and haemolytic uremic syndrome.

PS Claim 1; Fig 2; 47pp; English.

XX The Shiga toxin (Stx) peptides (AAW58827-W58830) were histine-tagged to
 CC simplify and expedite purification. Non toxic Shiga toxoids, Fusion
 CC proteins of His-tagged Shiga toxins/toxoids and antibodies can be used in
 CC the treatment, diagnosis or prevention of infections mediated by toxins
 CC of the Stx family. These are associated with haemorrhagic colitis and the
 CC life-threatening sequelae, haemolytic uremic syndrome. Shiga antibodies
 CC are also useful for the treatment, diagnosis and prevention of disease
 CC and infections by pathogenic Escherichia coli

XX Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 9e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
 |||||
 DB 242 CHHHASRVARMASDEFPSSMC 261

RESULT 3
 AAY39393
 ID AAY39393 standard; protein; 293 AA.

XX AAY39393;

DT 20-DEC-1999 (first entry)

XX Shiga-like Toxin 1, A subunit.

XX Shiga toxin; ShT; Shiga-like toxin; SLT; A subunit; B subunit; ricin;
 KW microorganism clone; combinatorial library; therapeutic protein;
 KW medicament; target cell; binding specificity.

OS Shigella dysenteriae.

PN WO9940185-A1.

XX 12-AUG-1999.

PF 08-DEC-1998; 98WO-CA001137.

PR 04-FEB-1998; 98CA-02222993.

XX (ONTA-) ONTARIO CANCER INST.

PI Garipey J, Bray MR;

XX WPI; 1999-590695/50.

XX Production of cytotoxic heteromeric protein combinatorial libraries,
 PT useful for ability to specifically bind to and kill a target cell.

PS Example 1; Fig 1a; 61pp; English.

XX This is the Shiga-like toxin (SLT) subunit A amino acid sequence. SLT is
 CC a bacterial toxin related to the Shiga toxin (ShT). SLT and ShT have the
 CC smallest known B subunit of all AB toxins, and the A subunit has
 CC identical catalytic activity as the corresponding subunit in ricin. The B
 CC subunit (AAY39394) is identical for both ShT and SLT. Both the A and B
 CC subunit amino acid sequences are used in the methods of the invention,
 CC which relates to the creation of a library of microorganism clones
 CC producing mutant proteins which are then screened for their ability to
 CC specifically bind to and kill target cell. AAY39395-Y39389 and AAY43001-
 CC Y43024 are examples of mutant B subunits identified by the methods of the
 CC invention. The B subunit of the toxin has high binding specificity, and
 CC therefore mutant versions of the B subunit may target the toxin to a
 CC specific cell. Cytotoxic mutant proteins identified by the method can be
 CC used to identify therapeutic proteins and medicaments having binding
 CC specificity for a target cell. The cytotoxic mutants can also be used to
 CC construct diagnostic probes for detecting the presence of cell surface
 CC markers. These medicaments can be used to target medicines to target
 CC cells in host organisms

XX Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 9e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
 |||||
 DB 242 CHHHASRVARMASDEFPSSMC 261

RESULT 4
 AAY69046
 ID AAY69046 standard; protein; 293 AA.

XX AAY69046;

DT 30-MAY-2000 (first entry)

DE Amino acid sequence of exemplary cell toxin shiga toxin A-chain.
 XX
 KW Chemokine receptor; ligand; inflammatory response; immune effector cell;
 KW secondary tissue damage; central nervous system injury; shiga;
 KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
 KW inflammatory eye disease; inflammatory bowel disease; PCR primer;
 KW inflammatory joint disease; inflammatory kidney; renal disease;
 KW inflammatory lung disease; inflammatory nasal disease; thyroiditis;
 KW inflammatory thyroid disease; cytokine-regulated cancer; ss.
 XX
 OS Shigella dysenteriae.
 XX
 PN WO200004926-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-CA000659.
 XX
 PR 22-JUL-1998; 98US-00120523.
 XX
 PA (OSPR-) OSPREY PHARM LTD.
 XX
 PI McDonald JR, Coggins PJ;
 XX
 DR WPI; 2000-182542/16.
 XX
 PT A new therapeutic agent comprising a conjugate for treating secondary
 PT tissue damage and other disease conditions like Alzheimer's disease,
 PT stroke, Parkinson's disease and atherosclerosis.
 XX
 PS Disclosure; Page 67; 204pp; English.
 XX
 CC The present sequence represents an exemplary cell toxin, which can be
 CC incorporated into the conjugates of the invention. The specification
 CC describes a conjugate, comprising a targeted agent and a chemokine
 CC receptor ligand. The conjugate binds to a chemokine receptor resulting in
 CC internalisation of the targeted agent in cells bearing the receptor. The
 CC conjugates are used for formulating a medicament or for treating
 CC disorders associated with inflammatory responses resulting from
 CC activation, proliferation and migration of immune effector cells. The
 CC disorders or disease states comprise secondary tissue damage such as
 CC central nervous system (CNS) injury, CNS inflammatory diseases,
 CC neurodegenerative disorders, heart disease, inflammatory diseases,
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
 CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
 CC regulated cancers
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 114; DB 3; Length 293;
 Best Local Similarity 100.0%; Pred. No. 9e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFPSC 20
 DB 242 CHHHASRVARMASDEFPSC 261
 RESULT 5
 AAW06403
 ID AAW06403 standard; protein; 315 AA.
 XX
 AC AAW06403;
 XX
 DT 25-FEB-1997 (first entry)
 XX
 DE Verotoxinigenic E. coli toxin (VT1) subunit A.
 XX
 KW Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
 KW haemolytic uraemic syndrome; detection.
 XX
 OS Escherichia coli.

XX WO9630043-A1.
 PN
 XX 03-OCT-1996.
 PD
 XX 25-MAR-1996; 96WO-US004093.
 PF
 XX 24-MAR-1995; 95US-00410058.
 PR
 XX (OPHI-) OPHIDIAN PHARM INC.
 PA
 XX Carroll SB, Stafford DC, Padhye NV;
 PI
 XX WPI; 1996-505779/50.
 DR N-PSDB; AAT42649.
 XX
 PT Compan. contg. neutralising antitoxin against E.coli vero-toxin - used to
 PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
 PT disease or extra-intestinal complications of E.coli infection.
 XX
 PS Example 6; Page 51; 101pp; English.
 XX
 CC Compositions containing neutralising antitoxin against one or more E.
 CC coli verotoxin (VT) can be used to treat intoxicated adults and children
 CC with enteric bacterial infections. They may also be used as prophylactics
 CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
 CC -intestinal complications of E.coli infection, especially haemolytic
 CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
 CC a sample. The VT is recombinant, preferably a fusion protein containing a
 CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence
 XX
 SQ Sequence 315 AA;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFPSC 20
 DB 264 CHHHASRVARMASDEFPSC 283
 RESULT 6
 AAW21702
 ID AAW21702 standard; protein; 315 AA.
 XX
 AC AAW21702;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 26-SEP-1997 (first entry)
 XX
 DE Shiga-like toxin (SLT-1) RIP.
 XX
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat;
 KW ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
 XX
 OS Bacteriophage H-19B.
 XX
 FH Key Location/Qualifiers
 FT Region 145..155
 FT /note= "Position of possible insertion of internal
 FT peptide linker sequence"
 XX
 XX US5635384-A.
 PN
 XX 03-JUN-1997.
 PD
 XX 26-JAN-1995; 95US-00378761.
 PF
 XX 11-JUN-1990; 90US-00535636.
 PR

PR 09-DEC-1992; 92US-00987927.
 XX (DOWC) DOWELANCO.
 XX
 XX Hey TD, Morgan AER, Walsh TA;
 XX WPI; 1997-309831/28.
 DR
 XX Inactive precursor of maize ribosome-inactivating protein - also chimeric
 PT ribosome-inactivating protein precursors containing internal linker
 PT sequences.
 XX
 XX Claim 2; Col 113-116; 121pp; English.
 PS
 XX The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIP's), which may be used in the construction of the proRIP of
 CC the invention. The proRIP has a selectively removable, internal peptide
 CC linker. The precursor sequence is incapable of inactivating eukaryotic
 CC ribosomes, but can be converted by removal of the linker into a protein
 CC having alpha and beta fragments and being capable of inactivating
 CC eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein
 CC synthesis. They possess a highly specific N-glycosidase activity which
 CC cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S
 CC RNA. RIP's selectively inhibit cellular proliferation of cells, e.g.
 CC cancer cells and HIV-infected T cells. The inactive proRIP proteins make
 CC it possible to provide protein synthesis inhibitors with uses in
 CC practical and improved ways not before possible. The RIP can be used to
 CC make cytotoxic conjugates. (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 XX SQ Sequence 315 AA;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFFPSMC 20
 |||||
 DB 264 CHHHASRVARMASDEFFPSMC 283
 RESULT 7
 AAW25139
 ID AAW25139 standard; protein; 315 AA.
 XX
 XX AAW25139;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-DEC-1997 (first entry)
 DE
 DE SLT-1 (a ribosome inhibitory protein) inactive precursor.
 XX
 XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.
 XX
 XX Synthetic.
 OS
 XX US5646026-A.
 PN
 XX 08-JUL-1997.
 PD
 XX 07-JUN-1995; 95US-00485286.
 PF
 XX 11-JUN-1990; 90US-00535636.
 PR 09-DEC-1992; 92US-00987927.
 PR 26-JAN-1995; 95US-00378761.
 XX
 XX (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;
 XX WPI; 1997-362934/33.
 DR
 XX DNA encoding pro-ribosome inactivating proteins - inactive precursors of
 PT ribosome inactivating proteins; can be expressed in eukaryotic cells
 PT without causing cell death.
 XX
 XX Claim 4; Col 115-116; 186pp; English.
 PS
 XX AAW25139 represents an SLT-1 (a ribosome inhibitory protein, RIP) protein
 CC which was engineered to contain a selectively removable internal peptide
 CC linker sequence separating the alpha and beta units of the RIP. When
 CC separated the two units regain activity and are capable of inactivating
 CC eukaryotic ribosomes and hence preventing protein production. Many
 CC different RIPs may be produced with an internal linker including maize
 CC RIP, Trichosanthin, Ricin A-chain, Abrin-A-chain and Saporin. The RIPs
 CC can be used in the construction of therapeutic toxins targeted to
 CC specific cells such as tumour cells via the attachment of a targeting
 CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
 CC (see US4869903). There is interest in expressing RIP recombinantly in
 CC host eukaryotic cells, because of the capacity to provide correct post-
 CC translational processing. However, RIPs effectively inhibit protein
 CC synthesis in eukaryotic cells resulting in cell death. Since the inactive
 CC RIP proteins are not cytotoxic to eukaryotic cells, they can be
 CC recombinantly expressed in such cells and then converted to active RIP
 CC proteins. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX SQ Sequence 315 AA;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFFPSMC 20
 |||||
 DB 264 CHHHASRVARMASDEFFPSMC 283
 RESULT 8
 AAY96681
 ID AAY96681 standard; protein; 315 AA.
 XX
 XX AAY96681;
 XX
 XX 26-SEP-2000 (first entry)
 DT
 DE E. coli verotoxin 1 subunit A.
 DE
 KW VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
 KW recombinant production; screening; dairy; anti-bacterial; vaccine.
 KW
 OS Escherichia coli.
 XX
 XX US6080400-A.
 PN
 XX 27-JUN-2000.
 PD
 XX 13-MAR-1997; 97US-00816977.
 PF
 XX 24-MAR-1995; 95US-00410058.
 PR
 XX (OPHI-) OPHIDIAN PHARM INC.
 XX
 XX Williams JA, Byrne LM;
 PI
 XX WPI; 2000-451195/39.
 DR
 XX N-PSDB; AAA51194.
 XX
 XX Bacterial cell for recombinantly expressing bacterial toxins in large
 PT quantities useful for immunization and treatment of bacterial infections,
 PT comprises expression vector encoding bacterial toxin.

XX Example 6; Col 69-71; 83pp; English.

XX The invention relates to antitoxin therapy for humans and other animals.

CC Antitoxins which neutralize the pathologic effects of *Escherichia coli*

CC toxins are generated by immunization of avian hosts with recombinant

CC toxin fragments. The recombinant *E. coli* verotoxin (VT) is a fusion

CC protein comprising a non-verotoxin protein (especially an affinity tag)

CC fused to a portion of the VT-1 or VT-2 sequence. The VT B chains are

CC small proteins (approximately 8 kDa), so use of a small affinity tag was

CC preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates

CC single step affinity purification of subunits from periplasmic extracts.

CC However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,

CC expression of maltose binding protein (MBP) fused subunits was

CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced

CC promoter control is necessary to permit cell viability. Bacterial host

CC cells expressing a recombinant expression vector encoding a polyhistidine

CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is

CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"

CC indicates that the vector encodes the preprotein form of the protein and

CC "L-" indicates that the vector encodes the mature form of the protein.

CC The bacterial cell is capable of expressing large quantities (40 mg/l) of

CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting

CC bacterial toxins in environmental samples including soil, water,

CC industrial samples, biological samples and samples obtained from food and

CC dairy processing instruments

XX Sequence 315 AA;

Query Match 100.0%; Score 114; DB 3; Length 315;

Best Local Similarity 100.0%; Pred. No. 9.8e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFFPSMC 20

DB 264 CHHHASRVARMASDEFFPSMC 283

RESULT 9

ID AAU77817

XX AAU77817 standard; protein; 315 AA.

AC AAU77817;

DT 05-JUN-2002 (first entry)

DE *E. coli* verotoxin VT1-A chain protein.

XX Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic;

KW vaccine; haemorrhagic cystitis; balanitis; haemolytic uremic syndrome;

KW thrombotic thrombocytopenic purpura.

XX *Escherichia coli*.

OS US2002012658-A1.

XX 31-JAN-2002.

XX 16-JUN-1999; 99US-00334477.

XX 13-MAR-1997; 97US-00816977.

XX (WILL/) WILLIAMS J A.

PA (BYRN/) BYRNE L M.

PA (PUGH/) PUGH C S G.

XX Williams JA, Byrne LM, Pugh CSG;

PI WPI; 2002-205094/26.

DR N-PSDB; ABK11775.

XX New recombinant expression vector encoding affinity tag and *Escherichia*

PT *coli* type 1 or type 2 verotoxin, useful for treating or preventing

PT diseases due to *E. coli* verotoxins and in producing vaccines.

PS Example 6; Page 38-39; 98pp; English.

XX This invention relates to a recombinant expression vector encoding an

CC affinity tag and protein comprising at least a portion of a bacterial

CC toxin consisting of *Escherichia coli* type 1 or type 2 verotoxin. The

CC expression vector can be used to produce recombinant verotoxin protein

CC which can be used to create a vaccine against diseases caused by *E. coli*

CC such as verotoxin haemorrhagic cystitis and balanitis. The antitoxins

CC are useful for treating humans and animals intoxicated with a bacterial

CC toxin, particularly *E. coli* verotoxin. The antitoxins may also be used in

CC the preventative treatment and in diagnostic assays to detect the

CC presence of a toxin in a sample. The polypeptides derived from *E. coli*

CC verotoxins are useful as immunogens for the production of vaccines,

CC including multivalent vaccines and antitoxins, which can be administered

CC to a subject at risk of diarrhoeal disease or at risk of developing extra

CC intestinal complications of *E. coli* infections, e.g. haemolytic uremic

CC syndrome, thrombotic thrombocytopenic purpura. The present sequence

CC represents the *E. coli* verotoxin protein VT1-A used to create the

CC expression vectors of the invention

XX Sequence 315 AA;

Query Match 100.0%; Score 114; DB 5; Length 315;

Best Local Similarity 100.0%; Pred. No. 9.8e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFFPSMC 20

DB 264 CHHHASRVARMASDEFFPSMC 283

RESULT 10

ID ADC00545

XX ADC00545 standard; protein; 315 AA.

AC ADC00545;

DT 04-DEC-2003 (first entry)

DE Enterohaemorrhagic *E. coli* O157:H7-specific protein SEQ ID NO: 590.

XX enterohaemorrhagic; anti-bacterial.

OS *Escherichia coli*; O157:H7.

PN JP2002355074-A.

XX 10-DEC-2002.

XX 24-JAN-2002; 2002JP-00015959.

XX 24-JAN-2001; 2001JP-00112010.

PA (UYTS-) UNIV TSUKUBA.

XX WPI; 2003-451640/43.

XX Enterohaemorrhagic *Escherichia coli* O157:H7-specific nucleic acid molecule

PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

PS Claim 3; SEQ ID NO 590; 2067pp; Japanese.

CC The invention relates to a novel enterohaemorrhagic *Escherichia coli*

CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention

CC has anti-bacterial activity. The polypeptide can be used in detection

CC and/or treatment of O157:H7 infection. The nucleotide sequence of the

CC genome of Enterohaemorrhagic *E. coli* O157:H7 was determined. The present

CC sequence represents an *E. coli* O157:H7-specific polypeptide of the

CC invention.

XX Sequence 315 AA;

Query Match 100.0%; Score 114; DB 7; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
 |||||
 DB 264 CHHHASRVARMASDEFPSSMC 283

RESULT 11
 ADH34319
 ID ADH34319 standard; protein; 315 AA.
 XX
 AC ADH34319;
 XX
 DT 11-MAR-2004 (first entry)
 DE Verotoxin 1 (VT1) A subunit.
 XX
 XX Attenuated verotoxin; attenuated VT; mutant A subunit; troponin I;
 KW fusion protein; cancer; cytostatic; verotoxin 1; VT1; A subunit.
 XX
 XX Escherichia coli; O157:H7.
 OS
 XX WO2003066854-A1.
 PN
 PD 14-AUG-2003.
 XX
 XX 03-FEB-2003; 2003WO-JP001043.
 PR
 XX 04-FEB-2002; 2002JP-00026577.
 XX
 PA (YOSH/) YOSHIDA H.
 XX
 PI Yoshida H, Liu X;
 XX
 XX WPI; 2003-646309/61.
 DR
 XX
 XX Attenuated verotoxin controls tumor growth for treatment of cancer.
 PT
 XX
 PS Disclosure; Fig 3; 56pp; Japanese.
 CC
 CC The invention relates to attenuated verotoxins (VTs) comprising mutations
 CC in one or more of the regions spanning residues 167-172 or 202-207 of the
 CC mature verotoxin A subunit. The invention also relates to the mutant
 CC verotoxin A subunit and the DNA encoding it; anticancer agents containing
 CC the novel mutant A subunit; a fusion protein comprising the mutant
 CC verotoxin A subunit and a ligand, especially troponin I, which binds to a
 CC cancer cell; a fusion gene encoding the mutant A subunit/troponin I
 CC fusion protein; and vectors encoding either the mutant verotoxin A
 CC subunit, or the fusion gene of the invention. The attenuated verotoxins,
 CC A subunits, fusion proteins, and polynucleotides encoding them are useful
 CC in the treatment of cancer. The present sequence represents the A subunit
 CC of verotoxin 1 (VT1).
 XX
 XX Sequence 315 AA;
 SQ

Query Match 100.0%; Score 114; DB 7; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
 |||||
 DB 264 CHHHASRVARMASDEFPSSMC 283

RESULT 12
 AAW25786
 ID AAW25786 standard; protein; 316 AA.
 XX
 AC AAW25786;
 XX

DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 27-MAR-1998 (first entry)
 XX
 DE Phage H19B shiga-like toxin.
 XX
 XX Shiga-like toxin; sIt-A gene; hybrid protein; cell delivery;
 KW cell binding ligand; translocation domain; diphtheria toxin B';
 KW interleukin-2; T-cell lymphoma; organ rejection; therapy; ss.
 XX
 OS Bacteriophage H-19B.
 XX
 PN US5668255-A.
 XX
 PD 16-SEP-1997.
 XX
 PF 04-AUG-1993; 93US-00102387.
 XX
 PR 07-JUN-1984; 84US-00618199.
 PR 25-APR-1985; 85US-00726808.
 PR 07-JUN-1985; 85US-00742554.
 PR 22-DEC-1989; 89US-00456095.
 PR 14-JUN-1990; 90US-00538276.
 PR 27-JUN-1991; 91US-00722484.
 XX
 PA (SERA-) SERAGEN INC.
 XX
 PI Murphy JR;
 XX
 DR WPI; 1997-470103/43.
 DR N-PSDB; AAT91637.
 XX
 PT New hybrid molecules for delivery of agents to cells - comprise a binding
 PT domain of a cell binding ligand and a portion of a trans-location domain
 PT of a protein.
 XX
 PS Example 3; Fig 8A-C; 30pp; English.
 CC
 CC This protein comprises the Escherichia coli phage H19B Shiga-like toxin.
 CC DNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was
 CC used to construct a Shiga-like toxin A-diphtheria toxin B'-interleukin-2
 CC (SLTA-PTB'-IL2) gene that was expressed in E. coli. The hybrid protein
 CC can be isolated and used to treat conditions involving over-production of
 CC cells bearing IL2 receptors, such as certain T-cell lymphomas and organ
 CC transplant rejection crises. The hybrid inactivates ribosomes in cells
 CC bearing IL2 receptors, resulting in cessation of protein synthesis and
 CC death of target cells. Claimed hybrid proteins comprise a translocation
 CC domain and a cell binding domain from e.g. a hormone, growth factor or
 CC protein toxin. The hybrid molecules can be used for the delivery of
 CC agents (e.g. therapeutic genes, toxins, detectable labels) into cells.
 CC The use of a translocation mechanism ensures that the hybrid will be
 CC effective in relatively low doses, since a high proportion of the
 CC substance of interest will be taken into the targeted cells. The hybrid
 CC molecules can be manufactured as a single hybrid recombinant protein,
 CC permitting reproducibility, consistency, and the precise control of
 CC composition. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17
 CC -OCT-2003 to standardise OS field)
 XX
 SQ Sequence 316 AA;

Query Match 100.0%; Score 114; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHASRVARMASDEFPSSMC 20
 |||||
 DB 264 CHHHASRVARMASDEFPSSMC 283

RESULT 13
 AAW06407
 ID AAW06407 standard; protein; 323 AA.
 XX


```

KW thrombotic thrombocytopenic purpura.
OS Escherichia coli.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 316..323
FT /note= "C terminal peptide with HIS tag"
XX
XX US2002012658-A1.
XX
XX 31-JAN-2002.
XX
XX 16-JUN-1999; 99US-00334477.
XX
XX 13-MAR-1997; 97US-00816977.
XX
XX (WILL/) WILLIAMS J A.
XX (BYRN/) BYRNE L M.
XX (PUGH/) PUGH C S G.
XX
XX Williams JA, Byrne LM, Pugh CSG;
XX
XX WPI; 2002-205094/26.
XX N-PSDB; ABK11789.
XX
XX New recombinant expression vector encoding affinity tag and Escherichia
XX coli type 1 or type 2 verotoxin, useful for treating or preventing
XX diseases due to E. coli verotoxins and in producing vaccines.
XX
XX Claim 1; Page 48-49; 98pp; English.
XX
XX This invention relates to a recombinant expression vector encoding an
XX affinity tag and protein comprising at least a portion of a bacterial
XX toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The
XX expression vector can be used to produce recombinant verotoxin protein
XX which can be used to create a vaccine against diseases caused by E. coli
XX such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
XX are useful for treating humans and animals intoxicated with a bacterial
XX toxin, particularly E. coli verotoxin. The antitoxins may also be used in
XX the preventative treatment and in diagnostic assays to detect the
XX presence of a toxin in a sample. The polypeptides derived from E. coli
XX verotoxins are useful as immunogens for the production of vaccines,
XX including multivalent vaccines and antitoxins, which can be administered
XX to a subject at risk of diarrhoeal disease or at risk of developing extra
XX -intestinal complications of E. coli infections, e.g. haemolytic uraemic
XX syndrome, thrombotic thrombocytopenic purpura. The present sequence
XX represents the HIS tagged E.coli VTI-A verotoxin protein of the invention
XX
XX Sequence 323 AA;
XX
XX Query Match 100.0%; Score 114; DB 5; Length 323;
XX Best Local Similarity 100.0%; Pred. No. 1e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CHHHASRVARMASDEFPSSMC 20
XX |||||
XX Db 264 CHHHASRVARMASDEFPSSMC 263
XX
XX RESULT 16
XX AAW06413
XX ID AAW06413 standard; protein; 326 AA.
XX
XX AC AAW06413;
XX
XX 26-FEB-1997 (first entry)
XX
XX Flag tag/VT1 A subunit fusion protein.
XX
XX Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
XX haemolytic uraemic syndrome; detection.
XX

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OS Escherichia coli.
XX
XX WO9630043-A1.
XX
XX 03-OCT-1996.
XX
XX 25-MAR-1996; 96WO-US004093.
XX
XX 24-MAR-1995; 95US-00410058.
XX
XX (OPHI-) OPHIDIAN PHARM INC.
XX
XX Carroll SB, Stafford DC, Padhye NV;
XX
XX WPI; 1996-505779/50.
XX N-PSDB; AAT42673.
XX
XX Compan. contg. neutralising antitoxin against E.coli vero-toxin - used to
XX treat intoxicated individuals, and as a prophylactic against diarrhoeal
XX disease or extra-intestinal complications of E.coli infection.
XX
XX Example 6; Page 79; 101pp; English.
XX
XX Compositions containing neutralising antitoxin against one or more E.
XX coli verotoxin (VT) can be used to treat intoxicated adults and children
XX with enteric bacterial infections. They may also be used as prophylactics
XX e.g. as a vaccine, against diarrhoeal disease or the development of extra
XX -intestinal complications of E.coli infection, especially haemolytic
XX uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
XX a sample. The VT is recombinant, preferably a fusion protein containing a
XX non-VT protein sequence and part of the E.coli VTI or VT2 sequence. This
XX is a flag tag/VT1 A subunit fusion protein
XX
XX Sequence 326 AA;
XX
XX Query Match 100.0%; Score 114; DB 2; Length 326;
XX Best Local Similarity 100.0%; Pred. No. 1e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CHHHASRVARMASDEFPSSMC 20
XX |||||
XX Db 275 CHHHASRVARMASDEFPSSMC 294
XX
XX RESULT 17
XX AAY96692
XX ID AAY96692 standard; protein; 326 AA.
XX
XX AC AAY96692;
XX
XX 26-SEP-2000 (first entry)
XX
XX FLAG tag-VT-1 subunit A fusion protein.
XX
XX VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
XX recombinant production; screening; dairy; anti-bacterial; vaccine;
XX primer; FLAG tag.
XX
XX Escherichia coli.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Protein 34..326
XX /label= Mature_verotoxin-1_subunit_A
XX
XX US6080400-A.
XX
XX 27-JUN-2000.
XX
XX 13-MAR-1997; 97US-00816977.
XX
XX 24-MAR-1995; 95US-00410058.
XX

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XX PA (OPHI-) OPHIDIAN PHARM INC.

XX PI Williams JA, Byrne LM;

XX PA WPI; 2000-451195/39.

XX DR N-PSDB; AAA51218.

XX PT Bacterial cell for recombinantly expressing bacterial toxins in large

XX PT quantities useful for immunization and treatment of bacterial infections,

XX PT comprises expression vector encoding bacterial toxin.

XX PS Example 6; Col 119-122; 83pp; English.

XX CC E. coli verotoxin (VT) types 1 and 2 subunit A were cloned into pFLAG-1.

XX CC The flag tag is located between the OmpA secretion signal sequence and

XX CC the authentic N-terminal of the target protein in the pFlag-1 vector.

XX CC EcoRI/XhoI A subunit PCR fragments were cloned into identically cleaved

XX CC pFlag-1, to produce an expression construct using the OmpA signal peptide

XX CC for secretion of A subunit fusion proteins. After secretion the

XX CC periplasmic protein contains the N-terminal 8 amino acid flag tag,

XX CC followed by 4 vector-encoded amino acids fused to the recombinant A

XX CC subunit. VT B chains are small proteins (approximately 8 kDa), so use of

XX CC a small affinity tag was preferred (i.e. polyhistidine). A polyhistidine

XX CC affinity tag facilitates single step affinity purification of subunits

XX CC from periplasmic extracts. However, due to poor recovery of his-tagged VT

XX CC -1 A and VT-2 A chains, expression of MBP fused subunits was undertaken.

XX CC Due to the toxicity of the VT-2 B subunit, strict uninduced promoter

XX CC control is necessary to permit cell viability. Bacterial host cells

XX CC expressing a recombinant expression vector encoding a polyhistidine

XX CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is

XX CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"

XX CC indicates that the vector encodes the preprotein form of the protein and

XX CC "L-" indicates that the vector encodes the mature form of the protein.

XX CC The bacterial cell is capable of expressing large quantities (40 mg/l) of

XX CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting

XX CC bacterial toxins in environmental samples including soil, water,

XX CC industrial samples, biological samples and samples obtained from food and

XX CC dairy processing instruments

XX SQ Sequence 326 AA;

Query Match 100.0%; Score 114; DB 3; Length 326;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARVASDEFPSSMC 20

DB 275 CHHHSRVARVASDEFPSSMC 294

RESULT 18

AAU77828

ID AAU77828 standard; protein; 326 AA.

XX AC AAU77828;

XX DT 05-JUN-2002 (first entry)

XX DE Flag tag/VT1 fusion protein.

XX KW Verotoxin; antitoxin; antiarrheal; antibacterial; Flag tag/VT1;

XX KW haemostatic; vaccine; haemorrhagic cystitis; balantitis;

XX KW haemolytic uremic syndrome; thrombotic thrombocytopenic purpura.

XX OS Escherichia coli.

XX OS Synthetic.

XX PN US2002012658-A1.

XX PD 31-JAN-2002.

XX PF 16-JUN-1999; 99US-00334477.

XX PR 13-MAR-1997; 97US-00816977.

XX PA (WILL/) WILLIAMS J A.

XX PA (BYRN/) BYRNE L M.

XX PA (PUGH/) PUGH C S G.

XX PI Williams JA, Byrne LM, Pugh CSG;

XX DR WPI; 2002-205094/26.

XX DR N-PSDB; ABK11799.

XX PT New recombinant expression vector encoding affinity tag and Escherichia

XX PT coli type 1 or type 2 verotoxin, useful for treating or preventing

XX PT diseases due to E. coli verotoxins and in producing vaccines.

XX PS Example 6; Page 64-65; 98pp; English.

XX CC This invention relates to a recombinant expression vector encoding an

XX CC affinity tag and protein comprising at least a portion of a bacterial

XX CC toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The

XX CC expression vector can be used to produce recombinant verotoxin protein

XX CC which can be used to create a vaccine against diseases caused by E. coli

XX CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins

XX CC are useful for treating humans and animals intoxicated with a bacterial

XX CC toxin, particularly E. coli verotoxin. The antitoxins may also be used in

XX CC the preventative treatment and in diagnostic assays to detect the

XX CC presence of a toxin in a sample. The polypeptides derived from E. coli

XX CC verotoxins are useful as immunogens for the production of vaccines,

XX CC including multivalent vaccines and antitoxins, which can be administered

XX CC to a subject at risk of diarrhoeal disease or at risk of developing extra

XX CC -intestinal complications of E. coli infections, e.g. haemolytic uremic

XX CC syndrome, thrombotic thrombocytopenic purpura. The present sequence

XX CC represents the Flag-tag/VT1 fusion protein of the invention. This fusion

XX CC protein was created to facilitate purification of the recombinant

XX CC proteins of the invention

XX SQ Sequence 326 AA;

Query Match 100.0%; Score 114; DB 5; Length 326;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARVASDEFPSSMC 20

DB 275 CHHHSRVARVASDEFPSSMC 294

RESULT 19

AAW29294

ID AAW29294 standard; protein; 332 AA.

XX AC AAW29294;

XX DT 20-APR-1998 (first entry)

XX DE BPI peptide fusion protein pING3793 vector construct protein.

XX KW Bactericidal/permeability increasing peptide; BPI; fusion protein;

XX KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;

XX KW fungicidal; recombinant DNA; vector.

XX OS Synthetic.

XX OS Pectobacterium carotovorum.

XX OS Homo sapiens.

XX OS Chimeric.

XX PN WO9735009-A1.

XX PD 25-SEP-1997.

XX PF 18-MAR-1997; 97WO-US005287.

PR 22-MAR-1996; 96US-00621803.
 XX (XOMA) XOMA CORP.
 XX Better MD;
 XX WPI; 1997-480215/44.
 DR N-PSDB; AAT86332.
 XX Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX
 XX Example 1; Page 148-150; 186pp; English.
 XX
 CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI); (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the pING3793 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts
 XX
 SQ Sequence 332 AA;
 Query Match 100.0%; Score 114; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHHHSRVARVASDEFFPSMC 20
 |||||
 Db 277 CHHHSRVARVASDEFFPSMC 296
 |||||
 RESULT 20
 AAR13118
 ID AAR13118 standard; protein; 409 AA.
 XX
 AC AAR13118;
 XX
 DT 24-OCT-2003 (revised)
 DT 08-OCT-1991 (first entry)
 XX
 DE Shiga-like toxin subunit A.
 XX
 KW Hybrid; fusion; membrane translocation; binding region; HIV; infection;
 KW toxin; steroid; hormone; monoclonal antibody; antigen; diphtheria;
 KW exotoxin; phenylketonuria; cholera; interleukin; IL-2; protease;
 KW epidermal growth factor; ricin; tetanus; hexosaminidase;
 KW Shiga-like toxin A; SLT-A; ligand; insulin; nuclease.
 XX
 OS Vibrio cholerae.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 317
 FT /note= "encoded by stop codon"
 XX
 FN W09109971-A.
 XX
 PD 11-JUL-1991.
 XX
 XX 22-DEC-1989; 89US-00456095.
 PF
 XX 22-DEC-1989; 89US-00456095.
 PR
 PR 14-JUN-1990; 90US-00538276.

XX (SERA-) SERAGEN INC.
 XX Murphy JR;
 XX WPI; 1991-222845/30.
 DR N-PSDB; AAO12711.
 XX Hybrid molecules for targetting chemical entity to cell - have membrane
 PT trans-locating and cell binding-regions and used to treat HIV infection,
 PT genetic enzyme-deficiency disorders etc.
 XX
 PS Disclosure; Fig 8(1-3); 59pp; English.
 XX
 CC Hybrid molecules are produced by covalently linking (1) a portion (A) of
 CC the binding domain of a cell-binding ligand, allowing binding of the mol.
 CC to an animal cell; (2) a portion (B) of a translocation domain of a
 CC protein able to translocate (C) across the cell cytoplasmic membrane, and
 CC and (3) a portion (C) which is to be introduced into the cell. (A) is
 CC derived from a steroid or polypeptide hormone, a single-chain analogue of
 CC a monoclonal antibody able to bind an antigen expressed on the cell
 CC surface, or a polypeptide toxin. (B) is derived from a toxin (e.g.
 CC diphtheria toxin or Pseudomonas exotoxin A). (A) may be derived from
 CC insulin, interleukins 2, 3 or 6 or epidermal growth factor. Suitable
 CC enzymes in (C) include cholera toxin, ricin, tetanus toxin,
 CC hexosaminidase A, protease, nuclease, SLT-A, etc. Specified examples
 CC are CT-A/DT-B'/IL-2, SLTA/DT-B'/IL-2, ricin A/DT-B'/IL-2, HIVP-BP/DT-
 CC B'/IL-2 and the phenylalanine hydroxylase-DT-B' or their biologically
 CC active mutants. (CT-A= cholera toxin, DT-B'= truncated diphtheria toxin,
 CC SLTA= Shiga-like toxin A; HIVP-BP= HIV protease binding protein. See also
 CC AAO12710-12. (Updated on 24-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 409 AA;
 Query Match 100.0%; Score 114; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHHHSRVARVASDEFFPSMC 20
 |||||
 Db 264 CHHHSRVARVASDEFFPSMC 283
 |||||
 RESULT 21
 AAY55891
 ID AAY55891 standard; protein; 409 AA.
 XX
 AC AAY55891;
 XX
 DT 17-OCT-2003 (revised)
 DT 15-FEB-2000 (first entry)
 XX
 DE E.coli bacteriophage H19B Shiga-like toxin A subunit.
 XX
 KW Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria;
 KW translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus;
 KW shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV;
 KW cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison;
 KW adipocyte; cancer; virus; infection; antibody.
 XX
 OS Bacteriophage H-19B.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 317
 FT /note= "encoded by TGA"
 XX
 FN US5965406-A.
 XX
 PD 12-OCT-1999.
 XX
 XX 07-JUN-1995; 95US-00488246.
 PF
 XX 07-JUN-1984; 84US-00618199.
 PR

PR 25-APR-1985; 85US-00726808.
 PR 07-JUN-1985; 85US-00742554.
 PR 22-DEC-1983; 89US-00456095.
 PR 14-JUN-1990; 90US-00538276.
 PR 27-JUN-1991; 91US-00722484.
 PR 04-AUG-1993; 93US-00102387.
 XX
 PA (SERA-) SERAGEN INC.
 XX
 PI Murphy JR;
 XX
 XX WPI; 1999-632431/54.
 DR N-PSDB; AA230662.
 DR
 XX Recombinant DNA molecule encoding a three part hybrid protein used in the
 PT treatment of Aids and genetic deficiency diseases.
 XX
 XX Example 3; Fig 8; 3lpp; English.
 PS
 CC The invention relates to a recombinant DNA molecule encoding a hybrid
 CC protein comprising three parts: (a) the first part comprises a portion of
 CC the binding domain of a cell-binding polypeptide ligand allowing the
 CC hybrid protein to bind to an animal cell; (b) the second part comprises a
 CC portion of a translocation domain of a naturally occurring protein
 CC selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera
 CC toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus
 CC toxin, which translocate the third part of the across the cytoplasmic
 CC membrane into the cytosol of the cell; and (c) the third part comprises a
 CC polypeptide entity to be introduced into the cell, which is non-native to
 CC the naturally occurring protein of (b). This sequence represents the
 CC E.coli bacteriophage H19B Shiga-like toxin A subunit sequence for use in
 CC generating the hybrid of the invention. The hybrid molecule enables the
 CC direction of appropriate therapy to affected cells, allowing them to
 CC function properly and alleviate or cure the disease. The hybrid is
 CC especially used in treating genetic deficiency diseases, by delivering to
 CC affected cells an enzyme supplying the missing function, to supplementing
 CC cellular levels of a particular enzyme or a scarce precursor or cofactor,
 CC to directing toxins or other poisons to destroy particular cells (such as
 CC adipocytes, cancer cell, or virus infected-cells), to counteracting viral
 CC infections such as HIV, by introducing appropriate antibodies to viral
 CC proteins. It is also involved in the process of getting non-therapeutic
 CC substances such as detectable labels into cells. (Updated on 17-OCT-2003
 CC to standardise OS field)
 XX
 XX Sequence 409 AA;
 SQ
 Query Match 100.0%; Score 114; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFFPSMC 20
 DB 264 CHHHASRVARMASDEFFPSMC 283
 RESULT 22
 AAY78591
 ID AAY78591 standard; protein; 409 AA.
 XX
 AC AAY78591;
 XX
 XX 06-AUG-2003 (revised)
 DT 05-MAY-2000 (first entry)
 XX
 DE E. coli bacteriophage H19B shiga-like toxin amino acid sequence.
 XX
 KW Shiga-like toxin; hybrid protein; translocation domain; cell destruction;
 KW cell binding domain; genetic deficiency disease; cell targeting; cancer;
 KW adipocyte; enzyme delivery; anti-viral; HIV.
 XX
 OS Bacteriophage H-19B.
 XX
 XX Location/Qualifiers
 FH Key

FT Misc-difference 317
 FT /label= Unknown
 FT /note= "Encoded by TGA"
 XX
 PN US6022950-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 07-JUN-1995; 95US-00479510.
 XX
 PR 07-JUN-1984; 84US-00618199.
 PR 25-APR-1985; 85US-00726808.
 PR 07-JUN-1985; 85US-00742554.
 PR 22-DEC-1983; 89US-00456095.
 PR 14-JUN-1990; 90US-00538276.
 PR 27-JUN-1991; 91US-00722484.
 PR 04-AUG-1993; 93US-00102387.
 XX
 PA (SERA-) SERAGEN INC.
 XX
 PI Murphy JR;
 XX
 XX WPI; 2000-160390/14.
 DR N-PSDB; AA290018.
 XX
 PT New two-part hybrid protein comprising a translocation domain and a cell-
 PT binding domain, for treating genetic deficiency diseases, cancer and HIV
 PT infections.
 XX
 XX Example 3; Fig 8; 32pp; English.
 CC This sequence represents the bacteriophage H19B shiga-like toxin protein
 CC sequence. The toxin can be included in the hybrid protein of the
 CC invention and used to destroy or modify the cell that the hybrid protein
 CC is targeted to. The hybrid protein comprises a first part which is a
 CC portion of the binding domain of a cell-binding ligand, effective to
 CC cause the hybrid molecule to bind to a cell of an animal. The second part
 CC comprises a portion of a translocation domain of a naturally occurring
 CC protein (e.g. the translocation domain of diphtheria toxin), the second
 CC part translocates the third part across the cytoplasmic membrane and into
 CC the cytosol of the cell. The third part comprises a chemical entity to be
 CC introduced into the cell, where each of the first and third part is non-
 CC native with respect to naturally occurring protein, and the covalent bond
 CC attaching the second and third part is cleavable. The toxin represented
 CC by the present sequence can form part of the third portion of the hybrid
 CC protein. The cell binding domain binds to a specific cell and the
 CC translocation domain transfers the hybrid molecule across the cell
 CC membrane into the cytosol. The third part of the protein, linked to the
 CC translocation domain through a cleavable bond, can then carry out its
 CC function. The hybrid molecules are useful for treating genetic deficiency
 CC diseases by delivering to affected cells an enzyme supplying the missing
 CC function, to supplement cellular levels of a particular enzyme or a
 CC scarce precursor or cofactor, to direct toxins or other poisons to
 CC destroy particular cells (such as adipocytes, cancer cells, or virus-
 CC infected cells), and to counteract viral infections such as HIV by
 CC introducing into appropriate cells antibodies to viral proteins. (Updated
 CC on 06-AUG-2003 to correct OS field.)
 XX
 XX Sequence 409 AA;
 SQ
 Query Match 100.0%; Score 114; DB 3; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFFPSMC 20
 DB 264 CHHHASRVARMASDEFFPSMC 283
 RESULT 23
 AAY96694
 ID AAY96694 standard; protein; 690 AA.
 XX

AC AAY96694;
 DT 26-SEP-2000 (first entry)
 DE MBP-VT-1 subunit A fusion protein.
 KW VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
 KW recombinant production; screening; dairy; anti-bacterial; vaccine;
 KW primer; maltose binding protein; MBP.
 XX
 OS Escherichia coli.
 OS Synthetic.
 OS Chimeric.
 FN US6080400-A.
 XX 27-JUN-2000.
 PD 13-MAR-1997; 97US-00816977.
 XX 24-MAR-1995; 95US-00410058.
 PR (OPHI-) OPHIDIAN PHARM INC.
 XX Williams JA, Byrne LM;
 PI WPI; 2000-451195/39.
 DR N-PSDB; AAA51226.
 DR Bacterial cell for recombinantly expressing bacterial toxins in large
 PT quantities useful for immunization and treatment of bacterial infections,
 PT comprises expression vector encoding bacterial toxin.
 XX
 PS Example 7; Col 133-138; 83pp; English.
 XX
 CC E. coli verotoxin (VT) types 1 and 2 subunit A were cloned into pMal-p2,
 CC designed to allow expression of the native proteins as C-terminal fusions
 CC to a periplasmically-secreted version of maltose binding protein (MBP).
 CC VT B chains are small proteins (approximately 8 kDa), so use of a small
 CC affinity tag was preferred (i.e. polyhistidine). A polyhistidine affinity
 CC tag facilitates single step affinity purification of subunits from
 CC periplasmic extracts. However, due to poor recovery of his-tagged VT-1 A
 CC and VT-2 A chains, expression of MBP fused subunits was undertaken. Due
 CC to the toxicity of the VT-2 B subunit, strict uninduced promoter control
 CC is necessary to permit cell viability. Bacterial host cells expressing a
 CC recombinant expression vector encoding a polyhistidine affinity tag and a
 CC portion of the VT-2 B chain are claimed. The vector is chosen from
 CC pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+" indicates that
 CC the vector encodes the preprotein form of the protein and "L-" indicates
 CC that the vector encodes the mature form of the protein. The bacterial
 CC cell is capable of expressing large quantities (40 mg/l) of VT-2B. The
 CC toxins are useful for immunizing non-mammals and for detecting bacterial
 CC toxins in environmental samples including soil, water, industrial
 CC samples, biological samples and samples obtained from food and dairy
 CC processing instruments
 XX
 SQ Sequence 690 AA;
 Query Match 100.0%; Score 114; DB 3; Length 690;
 Best Local Similarity 100.0%; Pred. No. 2.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFPSC 20
 DB 639 CHHHASRVARMASDEFPSC 658
 RESULT 24
 ID AAU77830
 XX AAU77830 standard; protein; 690 AA.
 AC AAU77830;
 XX

DT 05-JUN-2002 (first entry)
 XX MBPNVT1-A fusion protein #2.
 KW Verotoxin; VT2-A; antitoxin; antidiarrheal; antibacterial; haemostatic;
 KW vaccine; haemorrhagic cystitis; balantitis; MBPNVT1-A;
 KW haemolytic uremic syndrome; thrombotic thrombocytopenic purpura.
 XX
 OS Escherichia coli.
 OS Synthetic.
 FN US2002012658-A1.
 XX 31-JAN-2002.
 XX 16-JUN-1999; 99US-00334477.
 PF 13-MAR-1997; 97US-00816977.
 XX (WILL/) WILLIAMS J A.
 PA (BYRN/) BYRNE L M.
 PA (PUGH/) PUGH C S G.
 XX Williams JA, Byrne LM, Pugh CSG;
 PI WPI; 2002-205094/26.
 DR N-PSDB; ABK11957.
 DR New recombinant expression vector encoding affinity tag and Escherichia
 PT coli type 1 or type 2 verotoxin, useful for treating or preventing
 PT diseases due to E. coli verotoxins and in producing vaccines.
 XX
 PS Claim 1; Page 72-73; 98pp; English.
 XX
 CC This invention relates to a recombinant expression vector encoding an
 CC affinity tag and protein comprising at least a portion of a bacterial
 CC toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The
 CC expression vector can be used to produce recombinant verotoxin protein
 CC which can be used to create a vaccine against diseases caused by E. coli
 CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
 CC are useful for treating humans and animals intoxicated with a bacterial
 CC toxin, particularly E. coli verotoxin. The antitoxins may also be used in
 CC the preventative treatment and in diagnostic assays to detect the
 CC presence of a toxin in a sample. The polypeptides derived from E. coli
 CC verotoxins are useful as immunogens for the production of vaccines,
 CC including multivalent vaccines and antitoxins, which can be administered
 CC to a subject at risk of diarrhoeal disease or at risk of developing extra
 CC -intestinal complications of E. coli infections, e.g. haemolytic uremic
 CC syndrome, thrombotic thrombocytopenic purpura. The present sequence
 CC represents the MBPNVT1-A protein #2 of the invention. This fusion protein
 CC was created to facilitate purification of the recombinant proteins of the
 CC invention
 XX
 SQ Sequence 690 AA;
 Query Match 100.0%; Score 114; DB 5; Length 690;
 Best Local Similarity 100.0%; Pred. No. 2.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHASRVARMASDEFPSC 20
 DB 639 CHHHASRVARMASDEFPSC 658
 RESULT 25
 ID AAW06411 standard; protein; 708 AA.
 XX AAW06411;
 AC AAW06411;
 XX 26-FEB-1997 (first entry)
 DT Maltose binding protein/VT1 A subunit fusion protein.
 DE

XX Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
 KW haemolytic uraemic syndrome; detection.
 XX
 OS Escherichia coli.
 PN WO9630043-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 25-MAR-1996; 96WO-US004093.
 XX
 PR 24-MAR-1995; 95US-00410058.
 XX
 PA (OPHI-) OPHIDIAN PHARM INC.
 XX
 PI Carroll SB, Stafford DC, Padhye NV;
 DR WPI; 1996-505779/50.
 XX
 DR N-PSDB; AAT42671.
 XX
 PS Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used to
 PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
 PT disease or extra-intestinal complications of E.coli infection.
 XX
 PS Example 6; Page 70-72; 101pp; English.
 XX
 CC Compositions containing neutralising antitoxin against one or more E.
 CC coli verotoxin (VT) can be used to treat intoxicated adults and children
 CC with enteric bacterial infections. They may also be used as prophylactics
 CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
 CC -intestinal complications of E.coli infection, especially haemolytic
 CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
 CC a sample. The VT is recombinant, preferably a fusion protein containing a
 CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence. This
 CC is a maltose binding protein/VT1 A subunit fusion protein
 XX
 SQ Sequence 708 AA;
 Query Match 100.0%; Score 114; DB 2; Length 708;
 Best Local Similarity 100.0%; Pred. No. 2.4e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHSRVARMASDEFPSC 20
 DB 657 CHHHSRVARMASDEFPSC 676
 RESULT 26
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 ID AAY96690 standard; protein; 708 AA.
 XX
 AC AAY96690;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE MBP-VT-1 subunit A fusion protein.
 XX
 KW VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
 KW recombinant production; screening; dairy; anti-bacterial; vaccine;
 KW primer; maltose binding protein; MBP.
 XX
 OS Escherichia coli.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Protein 1. .415
 FT /label= Maltose binding protein
 FT /note= "Acts as an affinity tag"
 FT 416. .708
 FT /label= Mature_verotoxin-1_subunit_A
 XX

PN US6080400-A.
 XX
 PD 27-JUN-2000.
 XX
 PF 13-MAR-1997; 97US-00816977.
 XX
 PR 24-MAR-1995; 95US-00410058.
 XX
 PA (OPHI-) OPHIDIAN PHARM INC.
 XX
 PI Williams JA, Byrne LM;
 XX
 DR WPI; 2000-451195/39.
 XX
 DR N-PSDB; AAA51216.
 XX
 PT Bacterial cell for recombinantly expressing bacterial toxins in large
 PT quantities useful for immunization and treatment of bacterial infections,
 PT comprises expression vector encoding bacterial toxin.
 XX
 PS Example 6; Col 105-110; 83pp; English.
 XX
 CC E. coli verotoxin (VT) types 1 and 2 subunit A were cloned into pMal-p2,
 CC designed to allow expression of the native proteins as C-terminal fusions
 CC to a periplasmically-secreted version of maltose binding protein (MBP).
 CC The vector contains an engineered factor Xa cleavage site, which permits
 CC the removal of the affinity tag (i.e. MBP) from the fusion protein after
 CC purification. VT B chains are small proteins (approximately 8 kDa), so
 CC use of a small affinity tag was preferred (i.e. polyhistidine). A
 CC polyhistidine affinity tag facilitates single step affinity purification
 CC of subunits from periplasmic extracts. However, due to poor recovery of
 CC his-tagged VT-1 A and VT-2 A chains, expression of MBP fused subunits was
 CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced
 CC promoter control is necessary to permit cell viability. Bacterial host
 CC cells expressing a recombinant expression vector encoding a polyhistidine
 CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is
 CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"
 CC indicates that the vector encodes the preprotein form of the protein and
 CC "L-" indicates that the vector encodes the mature form of the protein.
 CC The bacterial cell is capable of expressing large quantities (40 mg/l) of
 CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting
 CC bacterial toxins in environmental samples including soil, water,
 CC industrial samples, biological samples and samples obtained from food and
 CC dairy processing instruments
 XX
 SQ Sequence 708 AA;
 Query Match 100.0%; Score 114; DB 3; Length 708;
 Best Local Similarity 100.0%; Pred. No. 2.4e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHSRVARMASDEFPSC 20
 DB 657 CHHHSRVARMASDEFPSC 676
 RESULT 27
 AAU77826
 ID AAU77826 standard; protein; 708 AA.
 XX
 AC AAU77826;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE MBPNVT1-A fusion protein.
 XX
 KW Verotoxin; VT2-A; antitoxin; antidiarrheal; antibacterial; haemostatic;
 KW vaccine; haemorrhagic cystitis; Balantitis; MBPNVT1-A;
 KW haemolytic uraemic syndrome; thrombotic thrombocytopenic purpura.
 XX
 OS Escherichia coli.
 OS Synthetic.
 XX
 PN US2002012658-A1.

```
XX 31-JAN-2002.
XX
XX
XX PF 16-JUN-1999; 99US-00334477.
XX
XX PR 13-MAR-1997; 97US-00816977.
XX
XX (WILL/) WILLIAMS J A.
XX PA (BYRN/) BYRNE L M.
XX PA (PUGH/) PUGH C S G.
XX
XX PI Williams JA, Byrne LM, Pugh CSG;
XX
XX WPI; 2002-205094/26.
XX DR N-PSDB; ABK11797.
XX
XX
XX PT New recombinant expression vector encoding affinity tag and Escherichia
XX coli type 1 or type 2 verotoxin, useful for treating or preventing
XX diseases due to E. coli verotoxins and in producing vaccines.
XX
XX Example 6; Page 57-58; 98pp; English.
XX
XX CC This invention relates to a recombinant expression vector encoding an
XX affinity tag and protein comprising at least a portion of a bacterial
XX toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The
XX expression vector can be used to produce recombinant verotoxin protein
XX which can be used to create a vaccine against diseases caused by E. coli
XX such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
XX are useful for treating humans and animals intoxicated with a bacterial
XX toxin, particularly E. coli verotoxin. The antitoxins may also be used in
XX the preventative treatment and in diagnostic assays to detect the
XX presence of a toxin in a sample. The polypeptides derived from E. coli
XX verotoxins are useful as immunogens for the production of vaccines,
XX including multivalent vaccines and antitoxins, which can be administered
XX to a subject at risk of diarrhoeal disease or at risk of developing extra
XX -intestinal complications of E. coli infections, e.g. haemolytic uremic
XX syndrome, thrombotic thrombocytopenic purpura. The present sequence
XX represents the MBPNT1-A protein of the invention. This fusion protein
XX was created to facilitate purification of the recombinant proteins of the
XX invention
XX
XX SQ Sequence 708 AA;
XX
XX Query Match 100.0%; Score 114; DB 5; Length 708;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-10; Mismatches 0; Gaps 0;
XX Matches 20; Conservative 0; Indels 0;
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XX Db 657 CHHHSRVARWASDEFFPSMC 676
XX
XX Search completed: June 22, 2005, 07:11:20
XX Job time : 166 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:35:58 ; Search time 30 Seconds
(without alignments)
624.564 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSGKATYTYVNF.....AVDQVKPITALKEVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 414038

Minimum DB seq length: 0
Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	251	1 US-08-425-336-2	Sequence 2, Appli
2	1287	100.0	251	1 US-08-488-113B-2	Sequence 2, Appli
3	1287	100.0	251	1 US-08-477-484B-2	Sequence 2, Appli
4	1287	100.0	251	2 US-08-646-360-2	Sequence 2, Appli
5	1287	100.0	251	3 US-08-621-803-247	Sequence 247, App
6	1287	100.0	251	3 US-08-839-765-2	Sequence 2, Appli
7	1287	100.0	251	3 US-09-136-389-2	Sequence 2, Appli
8	1287	100.0	251	3 US-09-217-352-247	Sequence 247, App
9	1287	100.0	251	3 US-09-610-838-2	Sequence 2, Appli
10	1287	100.0	251	4 US-09-711-485-2	Sequence 2, Appli
11	1287	100.0	251	4 US-09-645-603B-2	Sequence 2, Appli
12	1284	99.8	251	1 US-07-901-707-2	Sequence 2, Appli
13	1284	99.8	251	1 US-07-988-430-2	Sequence 2, Appli
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15	1282	99.6	251	1 US-08-425-336-108	Sequence 108, App
16	1282	99.6	251	1 US-08-488-113B-108	Sequence 108, App
17	1282	99.6	251	1 US-08-477-484B-108	Sequence 108, App
18	1282	99.6	251	2 US-08-646-360-108	Sequence 108, App
19	1282	99.6	251	3 US-08-839-765-108	Sequence 108, App
20	1282	99.6	251	3 US-09-136-389-108	Sequence 108, App
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22	1282	99.6	251	4 US-09-711-485-108	Sequence 108, App
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27	1279	99.4	251	1 US-08-425-336-109	Sequence 109, App

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29 1279 99.4 251 1 US-08-488-113B-104 Sequence 104, App
30 1279 99.4 251 1 US-08-488-113B-105 Sequence 105, App
31 1279 99.4 251 1 US-08-488-113B-106 Sequence 106, App
32 1279 99.4 251 1 US-08-488-113B-109 Sequence 109, App
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42 1279 99.4 251 2 US-08-646-360-109 Sequence 109, App
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45 1279 99.4 251 3 US-08-839-765-105 Sequence 105, App

ALIGNMENTS

RESULT 1

US-08-425-336-2
; Sequence 2, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-2

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	TELEFAX:	312/707-9155	
	TELEX:	650 388-1248	
	INFORMATION FOR SEQ ID NO: 2:		
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	TYPE:	amino acid	
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	US-08-488-113B-2		
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	TELEFAX:	312/707-9155	
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	SEQUENCE CHARACTERISTICS:		
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	MOLECULE TYPE:	protein	
	US-08-488-113B-2		
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	Best Local Similarity	100.0%; Pred. No. 8.6e-125;	
	Matches 251; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
	TELEPHONE:	312/707-8899	
	TELEFAX:	312/707-9155	
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	INFORMATION FOR SEQ ID NO: 2:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	251 amino acids	
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	US-08-488-113B-2		
	Query Match	100.0%; Score 1287; DB 1; Length 251;	
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	TELEPHONE:	312/707-8899	
	TELEFAX:	312/707-9155	
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	TOPOLOGY:	linear	
	MOLECULE TYPE:	protein	
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	Query Match	100.0%; Score 1287; DB 1; Length 251;	
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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
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; TOPOLOGY: linear
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; US-08-477-484B-2.

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DB 181 FOORIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYYVTVADVQVKPKI 240
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; Sequence 2, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
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; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-360-2

Query Match          100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYYVNFNLRLVKLPKPEGNHSHGIPLLRKCDPDKGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATYYVNFNLRLVKLPKPEGNHSHGIPLLRKCDPDKGKCFVLVALSNDN 60
QY 61 GLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYYVTVADVQVKPKI 240
DB 181 FOORIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYYVTVADVQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5
US-08-621-803-247
; Sequence 247, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-621-803-247

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFLELVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFLELVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 6
US-08-839-765-2
; Sequence 2, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765

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; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-2

Query Match 100.0%; Score 1287; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFLELVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFLELVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 7
US-09-136-389-2
; Sequence 2, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago

```


STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM: disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,389
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-136-389-2

Query Match 100.0%; Score 1287; DB 3; Length 251;
 Best Local Similarity 100.0%; Pred. No. 8.6e-125;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVNSEAARFTFTENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVNSEAARFTFTENQIRNN 180
 QY 181 FQORIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
 DB 181 FQORIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
 QY 241 ALLKFVDKDKP 251
 DB 241 ALLKFVDKDKP 251

RESULT 8
 US-09-217-352-247
 ; Sequence 247, Application US/09217352

Patent No. 6274344
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM: disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,352
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/621,803
 FILING DATE: 22-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27129/33199
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 247:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-217-352-247

Query Match 100.0%; Score 1287; DB 3; Length 251;
 Best Local Similarity 100.0%; Pred. No. 8.6e-125;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVNSEAARFTFTENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVNSEAARFTFTENQIRNN 180
 QY 181 FQORIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
 DB 181 FQORIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
 QY 241 ALLKFVDKDKP 251
 DB 241 ALLKFVDKDKP 251

RESULT 9
 US-09-610-838-2
 ; Sequence 2, Application US/09610838
 ; Patent No. 6376217
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroli, Stephen F.
 APPLICANT: Studnika, Gary M.

```

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-2
Query Match 100.0%; Score 1287; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYVNFNLNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYVNFNLNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSVPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSVPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAISSLLVVIQWVSEAAFTTIEQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAISSLLVVIQWVSEAAFTTIEQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKKYVTVAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKKYVTVAVDQVKPKI 240
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QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 10
US-09-711-485-2
; Sequence 2, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-2
Query Match 100.0%; Score 1287; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GLDTSVSTKGATYITYVNFNLNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYVNFNLNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSVPSLEGEK 120
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Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 11
US-09-645-603B-2
; Sequence 2, Application US/09645603B
; Patent No. 6652861
; GENERAL INFORMATION:
; APPLICANT: LEE-HUANG, Sylvia
; TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of
; FILE OF INVENTION: map30 and gap31
; FILE REFERENCE: LEE-HUANG 4A
; CURRENT APPLICATION NUMBER: US/09/645,603B
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/150,885
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Gelonium multiflorum
US-09-645-603B-2

Query Match 100.0%; Score 1287; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSVFSFGKATYITYVNFNLRLVRLKPEGNHSHGIPILRRKCDPDKGKCFVLVALSNDN 60
Db 1 GLDTSVFSFGKATYITYVNFNLRLVRLKPEGNHSHGIPILRRKCDPDKGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 12
US-07-901-707-2
; Sequence 2, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; ; Composition and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-2

Query Match 99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSVFSFGKATYITYVNFNLRLVRLKPEGNHSHGIPILRRKCDPDKGKCFVLVALSNDN 60
Db 1 GLDTSVFSFGKATYITYVNFNLRLVRLKPEGNHSHGIPILRRKCDPDKGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 13
US-07-988-430-2
; Sequence 2, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping

;/ TITLE OF INVENTION: Materials Comprising and Methods of
;/ NUMBER OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
;/ NUMBER OF SEQUENCES: 101
;/ CORRESPONDENCE ADDRESS: 101
;/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;/ STREET: Two First National Plaza, 20 South Clark
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60603
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ FILING DATE: 19921209
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/901,707
;/ FILING DATE: 19-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/787,567
;/ FILING DATE: 04-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: NO. 5416202and, Greta E.
;/ REGISTRATION NUMBER: 35302
;/ REFERENCE/DOCKET NUMBER: 31133
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (312) 346-5750
;/ TELEFAX: (312) 984-9740
;/ TELEX: 25-3856
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 251 amino acids
;/ TYPE: AMINO ACID
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ PCT-US92-09487-2
;/ US-07-988-430-2

Query Match 99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	60
Db	1	GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	60
QY	61	GOLAEIADVTSVVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK	120
Db	61	GOLAEIADVTSVVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK	120
QY	121	AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIEQIRNN	180
Db	121	AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIEQIRNN	180
QY	181	FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	240
Db	181	FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	240
QY	241	ALLKFVDKDPK 251	
Db	241	ALLKFVDKDPK 251	

RESULT 14

PCT-US92-09487-2
; Sequence 2, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.

;/ APPLICANT: Better, Marc D.
;/ APPLICANT: Carroll, Stephen F.
;/ APPLICANT: Lane, Julie A.
;/ APPLICANT: Lei, Shau-Ping
;/ TITLE OF INVENTION: Materials Comprising and Methods of
;/ NUMBER OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
;/ CORRESPONDENCE ADDRESS: 101
;/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;/ STREET: Two First National Plaza, 20 South Clark
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60603
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US92/09487
;/ FILING DATE: 19921104
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/901,707
;/ FILING DATE: 19-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/787,567
;/ FILING DATE: 04-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Noland, Greta E.
;/ REGISTRATION NUMBER: 35302
;/ REFERENCE/DOCKET NUMBER: 31133
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (312) 346-5750
;/ TELEFAX: (312) 984-9740
;/ TELEX: 25-3856
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 251 amino acids
;/ TYPE: AMINO ACID
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ PCT-US92-09487-2

Query Match 99.8%; Score 1284; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-124; Mismatches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	60
Db	1	GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	60
QY	61	GOLAEIADVTSVVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK	120
Db	61	GOLAEIADVTSVVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSPSLEGEK	120
QY	121	AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIEQIRNN	180
Db	121	AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIEQIRNN	180
QY	181	FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	240
Db	181	FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	240
QY	241	ALLKFVDKDPK 251	
Db	241	ALLKFVDKDPK 251	

RESULT 15

US-08-425-336-108
; Sequence 108, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-108

Query Match 99.6%; Score 1282; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.8e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYIYVNFNLRLVKLPNGNSHGIPILRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYIYVNFNLRLVKLPNGNSHGIPILRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVQRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVQRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKLDENAINDKYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKLDENAINDKYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FQORIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:49:12
Job time : 31 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:34:33 ; Search time 25 Seconds
(without alignments)
966.016 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTVSFSTKGATYITYNF.....AVDQVKPKIALLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 130334

Minimum DB seq length: 0

Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	348.5	27.1	245	2 JC4840	rRNA N-glycosidase
2	329	25.6	251	2 C39761	abrin (clone 7.2)
3	315	24.5	247	2 JU0393	karasurin - Mongol
4	310	24.1	247	2 JC5032	karasurin-B - Tric
5	270	21.0	250	2 JN0108	luffin-b - smooth
6	195	15.2	40	2 S17574	rRNA N-glycosidase
7	149	11.6	236	2 S17932	rRNA N-glycosidase
8	121	9.4	106	2 B39761	abrin (clone 3.7)
9	80	6.2	220	2 D96702	unknown protein, 6
10	79.5	6.2	249	2 B95186	tRNA pseudouridine
11	78.5	6.1	234	2 B93957	HAD superfamily hy
12	78.5	6.1	249	2 B98053	pseudouridylylate sy
13	75.5	5.9	244	1 A28053	carboxyl reductase
14	73.5	5.7	246	2 F2769	hypothetical prote
15	73	5.7	249	2 T47996	hypothetical prote
16	72.5	5.6	194	2 T33345	hypothetical prote
17	72	5.6	180	2 D87031	probable acetyltra
18	72	5.6	245	2 B70247	conserved hypothet
19	71.5	5.6	204	2 AB3024	transcription regu
20	71	5.5	139	2 D86753	hypothetical prote
21	71	5.5	139	2 G86681	hypothetical prote
22	71	5.5	202	2 S26074	hypothetical prote
23	71	5.5	221	2 B81143	hypothetical prote
24	70.5	5.5	220	2 B82472	hypothetical prote
25	70	5.4	149	2 D72527	hypothetical prote
26	69.5	5.4	211	2 A64490	precorrin-6y methy
27	69	5.4	112	2 AG2275	hypothetical prote
28	69	5.4	145	2 AE1714	flavodoxin homolog
29	69	5.4	211	2 A84006	GTP pyrophosphokin

30	69	5.4	232	2 S47846	rfay protein - Esc
31	69	5.4	245	1 JQ1607	polyheadin - Antic
32	68.5	5.3	169	2 F82403	hypothetical prote
33	68.5	5.3	180	2 E97355	hypothetical prote
34	68.5	5.3	218	2 T36499	probable two-compo
35	68	5.3	122	1 MNIV23	nonstructural prot
36	68	5.3	185	2 D97187	tdDP-4-dehydroram
37	68	5.3	197	2 F96731	hypothetical prote
38	68	5.3	205	2 T16560	hypothetical prote
39	68	5.3	211	2 C90330	partial transposas
40	67.5	5.2	170	2 A43841	major fibrillar sub
41	67.5	5.2	181	2 A11682	conserved hypothet
42	67.5	5.2	191	2 C75011	hypothetical prote
43	67.5	5.2	222	2 AE1826	hypothetical prote
44	67.5	5.2	223	2 A90523	hypothetical prote
45	67.5	5.2	235	2 AB2613	orotidine 5'-monop

ALIGNMENTS

RESULT 1

JC4840
rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd
C:Species: Trichosanthes anguina (snake gourd)
C:Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C:Accession: JC4840; JT0701; JT0677
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Biomed. Sci. 3, 178-186, 1996
A:Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from 7
A:Reference number: JC4840
A:Accession: JC4840
A:Molecule type: protein
A:Residues: 1-132, 'S', 134-245 <CHO1>
A:Experimental source: seed
A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
submitted to JFID, August 1995
A:Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from
A:Reference number: JT0677
A:Accession: JT0701
A:Molecule type: protein
A:Residues: 1-50, 'L', 52-245 <CHO2>
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F:4-242/Domain: rRNA N-glycosidase homology <RNG>
F:51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:70,158,161/Active site: Tyr, Glu, Arg #status predicted
F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match	27.1%	Score	348.5;	DB	2;	Length	245;
Best Local Similarity	35.9%;	Pred. No.	1.4e-21;				
Matches	90;	Conservative	44;	Mismatches	96;	Indels	21;
Gaps	7;						
QY	5	VFSFSTKGATYITYNFNLRLVKLPKPNHSHGIPILRLKCDPDKCFVLVALSNDNGQLA	64				
DB	2	VSFDLSTAKSYSFITQLRDALPTQGTGYGIPLLPSTAGSQR-FRFFNLNTYNDTV	60				
QY	65	ETAIADVTSVYVGVYVRNRSYFFKDPADAAVYGLFKNTIKRLHFGGSYPSLE---GEKA	121				
DB	61	TVADVDTNVIYVAYRADAVSYFFEDTPAFAFKLIFAGTKTVKLPYSGNTDKLQSVVGKQ-	119				
QY	122	YRETTDLGIEPLRIGIKLDENAIDN---XKPEIASSLLVVIQMVSEARFTFIENQIR	178				
DB	120	-RDMIELGIPAL-----SSAITNMVYDYSQTAALLVLIQSTAAEARYKIEQVS	170				
QY	179	NNFQQRIRPANTTISLENKWKLSFOIRTSG--ANGMFSEAVELEERANGKKYIV--TAVD	234				
DB	171	SHISSNFYFNQAVISLENKWKLSQIQIARTNGHQFENPVELYNDGTRFSTVHTSAG	230				
QY	235	QVKPKIALLKPF	245				
DB	231	VVKGNIKLILLY	241				

C;Keywords: abortifacient
F:4-243/Domain: rRNA N-cl

Query Match	24.5%;	Score 315;	DB 2;	Length 247;
Best Local Similarity	38.8%;	Pred. No. 8.6e-19;		
Matches	94;	Conservative	33;	Mismatches 105; Indels 14; Gaps 8;
Qy	5	VSFSTKGATITYVNFELNLRVVKLKEPNSHGIPLLRKKKDDPG-KCFVLVALSNSDNGQL	63	
Db	2	VSPRLSGSSSYGVFISNLRKALPYERKLYDIPLLRSTL--PGSRYALIHLLTNVADET	59	
Qy	64	AETAIDVTSVYVGVQVRNRSYEFKDA-PDAAVEGLFKNT-IKTRHLFGSGSYSLSE-GEK	120	
Db	60	ISVAIDVTVNVGVYRAGDTSYFNSASATEAAKYVFKDKRKVTLPYSGNYERLQIAAG	119	
Qy	121	AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETASSLLVVVIQMVSEAAFTFFINRNN	180	
Db	120	KIRENIPGLPALDSAI-----TTLFVYVANSASALSMLVLQSTSEAAKYKFTIEQIGKR	174	
Qy	181	FQQRIPANNNTISLENKWKGLSFQIR-TSGANGWFSEAVELELRANGKYYVVTAVDQ--VK	237	
Db	175	VDKTFIPSLAILSLNSWSALSQIQIASYNNQFFTFPVVLINAQNRVTTITWVDAQVVT	234	
Qy	238	PKIALL	243	
Db	235	SNIALL	240	

RESULT 4
JC5032

karasin-B - *Trichosanthes kirilowii* var. *japonica*
 C/Species: *Trichosanthes kirilowii* var. *japonica*
 C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997
 C/Accession: JCS032
 R/Kondo, T.; Mizukami, H.; Takeda, T.; Oginhara, Y.
 Biol. Pharm. Bull. 19, 1485-1489, 1996
 A/Title: Amino acid sequences and ribosome-inactivating
 A/Reference number: JCS032; MUID:97108848; PMID:895
 A/Accession: JCS032
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-247 <RNG>
 A/Cross-references: UNIPROT:Q41216; UNIPROT:Q94K84;
 C/Comment: This protein belongs to type I ribosomal
 C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase
 F:4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match.	24.1%;	Score 310;	DB 2;	Length 247;
Best Local Similarity	37.8%;	Pred. NO. 2.2e-18;		
Matches	93;	Conservative 34;	Mismatches 105;	Indels 14; Gaps 8;
Qy	5	VSBSTKGATITYVYFNLNLRVLLKPGNSHGIPLLRKKCCDDPG-KCFVLVALSDNDNGQL	63	
Db	2	VSPRLSGATSSSYGVFISNLRKALPYERKLDYIPLLRSTL--PGSQRYALIHLTNYADET	59	
Qy	64	AETAIDVTSVVVGVYQVRNESYFFPKDA-PDAAVEGLFKNT-IKTRLHFGGSPSLSE-GEK	120	
Db	60	ISVAIDVTNVYGVYRAGDTSYFFNEASATEAKYVFKDAKRKVTLPYSGYERLQIAAG	119	
Qy	121	AYRETTDLGIPELRIGIKLIDENAINYKPTETASSLLVVVIQMVSEARFTFIENQIRNN	180	
Db	120	KIRENPLGHPALDSAI-----TTLPYFNANSASALLMWLIQSTSEARVKYFIEQIQIKR	174	
Qy	181	FQQRIRPANNTISLENKGLSPQIR-TSGANGWFSEAVELERANGKKYVYVADQ--VK	237	
Db	175	VDKTFPLSLAIISELSWSALSQIQIQTATNNQGFETFPVVLINAQNRVITITNAGVVT	234	
Qy	238	PXTALL	243	
Db	235	SNIALL	240	

RESULT 5

RESULT 2

C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C39761; S14471
R;Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
A;Accession: C39761
A;Molecule type: DNA
A;Residues: 1-251 <EVE>
A;Cross-references: UNIPROT:Q38760
R;Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Reference number: S14471
A;Accession: S14471
A;Molecule type: DNA
A;Residues: 'M', 1-251 <EV2>
A;Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F;1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted

Query Match	25.6%	Score 329;	DB 2;	Length 251;
Best Local Similarity	36.5%;	Pred. No. 6e-20;		
Matches	93; Conservative	40; Mismatches	104; Indels	18; Gaps
Qy	5	VSPSTKGATITVYVNFLEURVLKPEGNSHGIPLLRKKCDDPKC-----FVLVALSND	59	
Db	5	IKSTEGATSQSRYKFTEALRELR--GLIHDIPVLR----DPTVEERNRRIYTVELSNS	59	
Qy	60	NGQLAEIAIDVTSVYGVGYVRNRSYFFKDAPDAAYEGLFKNTIKTRLHPGGSYPSLE-G	118	
Db	60	ERESIEVGIDVTWAVYVAYAGSQSYFLRDAPASASTYLFTGTQRYSLAFDGSYGDLRW	119	
Qy	119	EKAVRTTDIGIRPLRGIKKLDENAIDNKYPEIASILLWIQMYSSEAAARFTTFENQR	178	
Db	120	AHQTRQISLGLQALTHAISFLSGASND---BEKARTLIVIIQMASEAARYRYSNRVG	176	
Qy	179	NNFQ--QRIRPANNTISLENKWGKLSFIQINTSGANGMFSEAVELERANGKYVVTA-V-DQ	235	
Db	177	VSRTGTGAFOFDPAMLSLSNWNINLSRGVOES--VOSTFPNAVTLREVNNOPVIVLSLTHQ	235	

RESULT 3
JUL0393

karasurin - Mongolian snake-gourd
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: J00393; PS0163
 R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.
 Chem. Pharm. Bull. 39, 1244-1249, 1991
 A:Title: The complete amino acid sequence of an abortifacient protein, karasurin.
 A:Reference number: J00393; PMID:92005921; PMID:1914000
 A:Accession: J00393
 A:Molecule type: protein
 A:Residues: 1-247 <TOY>
 A:Cross-references: UNIPROT:P24478
 A:Note: a sequence which lacks Ala-247 is also shown in this publication
 C:Superfamily: tRNA N-glycosidase; tRNA N-glycosidase homology


```

JN0108
luffin-b - smooth loofah
C:Species: Luffia cylindrica (smooth loofah)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: JN0108
R:Islam, M.R.; Hirayama, H.; Hirayama, G.
Agric. Biol. Chem. 55, 229-238, 1991
A:Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from
A:Reference number: JN0108; MUID:91248486; PMID:1368666
A:Accession: JN0108
A>Status: preliminary
A:Molecule type: protein
A:Molecule type: protein
A:Residues: 1-250 <ISL>
A:Cross-references: UNIPROT:P22851
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;5-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 21.0%; Score 270; DB 2; Length 250;
Best Local Similarity 31.3%; Pred. No. 4.8e-15;
Matches 79; Conservative 47; Mismatches 106; Indels 20; Gaps 8;

Qy 5 VFSESTKGATITYVYNFLNELRVKLKPGNSHGIFLLRKKCDPGKCFVLVALSNDNGQLA 64
Db 3 VFSLSGADSKSYSKFITALRKALPSEKVKSNIPLLPSASGASR-YILMQLSNYDAKAI 61
Qy 65 EIAIDVTSVVVGVQVNRNRSYFFKADDA--AYEGLFKNTIKTRLHFGSGSYPSLEGEKAY 122
Db 62 TMAIDVTNVYIMGYLVNSTSYFANES-DAKLASQYVFKGSTLVITIPYSGNTERLQNAAGK 120
Qy 123 RETTDLGIEPLRIGIKKLE--NAIDNVKPEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db 121 IR-----EKIPGFRALDSALTSIFHYDSTAAAFLLVILQTTAASRFKYEIQIIER 174
Qy 181 FQQRIRPANNTISLENK-WGKLSFQIRTSGA-NGMFSEAVELERANGKKYYVT-----A 232
Db 175 IPKNEVSPAAALSLENAWSLLSQIQLAQTNNGAFRTPVVIDNKGORVEITNLASKVQ 234
Qy 233 VDQVKPKIALLK 244
Db 235 IKDYNKSLLLNK 246

RESULT 6
S17574
rRNA N-glycosidase (EC 3.2.2.22) GAP31 - Gelonium multiflorum (fragment)
C:Species: Gelonium multiflorum
C>Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S17574
R:Lee-Huang, S.; Kung, H.; Huang, P.L.; Huang, P.L.; Li, B.Q.; Huang, H.I.;
FEBS Lett. 291, 139-144, 1991
A:Title: A new class of anti-HIV agents: GAP31, DAPS 30 and 32.
A:Reference number: S17574; MUID:92037998; PMID:1936243
A:Accession: S17574
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-40 <LEE>
A:Cross-references: UNIPROT:P24475
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase

Query Match 15.2%; Score 195; DB 2; Length 40;
Best Local Similarity 95.0%; Pred. No. 7.3e-10;
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDVTSPSTKGATITYVYNFLNELRVKLKPGNSHGIPLL 40
Db 1 GLDVTSPSTKGATITYVYNFLNELRVKTKPGNSHGIPSL 40

RESULT 7
S17932
rRNA N-glycosidase (EC 3.2.2.22) Sap3 - common soapwort (fragment)
N:Alternate names: saporin 3

```

70 VISIVVIGIQVKNKSI--FKKAFDFAVIGLFAVILKAKL--FGGGFSDLD--EAKAKL 125
 99 LVVNY-----RKYDYK--DAIYE-IPKLSKKYKLAVIDSDAWPSLSEGVFKA--- 142
 126 TDLGIEPLRIGIKKLDENAIQN-----YKPEIA--SSLVLVIQVMVSEAAARFTIENQIRN 179
 143 -----GLRKYFSFVLSSVKGVTKPNEMMYKTALSRLVLPBEA--VFIDDIRN 190
 180 NFQRIIRPANNNTISLENKWKGLSFQIRTSNGAMFSEAVE 219
 191 -----CEGAVKLGIKSFVLSRKSRIYAVNKLFNRRIK 222

RESULT 12
 B98053 pseudouridylylate synthase (EC 4.2.1.70) [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: B98053
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es-
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc-
 Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:22:52 ; Search time 111.5 Seconds
(without alignments)
1152.752 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTVSFSTKGATITTYVNF.....AVDQVKPKIALLKFDVKDKP 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 827211

Minimum DB seq length: 0

Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	320	24.9	251 2 Q7DM12	Q7dm12 abrus preca
2	316	24.6	247 2 Q6BQ4	Q6bq4 trichosan
3	315	24.5	247 2 Q9LRE3	Q9lre3 trichosan
4	314	24.4	251 2 Q96236	Q96236 abrus preca
5	313	24.3	251 2 Q96237	Q96237 abrus preca
6	311.5	24.2	249 2 Q8LQK5	Q8lqk5 viscum albu
7	310.5	24.1	249 2 Q8RXH7	Q8rxh7 viscum albu
8	307.5	23.9	251 2 Q8LQK4	Q8lqk4 viscum albu
9	307	23.9	251 2 Q96235	Q96235 abrus preca
10	297	23.1	203 2 Q8RY69	Q8ry69 gynosomma
11	290	22.5	248 2 Q7YIU7	Q7yiu7 gynosomma
12	286	22.2	248 2 Q7YIU5	Q7yiu5 gynosomma
13	280	21.4	237 2 Q6J3N3	Q6j3n3 phytolacca
14	276	21.4	237 2 Q6J3N4	Q6j3n4 phytolacca
15	276	21.4	237 2 Q9ATB3	Q9atb3 phytolacca
16	270	21.0	250 1 R1PB LUFY	P22851 luffa cylin
17	266	20.7	237 2 Q6J3N2	Q6j3n2 phytolacca
18	242	18.8	234 2 Q7SIF0	Q7sif0 trichosan
19	239	18.6	55 1 R1P3 GELMU	P24475 gelonium mu
20	235	18.3	172 2 Q7YIU6	Q7yiu6 gynosomma
21	197.5	15.3	136 2 Q8SAD7	Q8sad7 cucurbita m
22	187.5	14.6	136 2 Q84LJ9	Q84lj9 cucurbita m
23	187.5	14.6	136 2 Q84LJ0	Q84lj0 cucurbita m
24	186.5	14.5	136 2 Q8S2R5	Q8s2r5 cucurbita m
25	186.5	14.5	136 2 Q84LJ8	Q84lj8 cucurbita m
26	185.5	14.4	136 2 Q8SAGO	Q8sago benincasa h
27	167.5	13.0	251 2 Q48859	Q48859 amaranthus
28	149	11.6	236 1 R1P3 SAPOF	P27560 saponaria o
29	131	10.2	26 2 Q9S8P3	Q9s8p3 gelonium mu
30	92.5	7.2	205 2 Q6Z4E3	Q6z4e3 oryza sativ
31	91.5	7.1	222 2 Q6Z4Z5	Q6z4z5 oryza sativ

32	89.5	7.0	213	2 Q9K3E8	Q9k3e8 staphylococ
33	85	6.6	191	2 Q9XL9	Q9xl9 streptococ
34	84.5	6.6	187	2 Q7P521	Q7p521 fusobacteri
35	82.5	6.4	195	1 RS4_FUSNN	Q8re43 fusobacteri
36	81	6.3	198	2 Q7RSS9	Q7rss9 plasmodiu
37	80.5	6.3	240	1 HIS4_PYRFU	P58791 pyrococcus
38	80	6.2	189	1 SSB_MYCPE	Q8ewt6 mycoplasma
39	80	6.2	220	2 Q9C9W1	Q9c9w1 arabidopsis
40	80	6.2	228	2 Q6MRY4	Q6mry4 mycoplasma
41	80	6.2	249	2 Q8RMD6	Q8rmd6 mycoplasma
42	79.5	6.2	101	2 Q7YIU4	Q7yiu4 gynosomma
43	79.5	6.2	170	2 Q69HQ7	Q69hq7 ciona intes
44	79.5	6.2	204	2 Q81FY4	Q81fy4 bacillus ce
45	79.5	6.2	249	1 TRUA_STRPN	Q97p10 streptococ

ALIGNMENTS

RESULT 1

ID	Q7DM12	PRELIMINARY;	PRT;	251 AA.
AC	Q7DM12;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Abrin A-chain (Fragment).			
OS	Abrus precatorius (Indian licorice) (Crab's eye).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.			
OX	NCBI_TaxID=3816;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Seed;			
RX	MEDLINE=94139756; PubMed=8307038;			
RA	Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;			
RT	"Cloning and expression of three abrin A-chains and their mutants			
RT	derived by site-specific mutagenesis in Escherichia coli.";			
RL	Eur. J. Biochem. 219:83-87(1994).			
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			
CC	specific adenosine on the 28S rRNA.			
CC	-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.			
DR	EMBL; X76720; CAA54138.1; -.			
DR	HSSP; P11140; IABR.			
DR	GO; GO:0016787; F:hydrolase activity; IEA.			
DR	GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.			
DR	GO; GO:0006952; P:defense response; IEA.			
DR	GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR001574; RIP.			
DR	Pfam; PF00161; RIP; 1.			
DR	PRINTS; PR00396; SHIGARICIN.			
DR	PROSITE; PS00275; SHIGA_RICIN; 1.			
KW	Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.			
FT	NON_TER 1			
FT	NON_TER 251			
SQ	SEQUENCE 251 AA; 28098 NW; 817B8B5C2A4AECCE CRC64;			

Query Match	24.9%;	Score 320;	DB 2;	Length 251;
Best Local Similarity	35.7%;	Pred. No. 1.2e-18;		
Matches	91;	Conservative 39;	Mismatches 107;	Indels 18; Gaps 8;
QY	5	VSFSTKGATITTYVNFNLRLVKLPKGNHGHPILRLKCCDDPGKC-----FVLVALSND	59	
Db	5	IKFSTEGATSQYKQFIEALRRLR-GGLIHDPVL-----PDPTLQERNRITVELSNS	59	
QY	60	NCQLAEIADVTSVVVGQVNRNRYFFKADPAAYEGLFKNTIKRLHFGSGSPSE-LG	118	
Db	60	DTESIEVGIDVTNAVYVAYRAGTQSVFLRDAFSSASDYLFTGTDQSLSPFYGYGLRW	119	
QY	119	EKAYRETTDLEPIRIGIKKLDENAIIDNKTETATASSLLVVIOMVSEARFTFIENQIR	178	

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Db 120 AHQSRQOIPGLQALHTGISFFRSGNDN---EERKARTLIVIIQMVAAARPRYISNRVR 176
QY 179 NNFO--QRIRPANNTISLENKWKLSFOIRTSANGMSEAEVLELERANGKKYVTVAVDQ- 235
Db 177 VSIQTGTAPODAAISLENNDNISRGVQES-VODTFPNQVTLTNRNEPVIDSLSHP 235
QY 236 VKPKIALKLFVDKDP 250
Db 236 TVAVLALMLFVCNPP 250

RESULT 2
Q6BBO4
ID Q6BBO4 PRELIMINARY; PRT; 247 AA.
AC Q6BBO4
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Trichosanthin (Fragment).
GN Name=TCS;
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RA Mi S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;
RA "Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF669811; AA791090.1; -.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT CHAIN <1> 247 trichosanthin.
FT NON_TER 247
SQ SEQUENCE 247 AA; 27172 MW; BCBA762884F89CCE CRC64;

Query Match 24.6%; Score 316; DB 2; Length 247;
Best Local Similarity 37.1%; Pred. No. 2.6e-18;
Matches 91; Conservative 35; Mismatches 107; Indels 12; Gaps 7;

QY 5 VSFSTKGATYTYVNFNLRLVKLPKGNHSGIPLLRKKCDPDGKCFVLVALSNDNGQLA 64
Db 2 VSFRLSGATSSSYGVFISNLRKALPNERLYDIPLRSTLQSGSR-YALIHLTNYADETI 60
QY 65 EIAIDVTSVYVGVYQVRNRSYFFKDA-PDAAYEGLFKNTI-KTRLHFGGSYPSLE-GEKA 121
Db 61 SVAVDVTNVYVGVYQVRNRSYFFKDA-PDAAYEGLFKNTI-KTRLHFGGSYPSLE-GEKA 120
QY 122 YRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNF 181
Db 121 IRENIPGLPALDSAI-----TTLFYNNANSAASALMWLIQSTSEAAARKYFIEQIQIGKRA 175
QY 182 QQRIRPANNTISLENKWKLSFOIR-TSGANGMSEAEVLELERANGKKYVTVAVDQ--VKP 238
Db 176 DKTFLFSLAIISLNSWSALSQIQIQTASTNGQFETPPVVLINAQNRVAITNVDAGVVT 235

QY 239 KIAL 243
Db 236 NIAL 240

RESULT 3
Q9LRE3

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ID Q9LRE3 PRELIMINARY; PRT; 247 AA.
AC Q9LRE3
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Trichobakin (Fragment).
GN Name=TBK;
OS Trichosanthes sp. Bac Kan 8-98.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=118182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21476888; PubMed=11592913;
RA Van Chi P., Quoc Truong H., Thuy Ha N., Chung W.I., Binh L.T.;
RT "Characterization of trichobakin, a type I ribosome-inactivating
RT protein from Trichosanthes sp. Bac Kan 8-98.";
RL Biotechnol. Appl. Biochem. 34:85-92(2001).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AB039324; BAA92530.1; -.
DR HSP; P09989; 1J4G.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:00017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT NON_TER 247
SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match 24.5%; Score 315; DB 2; Length 247;
Best Local Similarity 38.2%; Pred. No. 3.2e-18;
Matches 94; Conservative 33; Mismatches 105; Indels 14; Gaps 8;

QY 5 VSFSTKGATYTYVNFNLRLVKLPKGNHSGIPLLRKKCDPDG-KCFVLVALSNDNGQL 63
Db 2 VSFRLSGATSSSYGVFISNLRKALPYERKLDIPLRSTL--PGSQRYALIHLTNYADET 59
QY 64 AEIADVTSVYVGVYQVRNRSYFFKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSLE-GEK 120
Db 60 ISVAIDVTNVYVGVYQVRNRSYFFKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSLE-GEK 119
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNF 180
Db 120 KIRENIPGLPALDSAI-----TTLFYNNANSAASALMWLIQSTSEAAARKYFIEQIQIGKR 174
QY 181 FQQRIRPANNTISLENKWKLSFOIR-TSGANGMSEAEVLELERANGKKYVTVAVDQ--VK 237
Db 175 VDKTFLFSLAIISLNSWSALSQIQIQTASTNGQFETPPVVLINAQNRVAITNVDAGVVT 234

QY 238 KIAL 243
Db 235 SNIAL 240

RESULT 4
Q96236
ID Q96236 PRELIMINARY; PRT; 251 AA.
AC Q96236
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Abrin A chain (E164A) (Fragment).
GN Name=pgDNAAC-1-E164A;
OS Abrus precatorius (Indian licorice) (Crab's eye).

```


CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF508915; AAM46933.1; -.
DR HSSP; P81446; 100L.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT SEQUENCE 249 AA; 27821 MW; 3C5870F8338BDB5 CRC64;
SQ
Query Match 24.2%; Score 311.5; DB 2; Length 249;
Best Local Similarity 35.4%; Pred. No. 6.3e-18;
Matches 90; Conservative 37; Mismatches 106; Indels 21; Gaps 7;
QY 5 VSFSTKGATYYTYNFMELRVKLKPEGNHSHGIPLLRKK---CDPDKCFVLVALSNDNG 61
DB 8 VTHQTTGQYF---KFITLLRDHVSGLSNQIPLLRQSTVPVSDTQR-FVLVELSNQGG 63
QY 62 QLAETAIDVTSVVVGYQVRNPSYFKDAPDAAYEGSLFKNTIKTRLHFGGSPSLGEKAY 121
DB 64 DSITAAIDVTNLYVAYQAGDSYFLRDAPGAERTYFTGTRSSLPFGSYDLERYAG 123
QY 122 YRETTDLGIEPLRIGIKLDENAIQNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNNF 181
DB 124 HRDQIPLGIDQL---IQVSALRFFGSTRQAQARSFIILLIQMISEARF---NPILWRA 176
QY 182 QQRIR-----PANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQ 235
DB 177 RQYISGGSFDPDTYILQLETSGWQQSTQVQHS-TDGVFNFPRLTISTGVFVTLNVRD 235
QY 236 VKPKIALLKFVDKD 249
DB 236 VIASLAIMLFVCE 249
RESULT 7
Q8RXH7 PRELIMINARY; PRT; 249 AA.
ID Q8RXH7
AC Q8RXH7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lectin chain A isoform 2 (fragment).
OS Viscum album (European mistletoe).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Santalaceae; Viscum.
OX NCBI_TaxID=3972;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Leaf;
RC TISSUE=Leaf;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY081148; AAL87005.1; -.
DR HSSP; P81446; 100L.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT CHAIN <1 >249 lectin chain A isoform 2.
FT NON_TER 249
SQ SEQUENCE 249 AA; 27944 MW; 89FAFB78309A83B3 CRC64;
Query Match 24.1%; Score 310.5; DB 2; Length 249;
Best Local Similarity 34.1%; Pred. No. 7.6e-18;
Matches 84; Conservative 42; Mismatches 109; Indels 11; Gaps 5;
QY 5 VSFSTKGATYYTYNFMELRVKLKPEGNHSHGIPLLRKK---DDPKCFVLVALSNDNGQ 62
DB 8 VTHQTTGDEYFRFITLLRDY---VSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNEGSD 64
QY 63 LAETAIDVTSVVVGYQVRNPSYFKDAPDAAYEGSLFKNTIKTRLHFGGSPSLGEKAY 122
DB 65 SITAAIDVTNLYVAYQAGDSYFLRDAPGAERHFTGTRSSLPFGSYDLERYAGH 124
QY 123 RETTDLGIEPLRIGIKLDENAIQNYKPTETIASLLVVIQMVSEAAARFTFIENQIRN--N 180
DB 125 RDQIPLGIEEL---IQVSALRYFGGSTRQAQARSFIILLIQMISEAARNPFWVRQDIN 181
QY 181 FQQRIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQPKPI 240
DB 182 SGESFLPDVYMLETSGWQQSTQVQOS-TDGVFNFPRLAISTGNFVTLNVRDVIASL 240
QY 241 ALLKFV 246
DB 241 AIMLFV 246
RESULT 8
Q8LKQ4 PRELIMINARY; PRT; 251 AA.
ID Q8LKQ4
AC Q8LKQ4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lectin chain A isoform 3 (fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Santalaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21566752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
RA "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AF508916; AAM46934.1; -.
DR HSSP; P81446; 100L.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1


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FT NON_TER 251 251
SQ SEQUENCE 251 AA; 28090 MW; A1177489012E989 CRC64;

Query Match 23.9%; Score 307.5; DB 2; Length 251;
Best Local Similarity 34.7%; Pred. No. 1.4e-17;
Matches 87; Conservative 40; Mismatches 111; Indels 13; Gaps 6;

QY 5 VSFSTKGATYIYVNFLENRLVKLPKGNHSHGIPILRKCD-DPGKCFVLVALSNDNGQL 63
DB 8 VTHQTGDEYF---RPIKLLRDSVSSGSFSDIPLLPSPVSSAQRFVLVELTINQLGKW 64

QY 64 AE---IAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGRK 120
DB 65 EDSITAAIDVTWLYVAYAGQOSYFLRDAPDGAERHLEFGTTRSLPENGSYADLERVA 124

QY 121 AVRETTDLGIEPLRIGIKKLDENAINDKYPTETIASLLVVIQMVSEAAARFTFIENQIRN 180
DB 125 GHRDRIPLGREPLIRSVSALD---YPGGSTRQAASSIIIVQMWSEAAARFNPILWRQY 181

QY 181 FQORIR--PANNTISLENKWKLSFOIRTSGANGMSEAEVELERANGKKYVYTAVDQVKP 238
DB 182 INSGVSLPDVYVMLEASWGQOSTQVQOS--TDGVFNNPIRLGISTGNFVWLSNRDVIA 240

QY 239 KIALKLFVDKD 249
DB 241 SLGIMVFCRD 251

RESULT 9
Q96235 PRELIMINARY; PRT; 251 AA.
AC Q96235;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE Abrin A chain E164A/R167L (Fragment).
GN Name=pcDNAC-1-E164A/R167L;
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID=3816;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94139756; PubMed=8307038;
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
RT "Cloning and expression of three abrin A-chains and their mutants
RT derived by site-specific mutagenesis in Escherichia coli.";
RL Eur. J. Biochem. 219:83-87(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; X76644; CAAS4092.1; -
DR HSSP; P11140; 1ABR.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:000598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1 1
FT NON_TER 251 251
SQ SEQUENCE 251 AA; 27997 MW; 3B60351839AEPB7E CRC64;

Query Match 23.9%; Score 307; DB 2; Length 251;
Best Local Similarity 34.9%; Pred. No. 1.5e-17;
Matches 89; Conservative 39; Mismatches 109; Indels 18; Gaps 8;

QY 5 VSFSTKGATYIYVNFLENRLVKLPKGNHSHGIPILRKCD-DPGKCFVLVALSND 59

RESULT 10
Q9RY69 PRELIMINARY; PRT; 203 AA.
AC Q9RY69;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type I ribosome-inactivating protein (fragment).
OS Gynostemma pentaphyllum (Glaogulan).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Cucurbitales; Cucurbitaceae; Gynostemma.
OX NCBI_TaxID=182084;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin Y., Wu Z.J., Lin Q.Y., Xie L.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY075115; AAL82822.2; -
DR HSSP; P24817; 1CF5.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:000598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1 1
FT NON_TER 203 203
SQ SEQUENCE 203 AA; 22692 MW; 8CCA3228286E09EF CRC64;

Query Match 23.1%; Score 297; DB 2; Length 203;
Best Local Similarity 38.3%; Pred. No. 8e-17;
Matches 80; Conservative 22; Mismatches 89; Indels 18; Gaps 4;

QY 5 VSFSTKGATYIYVNFLENRLVKLPKGNHSHG-----IPLARKKCD-DPGKCFVLVALS 58
DB 2 INFLAGADGGQTYNTFIARKLOEL-----SIGTKQVANITVLKHHVSSNTQRFSLINL 56

QY 59 DNGQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEG--LFGNTIKTRLHFGGSPSL 116
DB 57 YNNAKITGIDVDFVYVGVGLTGTSTYIFKEAPDLAYNQSLFPGVSRENLSYTGYYDDL 116

QY 117 EGKAYRETTDLGIEPLRIGIKKLDENAINDKYPTETIASLLVVIQMVSEAAARFTFIENQ 176
DB 117 ERGGARREDIPLGLPLPLNTAINTLPHR-----DSTSFRRSFIVIIQMVSEAAARFTFIENQ 171

QY 177 IRNNFQORIRPANNTISLENKWKLSFOI 205

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Db 172 IAKNLVGTGFKPDRAILSLNNWGLSKQI 200

RESULT 11

Q7YIU7 PRELIMINARY; PRT; 248 AA.

ID Q7YIU7

AC Q7YIU7

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Gynostemin-like protein (Fragment).

OS Gynostemma pentaphyllum (Jiaogulan).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosidia I; Cucurbitales; Cucurbitaceae; Gynostemma.

OX NCBI_TaxID=182084;

RN [1]

SEQUENCE FROM N.A.

RP Lin Y., Lin Q.Y., Xie L.H.;

RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

RL CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL; AY279104; AAP40648.1; -.

DR HSSP; P24817; 1CF5.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.

FT NON_TER 1

SQ SEQUENCE 248 AA; 27515 MW; 2ACBCE270B018203 CRC64;

Query Match 22.5%; Score 290; DB 2; Length 248;

Best Local Similarity 33.9%; Pred. No. 4e-16;

Matches 86; Conservative 31; Mismatches 91; Indels 46; Gaps 7;

QY 5 VSFSTKGATYTYVNFLELRLVKLKPENSHGIPLLRKKDDPGKCFVLVSLNDNGQLA 64

DB 2 INFLAGAGGQYKTFIAKLQE-----LSIGTQKVA 33

QY 65 ETADVTSTVYVGVQVRNRSYFFKADPAADAEV--LFRNTIKTRLHFGSGVPSLEGEKAY 122

DB 34 NIAVLKHVVYVVGFTGTNSYTFKEAPDLAYNKLSPFGSVRENLSYTGYYDGLRRGAG 93

QY 123 RETTDLGIEPLRIGIKLDENADINY---KPEIASSLLVVIQWSEARFTFIENQIRN 179

DB 94 REDIPGLGLPL-----DTAITNLFRRDSTFSRRSFIVIIQWSEARFKIEAKIAK 145

QY 180 NF--QQRIRPANNNTISLENKGLSFQI-RTSGANGMFSEAVELERANGKKYVY--TAVD 234

DB 146 NLYGENTFPDQAIIISLENNWGLSKQIQKQADRGVFPNLVTLTSSGKPLIRNDSDP 205

QY 235 QVQPKIALLKFVDK 248

DB 206 LVQNGIALLKYMSE 219

RESULT 12

Q7YIU7 PRELIMINARY; PRT; 248 AA.

ID Q7YIU7

AC Q7YIU7

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Gynostemin-like protein (Fragment).

OS Gynostemma pentaphyllum (Jiaogulan).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC eurosidia I; Cucurbitales; Cucurbitaceae; Gynostemma.

OX NCBI_TaxID=182084;

RN [1]

SEQUENCE FROM N.A.

RP Lin Y., Lin Q.Y., Xie L.H.;

RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

RL CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL; AY279104; AAP40648.1; -.

DR HSSP; P24817; 1CF5.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.

FT NON_TER 1

SQ SEQUENCE 248 AA; 27515 MW; 2ACBCE270B018203 CRC64;

Query Match 22.5%; Score 290; DB 2; Length 248;

Best Local Similarity 33.9%; Pred. No. 4e-16;

Matches 86; Conservative 31; Mismatches 91; Indels 46; Gaps 7;

QY 5 VSFSTKGATYTYVNFLELRLVKLKPENSHGIPLLRKKDDPGKCFVLVSLNDNGQLA 64

DB 2 INFLAGAGGQYKTFIAKLQE-----LSIGTQKVA 33

QY 65 ETADVTSTVYVGVQVRNRSYFFKADPAADAEV--LFRNTIKTRLHFGSGVPSLEGEKAY 122

DB 34 NIAVLKHVVYVVGFTGTNSYTFKEAPDLAYNKLSPFGSVRENLSYTGYYDGLRRGAG 93

QY 123 RETTDLGIEPLRIGIKLDENADINY---KPEIASSLLVVIQWSEARFTFIENQIRN 179

DB 94 REDIPGLGLPL-----DTAITNLFRRDSTFSRRSFIVIIQWSEARFKIEAKIAK 145

QY 180 NF--QQRIRPANNNTISLENKGLSFQI-RTSGANGMFSEAVELERANGKKYVY--TAVD 234

DB 146 NLYGENTFPDQAIIISLENNWGLSKQIQKQADRGVFPNLVTLTSSGKPLIRNDSDP 205

QY 235 QVQPKIALLKFVDK 248

DB 206 LVQNGIALLKYMSE 219

DR GO:0016787; F:hydrolase activity; IEA.
 DR GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO:0006952; P:defense response; IEA.
 DR GO:00017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 26710 MW; A274F9BA402031DA CRC64;

Query Match 21.8%; Score 280; DB 2; Length 237;
 Best Local Similarity 30.6%; Pred. No. 2.6e-15;
 Matches 76; Conservative 44; Mismatches 96; Indels 32; Gaps 8;

QY 2 LDTVSFSTKGATYITYVNFNLRLVKLK-PEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 Db 1 MNTIYVGVSTTSISKYATFLDLRLNEAKDPSLKCYGIPMLPNTNTPK--YVLVELQGSN 58
 QY 61 GOLAEIAIDVTSVYVVGQ-----VNRSYFFKD-----APDAAYEGLFKNT 102
 Db 59 KKTITLMLRNNLYVMGYSDPFTNKRVIHFNDSIGTERQDVETTLCPNA-----NSR 112
 QY 103 IKTRLHFGGSYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENADINYKPTIASSLLVV 160
 Db 113 VSRNINFDISRYPTLSKAGVKSRSQVLGIQILDNSNIGKI--SGVMSFTEKTEAEFLVA 170
 QY 161 IQMVSEARFTIENQIRNFOORIPANNITISLENKMGKLSFQIRTSANGMFSEAVEL 220
 Db 171 IQMVSEARFKYIENQVNFNFRAFPNPKVNLQETWGIKSTAIH-DKANGVLPKPLEL 229
 QY 221 ERANGKKY 228
 Db 230 VDASGAKW 237

RESULT 14
 Q6J3N4 PRELIMINARY; PRT; 237 AA.

ID Q6J3N4
 AC Q6J3N4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Antiviral protein PAP (Fragment).
 GN Name=pap;
 OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Phytolaccaceae; Phytolacca.
 OX NCBI_TaxID=3527;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen G., Lei J., Cao B., Zeng G.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AY603352; AAT12447.1; -.
 DR HSP; Q03464; LAPA.
 DR GO:0016787; F:hydrolase activity; IEA.
 DR GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO:0006952; P:defense response; IEA.
 DR GO:00017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 FT NON_TER 1

SQ SEQUENCE 237 AA; 26622 MW; FE576A3C96A1F6C6 CRC64;

Query Match 21.4%; Score 276; DB 2; Length 237;
 Best Local Similarity 30.2%; Pred. No. 5.6e-15;
 Matches 75; Conservative 45; Mismatches 96; Indels 32; Gaps 8;

QY 2 LDTVSFSTKGATYITYVNFNLRLVKLK-PEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 Db 1 VNTIYVGVSTTSISKYATFLDLRLNEAKDPSLKCYGIPMLPNTNTPK--YVLVELQGSN 58
 QY 61 GOLAEIAIDVTSVYVVGQ-----VNRSYFFKD-----APDAAYEGLFKNT 102
 Db 59 KKTITLMLRNNLYVMGYSDPFTNKRVIHFNDSIGTERQDVETTLCPNA-----NSR 112
 QY 103 IKTRLHFGGSYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENADINYKPTIASSLLVV 160
 Db 113 VSKNINFDISRYPTLSKAGVKSRSQVLGIQILDNSNIGKI--SGVMSFTEKTEAEFLVA 170
 QY 161 IQMVSEARFTIENQIRNFOORIPANNITISLENKMGKLSFQIRTSANGMFSEAVEL 220
 Db 171 IQMVSEARFKYIENQVNFNFRAFPNPKVNLQETWGIKSTAIH-DKANGVLPKPLEL 229
 QY 221 ERANGKKY 228
 Db 230 VDASGAKW 237

RESULT 15
 Q9ATB3 PRELIMINARY; PRT; 237 AA.

ID Q9ATB3
 AC Q9ATB3;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Antiviral protein (Fragment).
 GN Name=mpap;
 OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Phytolaccaceae; Phytolacca.
 OX NCBI_TaxID=3527;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen D., Wang X., Zhou G.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AF338910; AAK21951.1; -.
 DR HSP; F10297; IDGA.
 DR GO:0016787; F:hydrolase activity; IEA.
 DR GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO:0006952; P:defense response; IEA.
 DR GO:00017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 26534 MW; FE4ADCEE03464783 CRC64;

Query Match 21.4%; Score 276; DB 2; Length 237;
 Best Local Similarity 30.2%; Pred. No. 5.6e-15;
 Matches 75; Conservative 45; Mismatches 96; Indels 32; Gaps 8;

QY 2 LDTVSFSTKGATYITYVNFNLRLVKLK-PEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 Db 1 VNTIYVGVSTTSISKYATFLDLRLNEAKDPSLKCYGIPMLPNTNTPK--YVLVELQGSN 58
 QY 61 GOLAEIAIDVTSVYVVGQ-----VNRSYFFKD-----APDAAYEGLFKNT 102

Db	59	KKTITLMLRRNNLYVMGYSDPPEANKCRVHFNDISGTERQDVETTLCPNA-----NSR	112
Qy	103	IKTRLHFGGSYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENAIKNYKPTIASSILVW	160
Db	113	VSKNINFDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKI--SGVMSFTEKTEAEFLVA	170
Qy	161	IQMVSEAAARFTFIENQIRNNFOORIRPANNTISLENKWGLSFQIRTSANGMFSEAVEL	220
Db	171	IQMVSEAAARFKYIENQVKTNFNRAFNPNPKVLNQETWGTKYSTAIH-GAKNGVLPKPLEL	229
Qy	221	ERANGKY	228
Db	230	VDASGAKW	237

Search completed: June 20, 2005, 09:47:11
Job time : 113.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:21:47 ; Search time 113.5 Seconds
(without alignments)
855,303 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDVSFSTKGNITYTYNF.....AVDQVKPKIALLKFDKDKP 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1545266

Minimum DB seq length: 0

Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	251	2 AAR63903	Aar63903 Type I ri
2	1287	100.0	251	8 ADG63044	Adg63044 Gelonin
3	1282	99.6	251	2 AAR63923	Aar63923 Type I RI
4	1279	99.4	251	2 AAR63921	Aar63921 Type I RI
5	1279	99.4	251	2 AAR63918	Aar63918 Type I RI
6	1279	99.4	251	2 AAR63920	Aar63920 Type I RI
7	1279	99.4	251	2 AAR63919	Aar63919 Type I RI
8	1279	99.4	251	2 AAR63924	Aar63924 Type I RI
9	1278	99.3	251	2 AAR63922	Aar63922 Type I RI
10	1278	99.3	251	2 AAR63917	Aar63917 Type I RI
11	1278	99.3	251	2 AAR63912	Aar63912 Type I RI
12	1275	99.1	251	2 AAR74177	Aar74177 Type I ri
13	1269	98.6	251	2 AAR37291	Aar37291 Plant typ
14	1269	98.6	251	2 AAR63914	Aar63914 Type I RI
15	1261	98.0	251	2 AAR63915	Aar63915 Type I RI
16	1252	97.3	251	2 AAR63916	Aar63916 Type I RI
17	1176	91.4	235	2 AAR63913	Aar63913 Type I RI
18	321	24.9	247	3 AAR69048	Aay69048 Amino aci
19	321	24.9	248	2 AAR07518	Aar07518 Synthetic
20	321	24.9	248	2 AAR25573	Aar25573 Mature al
21	320	24.9	247	2 AAR67359	Aar67359 Trichosan
22	315	24.5	247	2 AAR21605	Aar21605 Antitumou
23	315	24.5	251	2 AAW14228	Aaw14228 Mature po
24	314	24.4	247	2 AAW14232	Aaw14232 Mature po
25	314	24.4	248	2 AAW14231	Aaw14231 Mature po

26	314	24.4	249	2 AAW14230	Aaw14230 Mature po
27	314	24.4	250	2 AAW14229	Aaw14229 Mature po
28	314	24.4	251	3 AAB19267	Aab19267 Amino aci
29	314	24.4	251	7 ADC24290	Adc24290 A. precat
30	307.5	23.9	250	2 AAW21700	Aaw21700 Abrin-A A
31	307.5	23.9	250	2 AAW25137	Aaw25137 Abrin-A A
32	307	23.9	244	2 AAW14235	Aaw14235 Mature po
33	307	23.9	245	2 AAW14234	Aaw14234 Mature po
34	307	23.9	246	2 AAW14233	Aaw14233 Mature po
35	307	23.9	247	3 AAY69043	Aay69043 Amino aci
36	307	23.9	248	4 AAB36824	Aab36824 Residues
37	301	23.4	243	2 AAW14236	Aaw14236 Mature po
38	300	23.3	246	2 AAR52636	Aar52636 Bioactive
39	297	23.1	242	2 AAW14237	Aaw14237 Mature po
40	291	22.6	241	2 AAW14238	Aaw14238 Mature po
41	289	22.5	240	2 AAW14239	Aaw14239 Mature po
42	288.5	22.4	233	2 AAW14246	Aaw14246 Mature po
43	288.5	22.4	234	2 AAW14245	Aaw14245 Mature po
44	288.5	22.4	235	2 AAW14244	Aaw14244 Mature po
45	288.5	22.4	236	2 AAW14243	Aaw14243 Mature po

ALIGNMENTS

RESULT 1

AAR63903
ID AAR63903 standard; protein; 251 AA.

XX AAR63903;

XX 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)

XX Type I ribosome-inactivating protein gelonin.

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

XX N-PSDB; AAQ75532.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
are suitable for use as components of cytotoxic therapeutic agents.

XX Example 1; Fig 1; 221pp; English.

XX AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
components of cytotoxic therapeutic agents (CTAs), which include gene
fusion products and immunoconjugates. CTAs may be used to selectively
eliminate any cell type to which a RIP component is targeted, by the
specific binding capacity of the second component of the agent. They can
be used in the treatment of diseases where the elimination of a
particular cell type is desired, such as autoimmune disease, cancer and
graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 251 AA;

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFLELRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTPIASLLVVIOMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTPIASLLVVIOMVSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTVAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2
ADG63044
ID ADG63044 standard; protein; 251 AA.
AC ADG63044;
DT 11-MAR-2004 (first entry)
DE Gelonium anti-HIV protein 3kDa (GAP31).
KW anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
KW GAP31; HIV; tumour; gelonium anti-HIV protein 3kDa.
OS Gelonium multiflorum.
XX US6652861-B1.
XX 25-NOV-2003.
XX 25-AUG-2000; 2000US-00645603.
XX 26-AUG-1999; 99US-0150885P.
XX (UYNV) UNIV NEW YORK STATE.
PI Lee-Huang S;
XX WPI; 2004-050519/05.
XX New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
PT antiviral activity, useful for treating human immunodeficiency virus
PT infection or tumor.
XX
XX Example 1; SEQ ID NO 2; 22pp; English.
PS The invention describes an isolated peptide or polypeptide having an anti
CC tumour and antiviral activity. Also described is a composition
CC comprising the isolated peptide or polypeptide, and a carrier, excipient
CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
CC polypeptides. The peptide or polypeptide is useful for treating HIV
CC infection, and tumour. This is the amino acid sequence of Gelonium anti-
CC HIV protein 30kDa (MAP30).
XX
XX Sequence 251 AA;

Query Match 100.0%; Score 1287; DB 8; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.6e-125;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFLELRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTPIASLLVVIOMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTPIASLLVVIOMVSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTVAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3
AAR63923
ID AAR63923 standard; protein; 251 AA.
XX AAR63923;
AC AAR63923;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX Type I RIP gelonin analog Gel(C103).
XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX Gelonium multiflorum.
XX WO9426910-A1.
XX 24-NOV-1994.
XX 12-MAY-1994; 94WO-US005348.
XX 12-MAY-1993; 93US-00064691.
XX (XOMA) XOMA CORP.
XX Better MD, Carroll SP, Studnicka GM;
XX WPI; 1995-006804/01.
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX Example 3; Page 187-188; 221pp; English.
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 251 AA;

Query Match 99.6%; Score 1282; DB 2; Length 251;

	Best Local Similarity	99.6%; Pred. No. 5.3e-125;	Matches 250;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	GLDTVSFSTKGATYYTVN	FLNELRVKLPKPGNSHGIP	LLRKKCCDDPKCFVL	VALSNDN	60	
Db	1	GLDTVSFSTKGATYYTVN	FLNELRVKLPKPGNSHGIP	LLRKKCCDDPKCFVL	VALSNDN	60	
Qy	61	GQLAEIAIDVTSVVVVG	YQVRNRSYFFKDAPDAAYEGL	FKNTIKTRLHFGGSYPSL	SGEK	120	
Db	61	GQLAEIAIDVTSVVVVG	YQVRNRSYFFKDAPDAAYEGL	FKNTIKTRLHFGGSYPSL	SGEK	120	
Qy	121	AYRETTDLGTEPLRIGIK	KL DENAIDN	YKPTETIASSLLV	IQMYSEARFTFIENQ	180	
Db	121	AYRETTDLGTEPLRIGIK	KL DENAIDN	YKPTETIASSLLV	IQMYSEARFTFIENQ	180	
Qy	181	FQQRIRPANNTISLENK	WGKLSFOIRTSGANGMFSEAV	ELERANGKKYYVTAVDQV	KPKI	240	
Db	181	FQQRIRPANNTISLENK	WGKLSFOIRTSGANGMFSEAV	ELERANGKKYYVTAVDQV	KPKI	240	
Qy	241	ALLKFVDKDPK	251				
Db	241	ALLKFVDKDPK	251				

RESULT 4	
AAR63921	
ID	AAR63921 standard; protein; 251 AA.
XX	
XX	AAR63921;
XX	
DT	25-MAR-2003 (revised)
DT	27-JUL-1995 (first entry)
XX	
XX	Type I RIP gelonin analog Gel(C10).
XX	
XX	Type I ribosome-inactivating proteins; RIPS; gelonin;
KW	cytotoxic therapeutic agents; autoimmune disease; cancer;
KW	graft-versus-host disease.
XX	
XX	
OS	Gelonium multiflorum.
XX	
XX	WO9426910-A1.
PN	
XX	
PD	24-NOV-1994.
XX	
XX	12-MAY-1994; 94WO-US005348.
PF	
XX	
XX	12-MAY-1993; 93US-00064691.
PR	
XX	
XX	(XOMA) XOMA CORP.
PA	
XX	
PI	Better MD, Carroll SF, Studnicka GM;
PI	
DR	WPI; 1995-006804/01.
DR	
XX	
PT	Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT	are suitable for use as components of cytotoxic therapeutic agents.
XX	
PS	Example 3; Page 186; 221pp; English.
PS	
XX	
CC	AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC	protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC	RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC	include gene fusion products and immunoconjugates. CTAs may be used to
CC	selectively eliminate any cell type to which a RIP component is
CC	targeted. By the specific binding capacity of the second component of
CC	the agent. They can be used in the treatment of diseases where the
CC	elimination of a particular cell type is desired, such as autoimmune
CC	disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC	correct PN field.)
XX	
SQ	Sequence 251 AA;
SQ	

Query Match	99.4%;	Score 1279;	DB 2;	Length 251;
Best local Similarity	99.6%;	Pred. No. 1.le-124;		
Matches 250;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1	GLDTVSFSTKGATVITYVNFNLNLRVVKLKEPGRSHGIPLLRKCKDDPKGKCFVLVALSNDN	60	
DB	1	GLDTVSFSTGCAYITYVNFNLNLRVVKLKEPGRSHGIPLLRKCKDDPKGKCFVLVALSNDN	60	
QY	61	GQLAEIAIDVTSVVVVGYYQVRNRSYFFKDPADPAAYEGLFKNITKTRLHFGGSYPSLEGEK	120	
DB	61	GQLAEIAIDVTSVVVVGYYQVRNRSYFFKDPADPAAYEGLFKNITKTRLHFGGSYPSLEGEK	120	
QY	121	AYRETTDLGTEPIRIGIKKLDENAIDNRYKPTETASSLLVVIQWYSEAAARFTFIENQIRNN	180	
DB	121	AYRETTDLGTEPIRIGIKKLDENAIDNRYKPTETASSLLVVIQWYSEAAARFTFIENQIRNN	180	
QY	181	FQQRIRPANNTISLENKWKGLSFQIRTSYGANGWPFSEAVELERANGKYYVTVAVDQVKPKI	240	
DB	181	FQQRIRPANNTISLENKWKGLSFQIRTSYGANGWPFSEAVELERANGKYYVTVAVDQVKPKI	240	
QY	241	ALLKFVDKPK 251		
DB	241	ALLKFVDKPK 251		
RESULT 5				
AAAR63918		ID	AAAR63918	standard; protein; 251 AA.
XX		AC	AAAR63918;	
XX		DT	25-MAR-2003	(revised)
XX		DT	27-JUL-1995	(first entry)
XX		DE	Type I RIP gelonin analog Gel(C248).	
XX		KW	Type I ribosome-inactivating proteins; RIPs; gelonin;	
XX		KW	cytotoxic therapeutic agents; autoimmune disease; cancer;	
XX		KW	graft-versus-host disease.	
XX		OS	Gelonium multiflorum.	
XX		PN	W09426910-A1.	
XX		PD	24-NOV-1994.	
XX		PF	12-MAY-1994; 94WO-US005348.	
XX		PR	12-MAY-1993; 93US-00064691.	
XX		PA	(XOMA) XOMA CORP.	
XX		PI	Better MD, Carroll SF, Studnicka GM;	
XX		DR	WPI; 1995-006804/01.	
XX		PT	Polynucleotide(s) encoding type I ribosome-inactivating proteins - which	
XX		PS	are suitable for use as components of cytotoxic therapeutic agents.	
XX		PS	Example 3; Page 183-184; 221pp; English.	
XX		CC	AAAR63912-R63924 are analogs of AAAR63903 type I ribosome-inactivating	
XX		CC	protein (RIP) gelonin, one of the nine RIPs described in AAAR63903-R63911.	
XX		CC	RIPs are key components of cytotoxic therapeutic agents (CTAs), which	
XX		CC	include gene fusion products and immunoconjugates. CTAs may be used to	
XX		CC	selectively eliminate any cell type to which a RIP component is	
XX		CC	targeted, by the specific binding capacity of the second component of	
XX		CC	the agent. They can be used in the treatment of diseases where the	
XX		CC	elimination of a particular cell type is desired, such as autoimmune	
XX		CC	disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to	
XX		CC	correct FN field.)	
XX		CC	Sequence 251 AA;	
XX		CC	Sequence 251 AA;	

Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60

QY 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 6
AAR63920
ID AAR63920 standard; protein; 251 AA.
AC AAR63920;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C244).
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
XX 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
XX
PS Example 3; Page 185; 221pp; English.
XX
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
XX correct PN field.)

SQ Sequence 251 AA;
Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60

QY 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVVVGQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 7
AAR63919
ID AAR63919 standard; protein; 251 AA.
XX
AC AAR63919;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C239).
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
XX 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
XX
PS Example 3; Page 184; 221pp; English.
XX
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
XX correct PN field.)

XX Sequence 251 AA;
 SQ
 Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.1e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GLDTSFSFGKATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
 DB 1 GLDTSFSFGKATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSSVPSLEGEK 120
 DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSSVPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 8
 AAR63924
 ID AAR63924 standard; protein; 251 AA.
 XX
 AC AAR63924;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 DE Type I RIP gelonin analog Gel (C184).
 XX
 KW Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 OS Gelonium multiflorum.
 XX
 PN WO9426910-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US005348.
 XX
 PR 12-MAY-1993; 93US-00064691.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD, Carroll SF, Studnicka GM;
 XX
 DR WPI; 1995-006804/01.
 XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.
 XX
 PS Example 3; Page 188-189; 221pp; English.
 XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

CC correct PN field.)
 XX Sequence 251 AA;
 SQ
 Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.1e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GLDTSFSFGKATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
 DB 1 GLDTSFSFGKATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
 QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSSVPSLEGEK 120
 DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSSVPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 9
 AAR63922
 ID AAR63922 standard; protein; 251 AA.
 XX
 AC AAR63922;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 DE Type I RIP gelonin analog Gel (C60).
 XX
 KW Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 OS Gelonium multiflorum.
 XX
 PN WO9426910-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US005348.
 XX
 PR 12-MAY-1993; 93US-00064691.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD, Carroll SF, Studnicka GM;
 XX
 DR WPI; 1995-006804/01.
 XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.
 XX
 PS Example 3; Page 187; 221pp; English.
 XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 99.3%; Score 1278; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKKCDPDKCFVLVALSND 60
QY 61 GOLAEIADVTSVVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIADVTSVVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 10
AAR63917
ID AAR63917 standard; protein; 251 AA.
XX
AC AAR63917;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C247).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 182-183; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the

CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 99.3%; Score 1278; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRVCLKPEGNHGIPLLRKKCDPDKCFVLVALSND 60
QY 61 GOLAEIADVTSVVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIADVTSVVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
AAR63912
ID AAR63912 standard; protein; 251 AA.
XX
AC AAR63912;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (A50/C44).
XX
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 179-180; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of

CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 99.3%; Score 1278; DB 2; Length 251;
 Best Local Similarity 99.8%; Pred. No. 1.4e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLNLRVRLKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYTYVNFNLNLRVRLKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLHFGGSPVLEGEK 120
 DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLHFGGSPVLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAFTFIENQIRNN 180

QY 181 FQORIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240
 DB 181 FQORIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240

QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 12
 AAR74177
 ID AAR74177 standard; protein; 251 AA.
 XX
 AC AAR74177;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-JAN-1980 (first entry)
 XX
 DE Type I ribosome-inactivating protein gelonin.
 XX
 KW Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin.
 XX
 OS Gelonium multiflorum.
 FH Key Location/Qualifiers
 FT Misc-difference 10 /label= Cys in claimed analogue
 FT Misc-difference 17 /label= invariant residue
 FT /note= "in ricin A-chain and the Type I RIPS"
 FT Misc-difference 25 /label= see above
 FT Misc-difference 44 /label= non-Cys residue in claimed analogue
 FT Misc-difference 44 /label= Ala in claimed analogue
 FT Misc-difference 50 /label= Non-Cys residue in claimed analogue
 FT Misc-difference 50 /label= see above
 FT Misc-difference 60 /label= Cys in claimed analogue
 FT Misc-difference 74 /label= see above
 FT Misc-difference 113 /label= see above
 FT Misc-difference 133 /label= see above
 FT Misc-difference 166..167 /label= see above

FT Misc-difference 169 /label= see above
 FT Misc-difference 198 /label= see above
 FT Misc-difference 239..251 /label= location of Cys in claimed analogue
 FT Misc-difference 239 /label= see above
 FT Misc-difference 244 /label= Cys in claimed analogue
 FT Misc-difference 247..248 /label= see above
 FT Misc-difference 247 /label= see above
 XX
 PN US5416202-A.
 XX
 PD 16-MAY-1995.
 XX
 XX 09-DEC-1992; 92US-00988430.
 PF
 PR 04-NOV-1991; 91US-00787567.
 PR 19-JUN-1992; 92US-00901707.
 XX
 PA (XOMA) XOMA CORP.
 XX
 XX Lei S, Carroll SF, Lane JA, Bernhard SL, Better MD;
 XX WPI; 1995-193480/25.
 DR
 XX Polynucleotide(s) encoding gelonin analogues - having a cysteine residue
 PT for intermolecular bonding for the prodn. of immuno-toxin(s).
 PT
 XX Claim 1; Fig 1; 66pp; English.
 PS
 XX Analogues of Type I RIP are defined as non-naturally occurring
 CC polypeptides that share the ribosome-inactivating activity of the natural
 CC protein but differ in AA sequence. Preferred analogues have a Cys
 CC available for disulfide bonding located at a posn. it its AA sequence
 CC from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy
 CC terminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA,
 CC which is a Type II RIP). The primary AA sequence of the Type I RIPS
 CC gelonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural
 CC Biological Chem., 54(5) 1343-45 1991], alphatrachosanthin [see Chow et
 CC al., J. Biol. Chem., 265, 8670-74 1990], momordin I [see Ho et al., BBA,
 CC 1088, 311-14 1991], Mirabilis antiviral protein [see Habuka et al., J.
 CC Biol. Chem., 264(12) 6629-37 1989], pokeweed antiviral protein isolated
 CC from seeds [see Kung et al., Agric. Biol. Chem., 54(12), 3301-18 1990]
 CC and saporin [see Banatti et al., Eur. J. Biochem., 183, 465-70 1989] are
 CC individually aligned with the primary sequence of the ricin A-chain [see
 CC Halling et al., Nucleic Acids Res., 13, 8019-8033 1985] respectively in
 CC Figures 1-9. The AAs invariant among the ricin A-chain and the type I
 CC RIPS are indicated in FT. Also indicated are the preferred sites of Cys
 CC substitution. It is also preferred that the gelonin cysteine residues at
 CC positions 44 and 50 be replaced with alanine residues. (Updated on 25-MAR
 CC -2003 to correct PR field.)
 XX
 SQ Sequence 251 AA;

Query Match 99.1%; Score 1275; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 2.8e-124;
 Matches 249; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLNLRVRLKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYTYVNFNLNLRVRLKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLHFGGSPVLEGEK 120
 DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTLHFGGSPVLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
 |||||
 Db 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
 |||||
 QY 241 ALLKFVDKDPK 251
 |||||
 Db 241 ALLKFVDKDPK 251
 |||||

RESULT 13
 AAR37291
 ID AAR37291 standard; protein; 251 AA.
 XX
 AC AAR37291;
 DT 25-MAR-2003 (revised)
 DT 13-SEP-1993 (first entry)
 XX
 XX Plant type I RIP Gelonin.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
 KW autoimmune disease; cell killing; toxin; Euphorbiaceae family.

XX Gelonium multiflorum.
 OS WO9309130-A1.
 PN
 XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.
 PF
 XX 04-NOV-1991; 91US-00787567.
 PR 19-JUN-1992; 92US-00901707.
 XX
 XX (XOMA) XOMA CORP.

XX Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
 PI WPI; 1993-167617/20.
 XX

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic
 PT agents, immuno toxins for treating auto immune diseases, cancer, graft
 PT versus host disease and selective cell killing in-vivo.

PS Claim 2; Page 93; 163pp; English.

XX The invention covers analogues of Type I RIPs. Gelonin is a Type I RIP
 CC and the analogues of the invention have a cysteine available for
 CC intermolecular disulphide bonding at an amino acid position corresp. to a
 CC position not naturally available for bonding; the cys residue is located
 CC in the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX

SQ Sequence 251 AA;

Query Match 98.6%; Score 1269; DB 2; Length 251;
 Best Local Similarity 98.8%; Pred. No. 1.2e-123;
 Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYYNFLNELRVKLKPEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||

Db 1 GLDTSFSTKGATYITYYNFLNELRVKLKPEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
 |||||

Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
 |||||

QY 121 AYRETTDLGIEPLRIGIKKLDENAINDKYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 |||||

Db 121 AYRETTDLGIEPLRIGIKKLDENAINDKYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 |||||

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
 |||||
 Db 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
 |||||
 QY 241 ALLKFVDKDPK 251
 |||||
 Db 241 ALLKFVDKDPK 251
 |||||

RESULT 14
 AAR63914
 ID AAR63914 standard; protein; 251 AA.
 XX
 AC AAR63914;
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX
 XX Type I RIP gelonin analog Gel (A44/A50).

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

OS Gelonium multiflorum.

PN WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

PR 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

PI Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

PS Example 3; Page 181-182; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX

SQ Sequence 251 AA;

Query Match 98.6%; Score 1269; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 1.2e-123;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYYNFLNELRVKLKPEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||

Db 1 GLDTSFSTKGATYITYYNFLNELRVKLKPEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
 |||||

Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
 |||||

QY 121 AYRETTDLGIEPLRIGIKKLDENAINDKYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
 |||||

Db 121 AVRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKKYVYVTAVDQVKPKI 240
Db 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKKYVYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 15

AAR63915
ID AAR63915 standard; protein; 251 AA.

XX AAR63915;

XX 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel (C10/A44/A50).

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
XX graft-versus-host disease.

OS Gelonium multiflorum.

XX PN W09426910-A1.

XX PD 24-NOV-1994.

XX PF 12-MAY-1994; 94WO-US005348.

XX PR 12-MAY-1993; 93US-00064691.

XX PA (XOMA) XOMA CORP.

XX PI Better MD, Carroll SF, Studnicka GM;

XX DR WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.

XX Example 3; Page 189-190; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX Sequence 251 AA;

SQ

Query Match 98.0%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 8.2e-123;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITVYNFLNELRVKLPKGNHSHGIPLLRKKDDPDGKCFVLVALSNDN 60
Db 1 GLDTSFSTKGATYITVYNFLNELRVKLPKGNHSHGIPLLRKKDDPDGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120
QY 121 AVRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180

Db 121 AVRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKKYVYVTAVDQVKPKI 240
Db 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKKYVYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:43:20
Job time : 114.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:47:23 ; Search time 104.5 Seconds
(without alignments)
922.286 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDVSFSTKGNITYTYNF.....AVDQVKPKIALKFFVDKDKP 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1177303

Minimum DB seq length: 0
Maximum DB seq length: 251

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	251	9	US-09-765-527-247
2	1287	100.0	251	17	US-10-127-890-2
3	1287	100.0	251	14	US-10-717-243-2
4	1282	99.6	251	14	US-10-127-890-108
5	1282	99.6	251	17	US-10-717-243-103
6	1279	99.4	251	14	US-10-127-890-104
7	1279	99.4	251	14	US-10-127-890-105
8	1279	99.4	251	14	US-10-127-890-106
9	1279	99.4	251	14	US-10-127-890-109
10	1279	99.4	251	14	US-10-717-243-103
11	1279	99.4	251	17	US-10-717-243-103

12	1279	99.4	251	17	US-10-717-243-104	Sequence 104, App
13	1279	99.4	251	17	US-10-717-243-105	Sequence 105, App
14	1279	99.4	251	17	US-10-717-243-106	Sequence 106, App
15	1279	99.4	251	17	US-10-717-243-109	Sequence 109, App
16	1278	99.3	251	14	US-10-127-890-99	Sequence 99, Appl
17	1278	99.3	251	14	US-10-127-890-100	Sequence 100, App
18	1278	99.3	251	14	US-10-127-890-102	Sequence 102, App
19	1278	99.3	251	14	US-10-127-890-107	Sequence 107, App
20	1278	99.3	251	17	US-10-717-243-99	Sequence 99, Appl
21	1278	99.3	251	17	US-10-717-243-100	Sequence 100, App
22	1278	99.3	251	17	US-10-717-243-102	Sequence 102, App
23	1278	99.3	251	17	US-10-717-243-107	Sequence 107, App
24	1269	98.6	251	14	US-10-127-890-101	Sequence 101, App
25	1269	98.6	251	17	US-10-717-243-101	Sequence 101, App
26	1261	98.0	251	14	US-10-127-890-110	Sequence 110, App
27	1261	98.0	251	17	US-10-717-243-110	Sequence 110, App
28	1252	97.3	251	14	US-10-127-890-111	Sequence 111, App
29	1252	97.3	251	17	US-10-717-243-111	Sequence 111, App
30	321	24.9	247	9	US-09-792-793A-39	Sequence 39, Appl
31	321	24.9	247	15	US-10-375-209A-39	Sequence 39, Appl
32	316	24.6	247	14	US-10-127-890-6	Sequence 6, Appli
33	316	24.6	247	17	US-10-717-243-6	Sequence 6, Appli
34	314	24.4	251	14	US-10-282-935-3	Sequence 3, Appli
35	314	24.4	251	15	US-10-440-796-3	Sequence 3, Appli
36	307	23.9	247	9	US-09-792-793A-34	Sequence 34, Appl
37	307	23.9	247	15	US-10-375-209A-34	Sequence 34, Appl
38	273	21.2	248	14	US-10-127-890-5	Sequence 5, Appli
39	273	21.2	248	17	US-10-717-243-5	Sequence 5, Appli
40	246.5	19.2	190	14	US-10-083-336A-11	Sequence 11, Appl
41	245.5	19.1	200	14	US-10-083-336A-10	Sequence 10, Appl
42	243.5	18.9	188	14	US-10-083-336A-4	Sequence 4, Appli
43	243.5	18.9	188	14	US-10-083-336A-8	Sequence 8, Appli
44	243.5	18.9	189	14	US-10-083-336A-6	Sequence 6, Appli
45	242.5	18.8	198	14	US-10-083-336A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-765-527-247

; Sequence 247, Application US/09765527

; Patent No. US20020006638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of

; Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/09/765,527

; FILING DATE: 18-Jan-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803

; FILING DATE: <Unknown>

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

```
;
;
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 251 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match      100.0%; Score 1287; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.8e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITYVNFLELRVCLKPGENSHGIPLLRKKCDGPKCFVLVALSNDN 60
Db 1 GLDVSFSTKGATYITYVNFLELRVCLKPGENSHGIPLLRKKCDGPKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

US-10-127-890-2

RESULT 2
US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992

;
;
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 251 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match      100.0%; Score 1287; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.8e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITYVNFLELRVCLKPGENSHGIPLLRKKCDGPKCFVLVALSNDN 60
Db 1 GLDVSFSTKGATYITYVNFLELRVCLKPGENSHGIPLLRKKCDGPKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

US-10-127-890-2

RESULT 3
US-10-717-243-2
; Sequence 2, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
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; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match          100.0%; Score 1287; DB 17; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.8e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 4
US-10-127-890-108
; Sequence 108, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match          99.6%; Score 1282; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKKYVYVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5
US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/717,243
;; FILING DATE: 18-Nov-2003
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/839,765
;; FILING DATE: 15-APR-1997
;; APPLICATION NUMBER: US/08/425,336
;; FILING DATE: 18-APR-1995
;; APPLICATION NUMBER: US/08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION NUMBER: US/07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION NUMBER: US/07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US/07/787,567
;; FILING DATE: 04-NOV-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;;
;; INFORMATION FOR SEQ ID NO: 108:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 108:

US-10-717-243-108

Query Match 99.6%; Score 1282; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYYTYVNFNLRLVRLKPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATYYTYVNFNLRLVRLKPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIADVTSVVYGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIADVTSVVYGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARFTFIENQIRN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARFTFIENQIRN 180

QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 6

US-10-127-890-103

;; Sequence 103, Application US/10127890
;; Publication No. US20030166196A1
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; Carroll, Stephen F.
;; Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/127,890
;; FILING DATE: 23-Apr-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; APPLICATION NUMBER: US/08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION NUMBER: US/07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION NUMBER: US/07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US/07/787,567
;; FILING DATE: 04-NOV-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;;
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 103:

US-10-127-890-103

Query Match 99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYYTYVNFNLRLVRLKPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATYYTYVNFNLRLVRLKPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIADVTSVVYGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIADVTSVVYGVQVRNRSYFFKDPADAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARFTFIENQIRN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARFTFIENQIRN 180

QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
RESULT 7
US-10-127-890-104
; Sequence 104, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-890-104
Query Match 99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYYTVNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVLSNDN 60
Db 1 GLDTSFSTKGATYYTVNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVLSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLEFKNTIKTRLHFGGSPSLEGEK 120

Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLEFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTBIASSLLVVIQWVSEAAFTTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTBIASSLLVVIQWVSEAAFTTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
RESULT 8
US-10-127-890-105
; Sequence 105, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105


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;
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-127-890-109

Query Match          99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGVSPLSEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGVSPLSEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
US-10-717-243-103
; Sequence 103, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
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;
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-717-243-103

Query Match          99.4%; Score 1279; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGVSPLSEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGVSPLSEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12
US-10-717-243-104
; Sequence 104, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-717-243-104

Query Match 99.4%; Score 1279; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNITISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
DB 181 FOORIRPANNITISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
US-10-717-243-105
; Sequence 105, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; ;
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-717-243-105
Query Match 99.4%; Score 1279; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVVGQVRRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNITISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
DB 181 FOORIRPANNITISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
US-10-717-243-106
; Sequence 106, Application US/10717243

Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-10-717-243-106

Query Match 99.4%; Score 1279; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GLAEIAIDVTSVYVGYQVRNRSYFFKADPAAAYEGLFKNTIKTLRHFGGSPSLEGEK 120
DB 61 GLAEIAIDVTSVYVGYQVRNRSYFFKADPAAAYEGLFKNTIKTLRHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAINDKYPTETAIASSLLVVIQVMSAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAINDKYPTETAIASSLLVVIQVMSAARFTFIENQIRNN 180
QY 181 FQORIRPANNITSLNKGWKLSPQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNITSLNKGWKLSPQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 15
US-10-717-243-109
Sequence 109, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-717-243-109

Query Match 99.4%; Score 1279; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGTATYYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GLAEIAIDVTSVYVGYQVRNRSYFFKADPAAAYEGLFKNTIKTLRHFGGSPSLEGEK 120

Db	61	GOLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	120
Qy	121	AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIOMVSEAAFTFIENQIRNN	180
Db	121	AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIOMVSEAAFTFIENQIRNN	180
Qy	181	FQOCIRPANNTISLENKWKLSFQIRTSGANGMFSEAVELEERANGKYYVTVAVDQVKPKI	240
Db	181	FQOCIRPANNTISLENKWKLSFQIRTSGANGMFSEAVELEERANGKYYVTVAVDQVKPKI	240
Qy	241	ALLKFVDKDPK	251
Db	241	ALLKFVDKDPK	251

Search completed: June 20, 2005, 10:05:45
Job time : 105.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:10:06 ; Search time 30 Seconds
(without alignments)
624.564 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGTATITVNF.....AVDQVKPKIALKFFVDKPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1287	100.0	251	1 US-08-488-113B-2	Sequence 2, Appli
3	1287	100.0	251	1 US-08-477-484B-2	Sequence 2, Appli
4	1287	100.0	251	2 US-08-646-360-2	Sequence 2, Appli
5	1287	100.0	251	2 US-08-621-803-247	Sequence 247, App
6	1287	100.0	251	3 US-08-839-765-2	Sequence 2, Appli
7	1287	100.0	251	3 US-09-136-389-2	Sequence 2, Appli
8	1287	100.0	251	3 US-09-217-352-247	Sequence 247, App
9	1287	100.0	251	3 US-09-610-838-2	Sequence 2, Appli
10	1287	100.0	251	4 US-09-711-485-2	Sequence 2, Appli
11	1287	100.0	251	4 US-09-645-603B-2	Sequence 2, Appli
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13	1284	99.8	251	1 PCT-US92-09487-2	Sequence 2, Appli
14	1284	99.8	251	5 PCT-US92-09487-2	Sequence 259, App
15	1284	99.8	293	2 US-08-621-803-259	Sequence 259, App
16	1284	99.8	293	3 US-09-217-352-259	Sequence 259, App
17	1284	99.8	309	2 US-08-621-803-253	Sequence 253, App
18	1284	99.8	309	3 US-09-217-352-253	Sequence 253, App
19	1284	99.8	332	2 US-08-621-803-251	Sequence 251, App
20	1284	99.8	332	3 US-09-217-352-251	Sequence 251, App
21	1282	99.6	251	1 US-08-425-336-108	Sequence 108, App
22	1282	99.6	251	1 US-08-488-113B-108	Sequence 108, App
23	1282	99.6	251	1 US-08-477-484B-108	Sequence 108, App
24	1282	99.6	251	2 US-08-646-360-108	Sequence 108, App
25	1282	99.6	251	3 US-08-839-765-108	Sequence 108, App
26	1282	99.6	251	3 US-09-136-389-108	Sequence 108, App
27	1282	99.6	251	3 US-09-610-838-108	Sequence 108, App

28 1282 99.6 251 4 US-09-711-485-108 Sequence 108, App
29 1279 99.4 251 1 US-08-425-336-103 Sequence 103, App
30 1279 99.4 251 1 US-08-425-336-104 Sequence 104, App
31 1279 99.4 251 1 US-08-425-336-105 Sequence 105, App
32 1279 99.4 251 1 US-08-425-336-106 Sequence 106, App
33 1279 99.4 251 1 US-08-425-336-109 Sequence 109, App
34 1279 99.4 251 1 US-08-488-113B-103 Sequence 103, App
35 1279 99.4 251 1 US-08-488-113B-104 Sequence 104, App
36 1279 99.4 251 1 US-08-488-113B-105 Sequence 105, App
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41 1279 99.4 251 1 US-08-477-484B-105 Sequence 106, App
42 1279 99.4 251 1 US-08-477-484B-106 Sequence 109, App
43 1279 99.4 251 2 US-08-646-360-103 Sequence 103, App
44 1279 99.4 251 2 US-08-646-360-103 Sequence 104, App
45 1279 99.4 251 2 US-08-646-360-104 Sequence 104, App

ALIGNMENTS

RESULT 1

US-08-425-336-2

; Sequence 2, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; NUMBER OF INVENTIONS: Proteins

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,336

; FILING DATE: 18-APR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.

; REGISTRATION NUMBER: P-36,989

; REFERENCE/DOCKET NUMBER: 31394

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-425-336-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYTYVNFLELRLVKKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYTYVNFLELRLVKKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANKKKYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANKKKYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2

US-08-488-113B-2
; Sequence 2, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYTYVNFLELRLVKKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYTYVNFLELRLVKKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANKKKYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANKKKYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3
US-08-477-484B-2
; Sequence 2, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-477-484B-2

Query Match      100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPILRRKCDPDKGKCFVLVALSNDN 60
DB 1 GLDTVSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPILRRKCDPDKGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFOIRTSGANGMFSEAVLERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFOIRTSGANGMFSEAVLERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-2
/ Sequence 2, Application US/08646360
/ Patent No. 5837491
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/646,360
/ FILING DATE: 13-MAY-1996
/ CLASSIFICATION: 530
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/ APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-646-360-2

Query Match      100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPILRRKCDPDKGKCFVLVALSNDN 60
DB 1 GLDTVSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPILRRKCDPDKGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAFTFIENQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFOIRTSGANGMFSEAVLERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFOIRTSGANGMFSEAVLERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5
US-08-621-803-247
/ Sequence 247, Application US/08621803
/ Patent No. 5851802
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ TITLE OF INVENTION: Methods for Recombinant Microbial Production of
/ TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-621-803-247

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYYVNFLELRVCLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
Db |||||
Db 1 GLDVSFSTKGATYYVNFLELRVCLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db |||||
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTESIASSLVVIQMVSEAAARFTFIENQIRNN 180
Db |||||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTESIASSLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEFRANGKYYVTVAVDQVKPKI 240
Db |||||
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEFRANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db |||||
Db 241 ALLKFVDKDPK 251

RESULT 6
US-08-839-765-2
; Sequence 2, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-2

Query Match 100.0%; Score 1287; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYYVNFLELRVCLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
Db |||||
Db 1 GLDVSFSTKGATYYVNFLELRVCLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db |||||
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTESIASSLVVIQMVSEAAARFTFIENQIRNN 180
Db |||||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTESIASSLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEFRANGKYYVTVAVDQVKPKI 240
Db |||||
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEFRANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db |||||
Db 241 ALLKFVDKDPK 251

RESULT 7
US-09-136-389-2
; Sequence 2, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
```

STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-2

Query Match 100.0%; Score 1287; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIADVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIBPLRIGIKKLDENADNYKPTIASLLVVIQMVSEARFTFIEQIRNN 180
DB 121 AYRETTDLGIBPLRIGIKKLDENADNYKPTIASLLVVIQMVSEARFTFIEQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 8
US-09-217-352-247
; Sequence 247, Application US/09217352

Patent No. 6274344
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,352
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-217-352-247
Query Match 100.0%; Score 1287; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIADVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVYVGVQVRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIBPLRIGIKKLDENADNYKPTIASLLVVIQMVSEARFTFIEQIRNN 180
DB 121 AYRETTDLGIBPLRIGIKKLDENADNYKPTIASLLVVIQMVSEARFTFIEQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 9
US-09-610-838-2
; Sequence 2, Application US/09610838
; Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.

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/
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/
/ TITLE OF INVENTION: Proteins
/
/ NUMBER OF SEQUENCES: 173
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/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/
/ CITY: Chicago
/
/ STATE: Illinois
/
/ COUNTRY: USA
/
/ ZIP: 60661
/
/ COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: Patent In Release #1.0, Version #1.25
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/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/09/610,838
/
/ FILING DATE: 06-JUL-2000
/
/ CLASSIFICATION:
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/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US/09/136,389
/
/ FILING DATE: 18-AUG-1998
/
/ APPLICATION NUMBER: 08/646,360
/
/ FILING DATE: 13-MAY-1996
/
/ APPLICATION NUMBER: PCT/US94/05348
/
/ FILING DATE: 12-MAY-1994
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 08/064,691
/
/ FILING DATE: 12-MAY-1993
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 07/988,430
/
/ FILING DATE: 09-DEC-1992
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 07/901,707
/
/ FILING DATE: 19-JUN-1992
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 07/787,567
/
/ FILING DATE: 04-NOV-1991
/
/ NAME: McNicholas, Janet M.
/
/ REGISTRATION NUMBER: 32,918
/
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: 312/707-8889
/
/ TELEFAX: 312/707-9155
/
/ TELEX: 650 388-1248
/
/ INFORMATION FOR SEQ ID NO: 2:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 251 amino acids
/
/ TYPE: amino acid
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: protein
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/ US-09-610-838-2
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/ Query Match 100.0%; Score 1287; DB 3; Length 251;
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/ Best Local Similarity 100.0%; Pred. No. 8.6e-125;
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/ Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ Db 1 GLDTSVFSFGKATYTYVNFNLKPKGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
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/ QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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/ Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKDPAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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/ QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPTEIASLLVVIQWSEARFTFIENQIRNN 180
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/ Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPTEIASLLVVIQWSEARFTFIENQIRNN 180
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/ QY 181 FQOIRPANNTISLENKWGLSFQIRTSANGWFSEAVLEBRANGKYYVTAVDQVKPKI 240
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/ Db 181 FQOIRPANNTISLENKWGLSFQIRTSANGWFSEAVLEBRANGKYYVTAVDQVKPKI 240
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QY 241 ALLKFVDKDPK 251
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/ Db 241 ALLKFVDKDPK 251
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/ RESULT 10
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/ US-09-711-485-2
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/ Sequence 2, Application US/09/11485
/
/ Patent No. 6649742
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Better, Marc D.
/
/ APPLICANT: Carroll, Stephen F.
/
/ APPLICANT: Studnika, Gary M.
/
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/
/ TITLE OF INVENTION: Proteins
/
/ NUMBER OF SEQUENCES: 169
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/
/ CITY: Chicago
/
/ STATE: Illinois
/
/ COUNTRY: USA
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/ ZIP: 60661
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/ COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: Patent In Release #1.0, Version #1.25
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/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/09/711,485
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/ FILING DATE:
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/ CLASSIFICATION:
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/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: 08/839,765
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/ FILING DATE:
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/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 08/064,691
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/ FILING DATE: 12-MAY-1993
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/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 07/988,430
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/ FILING DATE: 09-DEC-1992
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/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 07/901,707
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/ FILING DATE: 19-JUN-1992
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/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 07/787,567
/
/ FILING DATE: 04-NOV-1991
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: McNicholas, Janet M.
/
/ REGISTRATION NUMBER: 32,918
/
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
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/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: 312/707-8889
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/ TELEFAX: 312/707-9155
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/ TELEX: 650 388-1248
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/ INFORMATION FOR SEQ ID NO: 2:
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/ SEQUENCE CHARACTERISTICS:
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/ LENGTH: 251 amino acids
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/ TYPE: amino acid
/
/ TOPOLOGY: linear
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/ MOLECULE TYPE: protein
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/ US-09-711-485-2
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/ Query Match 100.0%; Score 1287; DB 4; Length 251;
/
/ Best Local Similarity 100.0%; Pred. No. 8.6e-125;
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/ Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ QY 1 GLDTSVFSFGKATYTYVNFNLKPKGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
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/ Db 1 GLDTSVFSFGKATYTYVNFNLKPKGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
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Db 121 AYRETTDLGIEPLRIGIKKLDENAIQVYKPTIASSLLVVIQVMSAARFTFIENQIRNN 180
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Db 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 11

US-09-645-603B-2
; Sequence 2, Application US/09645603B
; Patent No. 6652861
; GENERAL INFORMATION:
; APPLICANT: LEE-HUANG, Sylvia
; TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of
; TITLE OF INVENTION: map30 and gap31
; FILE REFERENCE: LEE-HUANG 4A
; CURRENT APPLICATION NUMBER: US/09/645,603B
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/150,885
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Gelonium multiflorum
US-09-645-603B-2

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Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 GQLAEIADVTSVYVGYQVRNRSYFFKDPADAAVEGLFKNTIKTLHFGGSPSLEGEK 120
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Db 121 AYRETTDLGIEPLRIGIKKLDENAIQVYKPTIASSLLVVIQVMSAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240
Db 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 12

US-07-901-707-2
; Sequence 2, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; Composition and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-2

Query Match 99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 121 AYRETTDLGIEPLRIGIKKLDENAIQVYKPTIASSLLVVIQVMSAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240
Db 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 13

US-07-988-430-2
; Sequence 2, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping

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; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS: 101
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-988-430-2

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Query Match          99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 241 ALLKFVDKDPK 251

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RESULT 14

PCT-US92-09487-2

; Sequence 2, Application PC/TUS9209487

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

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; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS: 101
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-09487-2

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Query Match          99.8%; Score 1284; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
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RESULT 15

US-08-621-803-259
; Sequence 259, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-621-803-259

Query Match 99.8%; Score 1284; DB 2; Length 293;
Best Local Similarity 99.6%; Pred. No. 2.2e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVLERANGKYYVTAVDQVKPKI 262
QY 241 ALLKFVDKDPK 251
DB 263 ALLKFVDKDPK 273

Search completed: June 20, 2005, 09:22:43
Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 09:20:52 ; Search time 105.5 Seconds

(without alignments)
913.544 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGTATYYNF.....AVDQVKPKIALLKFDVKDKP 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1287	100.0	251	14	US-10-127-890-2 Sequence 2, Appli
3	1287	100.0	251	17	US-10-717-243-2 Sequence 2, Appli
4	1287	100.0	316	14	US-10-074-596-1 Sequence 1, Appli
5	1287	100.0	507	14	US-10-074-596-11 Sequence 11, Appl
6	1284	99.8	293	9	US-09-765-527-259 Sequence 259, App
7	1284	99.8	309	9	US-09-765-527-253 Sequence 253, App
8	1284	99.8	332	9	US-09-765-527-251 Sequence 251, App
9	1282	99.6	251	14	US-10-127-890-108 Sequence 108, App
10	1282	99.6	251	17	US-10-717-243-108 Sequence 108, App
11	1279	99.4	251	14	US-10-127-890-103 Sequence 103, App

12 1279 99.4 251 14 US-10-127-890-104 Sequence 104, App
13 1279 99.4 251 14 US-10-127-890-105 Sequence 105, App
14 1279 99.4 251 14 US-10-127-890-106 Sequence 106, App
15 1279 99.4 251 14 US-10-127-890-109 Sequence 109, App
16 1279 99.4 251 17 US-10-717-243-103 Sequence 103, App
17 1279 99.4 251 17 US-10-717-243-104 Sequence 104, App
18 1279 99.4 251 17 US-10-717-243-105 Sequence 105, App
19 1279 99.4 251 17 US-10-717-243-106 Sequence 106, App
20 1279 99.4 251 17 US-10-717-243-109 Sequence 109, App
21 1278 99.3 251 14 US-10-127-890-99 Sequence 99, Appli
22 1278 99.3 251 14 US-10-127-890-100 Sequence 100, App
23 1278 99.3 251 14 US-10-127-890-102 Sequence 102, App
24 1278 99.3 251 14 US-10-127-890-107 Sequence 107, App
25 1278 99.3 251 17 US-10-717-243-99 Sequence 99, Appl
26 1278 99.3 251 17 US-10-717-243-100 Sequence 100, App
27 1278 99.3 251 17 US-10-717-243-102 Sequence 102, App
28 1278 99.3 251 17 US-10-717-243-107 Sequence 107, App
29 1269 98.6 251 14 US-10-127-890-101 Sequence 101, App
30 1269 98.6 251 17 US-10-717-243-101 Sequence 101, App
31 1261 98.0 251 14 US-10-127-890-110 Sequence 110, App
32 1261 98.0 251 17 US-10-717-243-110 Sequence 110, App
33 1252 97.3 251 14 US-10-127-890-111 Sequence 111, App
34 1252 97.3 251 17 US-10-717-243-111 Sequence 111, App
35 346 26.9 263 14 US-10-127-890-4 Sequence 4, Appli
36 346 26.9 263 17 US-10-717-243-4 Sequence 4, Appli
37 343 26.7 267 14 US-10-282-935-1 Sequence 1, Appli
38 343 26.7 267 14 US-10-127-890-1 Sequence 1, Appli
39 343 26.7 267 15 US-10-440-796-1 Sequence 1, Appli
40 343 26.7 267 17 US-10-717-243-1 Sequence 1, Appli
41 343 26.7 576 14 US-10-083-336A-1 Sequence 1, Appli
42 324.5 25.2 312 16 US-10-467-009-2 Sequence 2, Appli
43 321 24.9 247 9 US-09-792-793A-39 Sequence 39, Appl
44 321 24.9 289 15 US-10-375-209A-39 Sequence 39, Appl
45 321 24.9 289 14 US-10-280-679B-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-765-527-247

; Sequence 247, Application US/09765527

; Patent No. US2002000638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/09/765,527

; APPLICATION NUMBER: 08/621,803

; FILING DATE: 18-Jan-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match 100.0%; Score 1287; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.8e-117; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0;

QY 1 GLDTSFSTKGATYITYVNFNLKVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLKVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASLLVVIQVMSAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASLLVVIQVMSAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDKP 251
DB 241 ALLKFVDKDKP 251

RESULT 2
US-10-127-890-2
Sequence 2, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

Query Match 100.0%; Score 1287; DB 14; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.8e-117; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0;

QY 1 GLDTSFSTKGATYITYVNFNLKVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLKVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFKDPADPAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASLLVVIQVMSAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTBIASLLVVIQVMSAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELELRANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDKP 251
DB 241 ALLKFVDKDKP 251

RESULT 3
US-10-717-243-2
Sequence 2, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765

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; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match      100.0%; Score 1287; DB 17; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.8e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYNFMNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDTSFSTKGATYITYNFMNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGFLFKNTIKTRLHFGGSPSLEGEK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGFLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 4
US-10-074-596-1
; Sequence 1, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-074-596-11

Query Match      100.0%; Score 1287; DB 14; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.5e-116;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYNFMNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 257 GLDTSFSTKGATYITYNFMNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 316
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGFLFKNTIKTRLHFGGSPSLEGEK 120
Db 317 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGFLFKNTIKTRLHFGGSPSLEGEK 376
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAARFTFIENQIRNN 180
Db 377 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAARFTFIENQIRNN 436
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 437 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 496
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 5
US-10-074-596-11
; Sequence 11, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-074-596-11

Query Match      100.0%; Score 1287; DB 14; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.5e-116;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYNFMNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 257 GLDTSFSTKGATYITYNFMNLRVKKLPEGNHGIPLLRKKDDPGKCFVLVALSNDN 316
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGFLFKNTIKTRLHFGGSPSLEGEK 120
Db 317 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGFLFKNTIKTRLHFGGSPSLEGEK 376
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAARFTFIENQIRNN 180
Db 377 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAARFTFIENQIRNN 436
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 437 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 496
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

Gelonium multiflorum
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Db 497 ALLKFVDKDPK 507

RESULT 6

US-09-765-527-259
; Sequence 259, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:

APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 259:

SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match 99.8%; Score 1284; DB 9; Length 293;
Best Local Similarity 99.6%; Pred. No. 1.4e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLDVSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	60
Db	23	GLDVSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	82
QY	61	GQLAEIADVTSVVVGQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK	120
Db	83	GQLAEIADVTSVVVGQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGTPSLEGEK	142
QY	121	AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRN	180
Db	143	AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRN	202
QY	181	FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	240
Db	203	FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	262
QY	241	ALLKFVDKDPK	251
Db	263	ALLKFVDKDPK	273

RESULT 7

US-09-765-527-253
; Sequence 253, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:

APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 253:

SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-765-527-253

Query Match 99.8%; Score 1284; DB 9; Length 309;
Best Local Similarity 99.6%; Pred. No. 1.5e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLDVSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	60
Db	23	GLDVSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN	82
QY	61	GQLAEIADVTSVVVGQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK	120
Db	83	GQLAEIADVTSVVVGQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGTPSLEGEK	142
QY	121	AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRN	180
Db	143	AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRN	202
QY	181	FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	240
Db	203	FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI	262
QY	241	ALLKFVDKDPK	251
Db	263	ALLKFVDKDPK	273

RESULT 8

US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:

```

; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match          99.8%; Score 1284; DB 9; Length 332;
Best Local Similarity 99.6%; Pred. No. 1.7e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 23 GLDTSVSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 82
QY 61 GLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 120
DB 83 GLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 142
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 202
QY 181 FQORIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 203 FQORIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262
QY 241 ALLKFVDKDKP 251
DB 263 ALLKFVDKDKP 273

RESULT 9
US-10-127-890-108
; Sequence 108, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
```

```

; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108

Query Match          99.6%; Score 1282; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLPKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQWSEAAFTFIENQIRNN 180
QY 181 FQORIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDKP 251
DB 241 ALLKFVDKDKP 251
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RESULT 10
US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108
Query Match 99.6%; Score 1282; DB 17; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVFSFKGATYITYVNFNLKPKGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSVFSFKGATYITYVNFNLKPKGNHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GQLAEIADVTSVYVGVQVRNRSFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120
DB 61 GQLAEIADVTSVYVGVQVRNRSFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120
QY 121 AYRETTDGLIEPLRIGIKKLDENADINVKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDGLIEPLRIGIKKLDENADINVKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180

RESULT 11
US-10-127-890-103
; Sequence 103, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103
Query Match 99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVFSFKGATYITYVNFNLKPKGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSVFSFKGATYITYVNFNLKPKGNHGIPLLRKKCDPDKCFVLVALSNDN 60
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QY 61 GQAEIAIDVTSVYVGVQVRNRSYFFKDDPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQAEIAIDVTSVYVGVQVRNRSYFFKDDPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12

US-10-127-890-104
; Sequence 104, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 104:

SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:

US-10-127-890-104

Query Match 99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSVFSFTKGATYITYVNFNLNLRVKKLPEGNHGIPLLRKKCDPDKGCFVLVALSNDN 60
DB 1 GLDTSVFSFTKGATYITYVNFNLNLRVKKLPEGNHGIPLLRKKCDPDKGCFVLVALSNDN 60
QY 61 GQAEIAIDVTSVYVGVQVRNRSYFFKDDPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GQAEIAIDVTSVYVGVQVRNRSYFFKDDPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13

US-10-127-890-105
; Sequence 105, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

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;
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105

Query Match          99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITYVNFNLRLVKLKPEGNHGIPLLRKCCDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATYITYVNFNLRLVKLKPEGNHGIPLLRKCCDDPGKCFVLVALSNDN 60

QY 61 QLAELAIADVTSVYVGVQVRNRSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QLAELAIADVTSVYVGVQVRNRSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
US-10-127-890-106
; Sequence 106, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
```

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;
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-10-127-890-106

Query Match          99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITYVNFNLRLVKLKPEGNHGIPLLRKCCDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATYITYVNFNLRLVKLKPEGNHGIPLLRKCCDDPGKCFVLVALSNDN 60

QY 61 QLAELAIADVTSVYVGVQVRNRSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QLAELAIADVTSVYVGVQVRNRSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAELELRANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 15
US-10-127-890-109
; Sequence 109, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-127-890-109

Query Match 99.4%; Score 1279; DB 14; Length 251;
Best Local Similarity 99.6%; Pred. No. 3 5e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLNELRVKLPNGNSHGIPLLRKKCDPDKCFVLVLSNDN 60
Db |||||
1 GLDTSFSTKGATYITYVNFNLNELRVKLPNGNSHGIPLLRKKCDPDKCFVLVLSNDN 60
QY 61 GOLAEITADVTSVYVVGQVRRRSYFFKDAPDAAYEGLEFKNTIKTELHFGGSYPSLEGEK 120
Db |||||
61 GOLAEITADVTSVYVVGQVRRRSYFFKDAPDAAYEGLEFKNTIKTELHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAINDKYPTETIASLLVVIQVSEAAFTFIENQIRNN 180
Db |||||
121 AYRETTDLGIEPLRIGIKKLDENAINDKYPTETIASLLVVIQVSEAAFTFIENQIRNN 180
QY 181 FQOCIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKKYVYTTAVDQVKPKI 240
Db |||||
181 FQOCIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKKYVYTTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db |||||
241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:39:26
Job time : 106.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 09:09:06 ; Search time 25.5 Seconds
(without alignments)
947.075 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGATYTYVNF.....AVDQVKPKTALLKFEVDKPK 251

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	316	2 JT0753	rRNA N-glycosidase
2	348.5	27.1	245	2 JCA4840	rRNA N-glycosidase
3	346	26.9	286	2 S25560	rRNA N-glycosidase
4	343	26.7	576	1 RLCSDB	ricin D precursor
5	341	26.5	286	2 JCA235	rRNA N-glycosidase
6	334.5	26.0	564	1 RLCSAG	agglutinin precursor
7	333.5	25.9	527	2 S32430	abrin-b precursor
8	330.5	25.7	294	2 S28421	rRNA N-glycosidase
9	329	25.6	251	2 C39761	abrin (Clone 7.2)
10	325	25.3	313	2 RL7757	rRNA N-glycosidase
11	321	24.9	289	1 RL72T	rRNA N-glycosidase
12	320	24.9	528	1 TZLSA	abrin-a precursor
13	315	24.5	247	2 JU0393	Karsaurin - Mongol
14	315	24.5	289	2 S16022	Karsaurin C - Tric
15	311.5	24.2	261	2 JE0401	antiviral protein
16	310	24.1	247	2 JC5032	Karsaurin-B - Tric
17	306.5	23.8	277	2 S22494	rRNA N-glycosidase
18	300.5	23.3	254	2 PD0018	mistletoe lectin I
19	298	23.2	528	2 S32431	abrin-d precursor
20	298	23.2	562	2 RLPUGG	rRNA N-glycosidase
21	291	22.6	286	1 S62627	agglutinin I precu
22	287.5	22.3	570	2 S62627	beta-luffin - smoo
23	283.5	22.0	278	2 S23519	luffin-b - smooth
24	270	21.0	250	2 JN0108	rRNA N-glycosidase
25	215.5	16.7	278	2 A39817	betavulgin - beet
26	210	16.3	272	2 JCA4811	ribose-inactivat
27	202	15.7	310	2 S46239	rRNA N-glycosidase
28	195	15.2	40	2 S17574	rRNA N-glycosidase
29	181.5	14.1	253	2 S28542	rRNA N-glycosidase

30	181.5	14.1	292	1 RLQHG2	rRNA N-glycosidase
31	181	14.1	289	2 T12573	rRNA N-glycosidase
32	179	13.9	293	2 S17519	rRNA N-glycosidase
33	177.5	13.8	283	2 S05205	rRNA N-glycosidase
34	176.5	13.7	253	2 S28541	rRNA N-glycosidase
35	176.5	13.7	253	2 S28539	rRNA N-glycosidase
36	176.5	13.7	253	2 S29931	rRNA N-glycosidase
37	171.5	13.3	253	2 A58923	rRNA N-glycosidase
38	149	11.6	236	2 S17932	rRNA N-glycosidase
39	121	9.4	106	2 B3761	abrin (Clone 3.7)
40	120.5	9.4	1948	2 B69511	N conserved hypoth
41	114.5	8.9	275	2 S33631	tritin - wheat
42	113.5	8.8	280	1 RL8H	rRNA N-glycosidase
43	104.5	8.1	281	2 B38664	30K ribosome inact
44	103	8.0	280	2 JCS848	protein synthesis
45	102.5	8.0	456	2 T05612	hypothetical prote

ALIGNMENTS

RESULT 1

JT0753

rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum

N:Alternate names: gelonin; type I ribosome-inactivating protein

C:Species: Gelonium multiflorum

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C:Accession: JT0753; S16489

Gene 134, 223-227, 1993

A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protei

A:Reference number: JT0753; MUID:94085781; PMID:7916721

A:Accession: JT0753

A:Molecule type: mRNA

A:Residues: 1-316 <NOL>

A:Cross-references: UNIPROT:P3186; GB:112243; NID:G388633; PIDN:AA16312.1; PID:G388634

R:Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stripe, F.; Soria, M.; Lappi, D.

Int. J. Pept. Protein Res. 33, 263-267, 1989

A:Title: N-terminal sequence of some ribosome-inactivating proteins.

A:Reference number: S16331; MUID:89326691; PMID:2753596

A:Accession: S16489

A:Molecule type: protein

A:Residues: 47-89, 'K', '91-92, 'D' <MON>

C:Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA there

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase

F:1-46/Domain: signal sequence #status predicted <SIG>

F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>

F:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 100.0%; Score 1287; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.1e-99;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLDTSFSTKGATYTYVNFNLRLVKLPENSHGIPILRLKCDPDKGCFVLVALSNDN	60
DB	47	GLDTSFSTKGATYTYVNFNLRLVKLPENSHGIPILRLKCDPDKGCFVLVALSNDN	106
QY	61	GQLAEITADVTSVYVGVYVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGSGSYPSLEGEK	120
DB	107	GQLAEITADVTSVYVGVYVRNRSYFFKDPADAAVEGLFKNTIKTLRHFGSGSYPSLEGEK	166
QY	121	AYRETTDLGIEPLRIGIKKLDENADINRYKPTETASLLVVIQWSEAAARFTFTIENIRNN	180
DB	167	AYRETTDLGIEPLRIGIKKLDENADINRYKPTETASLLVVIQWSEAAARFTFTIENIRNN	226
QY	181	FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKKYVYVAVDQVKPKI	240
DB	227	FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKKYVYVAVDQVKPKI	286
QY	241	ALLKFEVDKPK 251	

Db 287 ALLKFVDKDPK 297

RESULT 2

JC4840

rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd
C:Species: Trichosanthus anguina (snake gourd)
C:Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C:Accession: JC4840; J0701; J0677
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Biomed. Sci. 3, 178-186, 1996
A:Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from
A:Reference number: JC4840
A:Accession: JC4840
A:Molecule type: protein
A:Residues: 1-132, 'S', 134-245 <CHO1>
A:Experimental source: seed
A>Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
Submitted to JIPIID, August 1995
A:Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from
A:Reference number: J070677
A:Accession: J0701
A:Molecule type: protein
A:Residues: 1-50, 'L', 52-245 <CHO2>
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F:4-242/Domain: rRNA N-glycosidase homology <RNG>
F:51.201/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:70.158.161/Active site: Tyr, Glu, Arg #status predicted
F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 27.1%; Score 348.5; DB 2; Length 245;
Best Local Similarity 35.9%; Pred. No. 1.4e-21;
Matches 90; Conservative 44; Mismatches 96; Indels 21; Gaps 7;
QY 5 VSFSTKGTATYTYVNFNLRLVKLKEGNSHIGIPILLRKKCDPDKGCFVLVALSNDNGOLA 64
DB 2 VSFDLSTATKYSFIIQLRDLATQGTIVYGIPLLPSTAGSQR-FRFNLTNYNDTV 60
QY 65 EIAIDVTSVYVGVQVRNRSYFFKDAADAAEGLFPKNTIKRLHFGSGYPSLE---GEKA 121
DB 61 TVAVDVTNVIYVAYRADAVSYFFEDTPAEAFKLIIFAGTKTVKLPYSGNYDKLQSVVGKQ- 119
QY 122 YETDGLGIEPLRIGIKKLDEAIND---YKTEATASSLLVVIQMVSEARFTFIENQIR 178
DB 120 -RDMIELGIPAL-----SSAITNMVYDYQSTAAALLVLIQSTAEARYYKIEQQVS 170
QY 179 NNFQORIRPANNTISLENKWKLSFQIRTSG--ANGMFSEAVELEERANGKYYV--TAVD 234
DB 171 SHISSNFYVQNAVISENKGWALSQKIQIANHTGHQFENPVELYNDGTRFSVTHTSAG 230
QY 235 QVKPKIALKF 245
DB 231 VVKGNIKLLY 241

RESULT 3

S25560

rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple
C:Species: Momordica balsamina (balsam apple)
C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S25560
R:Ortigao, M.; Better, M.
Nucleic Acids Res. 20, 4662, 1992
A:Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homologous to the trichosanthin ribosome inactivating protein from Momordica
A:Reference number: S25560; MUID:93027170; PMID:1408771
A:Accession: S25560
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-286 <ORT>
A:Cross-references: UNIPROT:P29339; EMBL:Z12175; NID:g19525; PIDN:CAA78166.1; PID:g19526
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase
F:27-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match 26.9%; Score 346; DB 2; Length 286;
Best Local Similarity 37.4%; Pred. No. 2.8e-21;
Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;
QY 5 VSFSTKGTATYTYVNFNLRLVKLKEGNSHIGIPILLRKKCDPDKGCFVLVALSNDNGOLA 64
DB 25 VNFDLSTATATYTYKFIEDFRATLPFSHKVYDIPLLYXSTISD-SRRFILLDTSTVAYETI 83
QY 65 EIAIDVTSVYVGVQVRNRSYFFKDAADAAEGLFPKNTIKRLHFGSGYPSLE-GEKAYR 123
DB 84 SVAIDVTNVIYVAYRADAVSYFFEDTPAEAFKLIIFAGTKTVKLPYSGNYENLQTAHKIR 143
QY 124 ETTDLGIEPLRIGIKKLDEAINDYKPTETIASSLLVVIQMVSEARFTFIENQIRNFQO 183
DB 144 ENIDGLPALSSAI-----TTFYNAQSAPSAALLVLIQTAAEARFYIERHVKYAVAT 198
QY 184 RIRPANNTISLENKWKLSFOI-RTSGANGMFSEAVELEERANGKYYVTVAVDQ--VKPKI 240
DB 199 NFKNLAIISLENQWSALSQKIFLAQNGGKFRNPVDLIKPTGERFQVTNVDSDVVGNI 258
QY 241 ALL 243
DB 259 KLL 261

RESULT 4

RLCSD

ricin D precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2999712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <HAL>
A:Cross-references: UNIPROT:P02879; GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083
R:Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <TRE>
A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preprotricitin.
A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>
A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile ch
A:Reference number: A03372
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>
A>Note: this paper cites the others in the series providing experimental details for the
R:Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein

A:Residues: 315-383, 'PS', 386-576 <APA>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374

A:Molecule type: protein
A:Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405, 'S', 529-564, 'W', 566, 'H', 567-570, 'LI', 573-574, 'P', <FUN>
A:Note: This paper, one of a series, summarizes the experimental details for the determination of the primary structure of ricin D.
R:Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991

A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of ricin toxicity.
A:Reference number: A48237; PMID:91352006; PMID:1881883

A:Contents: annotation; active site
R:Kutenber, E.; Robertus, J.D.
Proteins 10, 260-269, 1991

A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A:Reference number: A48238; PMID:91352005; PMID:1881882

A:Contents: annotation; X-ray crystallography, 2.5 angstroms
R:Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991

A:Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; PMID:91352004; PMID:1881881

A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which natively the A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit of the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). This protein is cytotoxic and very poisonous to animals.

C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed

F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-302/Product: ricin D chain A #status experimental <ACH>
F:46-293/Domain: rRNA N-glycosidase homology <RNG>
F:315-576/Product: ricin D chain B #status experimental <BCH>
F:331-373/Product: ricin D chain B #status experimental <RNG>
F:45, 409, 449/Binding site: carbohydrate (asn) (covalent) #status experimental

F:115, 158, 243, 244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:122/Active site: Glu #status experimental
F:212/Active site: Glu #status predicted
F:294-318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental

F:336, 349, 360/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status experimental
F:548, 569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental

Query Match 26.7%; Score 343; DB 1; Length 576;
Best Local Similarity 36.8%; Pred. No. 1.2e-20;
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;

QY 5 VSFSTKGTATYTYVNFELNRLVKLPKPGN-SHGIPLLRKKCDPP-GKCFVIALSNDNCQ 62

DB 44 INFETAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNVRGLPINQRFILVELSNHAE 103

QY 63 LAEIAIDVTSVVVGVQVNRNRYFFKADPD-----AAVEGLFKNTIKTR--LHFGGSYPS 115

DB 104 SVTLADVTNAVGVYRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYRTAFGNYDR 160

QY 116 LEQEXA-VRETTDLGIEPLRIGIKKLDENADINRYKPTETIASLLVVIQMVSEAAFTFTFE 174

DB 161 LEQAGNLRNIELGNLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAARFOYIE 220

QY 175 NOIRN--NFQQRIPANNITISLENKWKLSFQIRSGANGMFSEAVELERANGKYYVTA 232

DB 221 GEMTRIRNRSAPDPSVITLNSWGRSLTAIQESN-QGAFASPIQLQRRNGSKFSVYD 279

QY 233 VQVVKPKIALKF 245

DB 280 VSILPIIALMWY 292

RESULT 5

JC4235

rRNA N-glycosidase (EC 3.2.2.22) map30 precursor - balsam pear

N:Alternate names: anti-HIV 30K protein

C:Species: Momordica charantia (balsam pear, bitter melon)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4235; S12869

R:Lee-Huang, S.; Huang, P.L.; Chen, H.C.; Huang, P.L.; Bourinbaier, A.; Huang, H.I.; Kung, Gene 161, 151-156, 1995

A:Title: Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter melon.

A:Reference number: JC4235; MUID:95394347; PMID:7665070

A:Accession: JC4235

A:Molecule type: DNA

A:Residues: 1-286 <LEB>

A:Cross-references: UNIPROT:P24817

A:Experimental source: mature seeds

R:Lee-Huang, S.; Huang, P.L.; Nara, P.L.; Chen, H.C.; Kung, H.; Huang, H.I.; FBS Lett. 272, 12-18, 1990

A:Title: MAP 30: a new inhibitor of HIV-1 infection and replication.

A:Reference number: S12869; MUID:91032105; PMID:1699801

A:Accession: S12869

A:Molecule type: protein

A:Residues: 24-36, 'T', 38-66, 'P' <LEW>

C:Comment: This plant protein has anti-HIV activity. It possesses antiviral action, anti-activation activities. It is capable of acting against multiple stages of the viral life cycle. This protein has conserved unique residues Trp-213 and Met-277.

C:Genetics:

C:Superfamily: map30

C:Keywords: rRNA N-glycosidase; rRNA N-glycosidase homology

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-286/Product: rRNA N-glycosidase (EC 3.2.2.22) map30 #status predicted <MAT>

F:27-264/Domain: rRNA N-glycosidase homology <RNG>

F:74/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:93, 181, 184/Active site: Tyr, Glu, Arg #status predicted

Query Match 26.5%; Score 341; DB 2; Length 286;
Best Local Similarity 37.0%; Pred. No. 7.2e-21;
Matches 90; Conservative 34; Mismatches 109; Indels 10; Gaps 5;

QY 5 VSFSTKGTATYTYVNFELNRLVKLPKPGN-SHGIPLLRKKCDPPGKCFVIALSNDNCQ 64

DB 25 VNFDLSTAKTYTTFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSYAYETI 83

QY 65 EIAIDVTSVVVGVQVNRNRYFFKADPDAAAYEGLFKNTIKRLHFGGSYPSLE-GEKAYR 123

DB 84 SVAIDVTNAVGVYRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYRTAFGNYDR 143

QY 124 ETTDLGIEPLRIGIKKLDENADINRYKPTETIASLLVVIQMVSEAAFTFTFIQIRNNFQ 183

DB 144 ENIDLGLPALSSAI-----TTLFYNAQSPALLVLIQTAEARFKYTERHVAVYAT 198

QY 184 RIRPANNITISLENKWKLSFQI-RTSGANGMFSEAVELERANGKYYVTAVDQ--VKPKI 240

DB 199 NFKPNLAIISLENQWSALSQIFLAQNQGGKFRNPVDLIKPTGERFQVNTVDSVVYKGI 258

QY 241 ALL 243

DB 259 KLL 261

RESULT 6

RLCSAG

agglutinin precursor - castor bean

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)

C:Species: Ricinus communis (castor bean)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A24261; A24210

R:Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.

J. Biol. Chem. 260, 15682-15686, 1985

A:Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.

A:Reference number: A24261; MUID:86059449; PMID:2999130

A:Accession: A24261

A:Molecule type: mRNA

A:Residues: 1-564 <ROB>

A:Cross-references: UNIPROT:P06750; GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701


```
Db      197 VSEARFYKIEQVKNFNRAFPYNAKVNLNEESWGKISTAIH-NAKGALTSPLLEKNA 255  
          :|||:::||:::||::|||::|||::|||::|||::|||:  
  
Qy     224 NGKKYYTAVDQVKPKIALLKFVD 247  
          |||::|||::|||::|||::|||::|||::|||:  
  
Db      256 NGSKWIVLRVDIEDPDGGLLKVN 279  
          |||::|||::|||::|||::|||::|||::|||:  
  
RESULT 9  
C39761  
N:Contains: rRNA N-glycosidase - Indian licorice (fragment)  
C:Species: Abrus precatorius (Indian licorice)  
C>Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004  
C:Accession: C39761; S14471  
R:Evensen, G.; Mathiesen, A.; Sundan, A.  
J. Biol. Chem. 266, 6848-6852, 1991  
A>Title: Direct molecular cloning and expression of two distinct abrin A-chains  
A:Reference number: A39761; MUID:91201329; PMID:2016300  
A:Accession: C39761  
A:Molecule type: DNA  
A:Residues: 1-251 <EV>  
A:CROSS-references: UNIPROT.Q38760  
R:Evensen, G.; Mathiesen, A.; Sundan, A.  
submitted to the EMBL Data Library, October 1990  
A>Description: Direct molecular cloning of two distinct abrin A-chains.  
A:Reference number: S14471  
A:Accession: S14471  
A:Molecule type: DNA  
A:Residues: 'M',1-251 <E2>  
A:CROSS-references: EMBL.X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089  
C:Superfamily: ricin; RNA N-glycosidase homology  
C:Keywords: duplication; glycosidase; hydrolase; lectin; toxin  
F:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>  
F:7-246/Domain: rRNA N-glycosidase homology <RNG>  
F:74,113,195,196/Binding site: substrate { Tyr, Tyr, Glu, Asn} #status predicted  
F:164,167/Active site: Glu, Arg #status predicted
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```
Query Match           25.6%; Score 329; DB 2; Length 251;  
Best Local Similarity 36.5%; Pred No. 6e-20;  
Matches   93; Conservative 40; Mismatches 104; Indels 18; Gaps 5;
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```
Qy    5 VSFTKGATITYYNFLNELRVKLPEGNHGIGILLRKCKDDPGKC-----FVLVALSND 59  
       :|||||::|||::|||::|||::|||::|||::|||::|||:  
Db    5 IKFSTEGATSQSQKQFIALARERLA-GGLIHDPVLR---DPTVEERNRYITVELSNS 59  
       :|||||::|||::|||::|||::|||::|||::|||::|||:  
  
Qy    60 NGQLAEIAIDTVSYVVGVQVNRNSFFPKADAPDAAYEGLFKNTIKRLHFSGSYPSLE-G 118  
       :|||||::|||::|||::|||::|||::|||::|||::|||:  
Db    60 ERSEIVEGDVTNAVVAIRAGSQSYFLRDAPASASTYLFTGTQRYSLFDFDSYGDLRW 119  
       :|||||::|||::|||::|||::|||::|||::|||::|||:  
  
Qy    119 EKAVRETTDLGIPIRGIGIKLDENAINDKYPEITASLLVVIQMVSAAARTTFIENOJR 178  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db    120 AHQTREQISLGQAUTHAISFLRSASND----EKAKRTDIVIIQWASEARYRIISRNVG 176  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
  
Qy    179 NNFO--QRIRPANNTISLENKWKLSFGIRTSGANGMFSEAVERFRANKGYTYTAV-DQ 235  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db    177 VSIRGTAFQPDPAMPMLSLNNWDNLSRGVQES-VQDTTFNAVTLRRVNNQPVIVDSLTHQ 235  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
  
Qy    236 VKPKIALLKFDXKP 250  
        ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db    236 SVAVILALMLFCNP 250  
        ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

```
RESULT 10  
SI7757  
rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed  
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ricilactonase  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004  
C:Accession: SI7757; S02792; S13469; S32611  
R:Liu, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.  
Plant Mol. Biol. 17, 609-614, 1991  
A>Title: Isolation and characterization of a cDNA clone encoding the anti-vira-
```

R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990

A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A;Reference number: A36274; PMID:90256790; PMID:2341400

A;Accession: A36274

A;Molecule type: DNA

A;Residues: 1-233,'T','235-246','M',248-289 <CHO>

A;Cross-references: GB:J05434; NID:g170534; PIDN:AAA34206.1; PID:g170535

R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.

Acta Genet. Sin. 21, 42-51, 1994

A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.

A;Reference number: JCI093; PMID:94271613; PMID:8003348

A;Accession: JCI093

A;Molecule type: DNA

A;Residues: 1-72,'V','74-90','S',92-233,'T','235-267','D',269-289 <ZHE>

A;Cross-references: GB:S70176; NID:G547148; PIDN:AAB31048.1; PID:G547149

R;Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
J. Biol. Chem. 265, 8665-8669, 1990

A;Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abn
A;Reference number: A36273; PMID:90256789; PMID:2341399

A;Accession: A36273

A;Molecule type: protein

A;Residues: 24-270 <COL>

R;Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986

A;Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A;Reference number: JT0003

A;Accession: JT0003

A;Molecule type: Protein

A;Residues: 24-56,'L',58-59,'I',61-71,'I',73-81,85-86,'L',88-92,'DAGLP RNAVL',93-142,'GL'
R;Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994

A;Reference number: A67091; PDB:1MRJ

A;Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
R;Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994

A;Reference number: A67092; PDB:1MRK

A;Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-
R;Xiong, J.P.; Xia, Z.X.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, December 1994

A;Reference number: A66711; PDB:1TCS

A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27-
R;Xiong, J.P.; Xia, Z.X.; Wang, Y.
Nat. Struct. Biol. 1, 695-700, 1994

A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A;Reference number: A58622; PMID:95360714; PMID:7634073

A;Contents: annotation; X-ray crystallography, 1.7 angstroms

C;Comment: Alpha-trichosanthin has been used to induce abortions.

C;Genetics:

A;Gene: tcs

C;Function:

A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C;Keywords: abortifacient; glycosidase; hydrolase; root; toxin

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-270/Product: trichosanthin alpha #status experimental <MAT>

F;271-266/Domains: rRNA N-glycosidase homology <RNG>

F;271-289/Domains: carboxyl-terminal propeptide #status predicted <CTP>

F;93,183,186/Active site: Tyr, Glu, Arg #status predicted

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIQVPTTEIASLLVVTQMWSEAAARFTTIEHQIRNN 180

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

143 KIRENIPLGLPALDSAI-----TTLFFYNANSAASALMVLIIQSTSEATSEAKYKIEQOIGKR 197

Qy 181 FQOIRPANNTISLENKWKLSFOIR-TSGANGWESEAVELERANGKKYVYTTAVDQ--VK 237

Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

198 VDKTFLEPLAISLENSWSALSQIQIQTASTNGQFESPVLINAQORVITITNDVAGVVT 257

Qy 238 PKIALL 243 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 258 SNIALL 263 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12

TZLSA

abrin-a precursor - Indian licorice (fragment)

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Abrus precatorius (Indian licorice)

C;Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004

C;Accession: S32429; J0202; A39761; JCI1398; S14472; S24133; S74110; S74111

R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.

J. Mol. Biol. 229, 263-267, 1993

A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing

A;Reference number: S32429; MUID:93132798; PMID:8421313

A;Accession: S32429

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 'E', 2-528 <HUN>

A;Cross-references: UNIPROT:P11140; GB:M98344; NID:g16294; PIDN:AAA32624.1; P

A;Note: the coding region for the sequence shown is preceded by an ATG codon

A;Note: residues 1-8 were derived from the synthesized primer

R;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.

Agric. Biol. Chem. 52, 1095-1097, 1988

A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic p

A;Reference number: JT0202

A;Accession: JT0202

A;Molecule type: protein

A;Residues: 1-201,203-251 <PUN>

A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore

E;Evensen, G.; Mathiesen, A.; Sundan, A.

J. Biol. Chem. 266, 6848-6852, 1991

A;Title: Direct molecular cloning and expression of two distinct abrin A-chain

A;Reference number: A39761; MUID:91201329; PMID:2016300

A;Accession: A39761

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 'E', 2-251 <EVE>

A;Cross-references: GB:X54872

A;Note: residues 1-8 were derived from the synthesized primer

R;Kimura, M.; Sumizawa, T.; Funatsu, G.

Biosci. Biotechnol. Biochem. 57, 166-169, 1993

A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abri

A;Reference number: JCI198; MUID:93169023; PMID:7763422

A;Contents: seeds

A;Accession: JCI198

A;Molecule type: protein

A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>

A;Experimental source: seed

R;Evensen, G.; Mathiesen, A.; Sundan, A.

submitted to the EMBL Data Library, October 1990

A;Description: Direct molecular cloning of two distinct abrin A-chains.

A;Reference number: S14471

A;Accession: S14472

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 'ME', 2-251 <EV2>

A;Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091

R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.

FEBS Lett. 309, 115-118, 1992

A;Title: The complete primary structure of abrin-a B chain.

A;Reference number: S24133; MUID:92371656; PMID:1505674

A;Accession: S24133

A;Molecule type: protein

	Query Match	24.5%; Score 315; DB 2; Length 247;
	Best Local Similarity	38.2%; Pred. No. 8.6e-19;
	Matches	94; Conservative 33; Mismatches 105; Indels 14; Gaps 8
Qy	5 VSFSTKGATITVYVFNFLNEIRVKLPKGNSHGIPLLRKKCCDDPG-KCFVLVALSNDNGQL 63	: : : : : : : : : : : :
Db	2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIFLLASTL--PSQRVALIHLTNYADET 59	: : : : : : : : : : : :
Qy	64 AETAI DVTSYVVVG YQVNRNSYFFKDA-PDAAYEGLPKNT-IKTRLHFGGSYP SLE-GEK 120	: : : : : : : : : : : :
Db	60 ISVAIDVTNVVMGYRAGDTSYFPNEASATEAAKYVPKDAKRKVTLTPYSGNVERLQIAAG 119	: : : : : : : : : : : :
Qy	121 AYRETTDLGTEPLRIGIKLDENAINDKPTEIASLLLVQMYS EAA RFTFIENQIRNN 180	: : : : : : : : : : : :
Db	120 KIRENIPLGPLADSAI-----TTLFYNNASAASALMVL I QSTSEAAKYRFIEOQIGKR 174	: : : : : : : : : : : :
Qy	181 FQORIRPANNTISLENKWGKL SFQIR-TSGANGMFSEAVELERANGKKYYTVAVDQ--VK 237	: : : : : : : : : : : :
Db	175 VDKTFLPSLAII SENSWALSLSKIQIQTASTNGQFETPPVLI NAQNQRVTITNVDAGVVT 234	: : : : : : : : : : : :
Qy	238 PKIALL 243	
Db	235 SNIAL L 240	
 RESULT 14 JC5606		
karasurin C - Trichosanthes kirilowii var. japonica		
N;Caratsin karasurin A		
C;Species: Trichosanthes kirilowii var. japonica		
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004		
C;Accession: JC5606; JCS033		
B;Mizukami, H.; Iida, K.; Kondo, T.; Ogi hara, Y.		
Bio l. Pharm. Bull. 20, 711-713, 1997		
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein from Trichosanthes kirilowii		
A;Reference number: JC5606; MUID:97356562; PMID:9212998		
A;Accession: JC5606		
A;Molecule type: DNA		
A;Residues: 1-289 <MI Z>		
A;Cross-references: UNIPROT:P24478; DDBJ:AB000666; NID:g2329830; PIDN:BAA21786		
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogi hara, Y.		
Bio l. Pharm. Bull. 19, 1485-1489, 1996		
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin		
A;Reference number: JC5032; MUID:97108848; PMID:8951169		
A;Accession: JC5033		
A>Status: preliminary		
A;Molecule type: protein		
A;Residues: 22-270 <KON>		
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic activity against various eukaryotic cells		
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology		
F;22-270/Product: karasurin C #status predicted <MAC>		
F;24-270/Product: karasurin A #status predicted <MAA>		
F;27-266/Domain: rRNA N-glycosidase homology <RNG>		
	Query Match	24.5%; Score 315; DB 2; Length 249;
	Best Local Similarity	38.2%; Pred. No. 1.1e-18;
	Matches	94; Conservative 33; Mismatches 105; Indels 14; Gaps 8
Qy	5 VSFSTKGATITVYVFNFLNEIRVKLPKGNSHGIPLLRKKCCDDPG-KCFVLVALSNDNGQL 63	: : : : : : : : : : : :
Db	25 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIFLLASTL--PSQRVALIHLTNYADET 82	: : : : : : : : : : : :
Qy	64 AETAI DVTSYVVVG YQVNRNSYFFKDA-PDAAYEGLPKNT-IKTRLHFGGSYP SLE-GEK 120	: : : : : : : : : : : :
Db	83 ISVAIDVTNVVMGYRAGDTSYFPNEASATEAAKYVPKDAKRKVTLTPYSGNVERLQIAAG 142	: : : : : : : : : : : :
Qy	121 AYRETTDLGTEPLRIGIKLDENAINDKPTEIASLLLVQMYS EAA RFTFIENQIRNN 180	: : : : : : : : : : : :
Db	143 KIRENIPLGPLADSAI-----TTLFYNNASAASALMVL I QSTSEAAKYRFIEOQIGKR 197	: : : : : : : : : : : :
Qy	181 FQORIRPANNTISLENKWGKL SFQIR-TSGANGMFSEAVELERANGKKYYTVAVDQ--VK 237	: : : : : : : : : : : :

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:00:50 ; Search time 114.5 Seconds
(without alignments)
1122.549 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDVSFSTKGATITYYVF.....AVDQVKPKIALKFKVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1287	100.0	316	1	RIPG_GELMU	P33186 gelonium mu
2	1242.5	96.5	258	2	Q9S9E4	Q9S9E4 gelonium mu
3	394.5	30.7	581	2	Q94BW5	Q94BW5 cinnamomum
4	393.5	30.6	580	2	Q94BW3	Q94BW3 cinnamomum
5	392.5	30.5	549	2	Q9FV22	Q9FV22 cinnamomum
6	388	30.1	299	2	Q8GZN9	Q8GZN9 euphorbia s
7	386.5	30.0	580	2	Q94BW4	Q94BW4 cinnamomum
8	361.5	28.1	563	2	Q8GT32	Q8GT32 sambucus ni
9	357.5	27.8	297	2	Q8GZP0	Q8GZP0 euphorbia s
10	352	27.4	563	1	NIGB_SAMNI	P33183 sambucus ni
11	352	27.4	563	2	Q945S2	Q945S2 sambucus ni
12	348.5	27.1	563	2	O04367	O04367 sambucus ni
13	346	26.9	264	2	Q684J5	Q684J5 momordica c
14	346	26.9	286	1	RIP2_MOMBA	P29339 momordica c
15	346	26.9	286	1	RIP3_MOMCH	P24817 momordica c
16	344	26.7	541	2	Q41174	Q41174 ricinus com
17	343	26.7	576	1	RICI_RICCO	P02879 ricinus com
18	341.5	26.5	265	1	RIP2_PHYDI	P34967 phytolacca
19	338.5	26.3	294	1	RIP1_TRIAN	P56626 trichosanthe
20	337.5	26.2	564	2	Q9AVR2	Q9AVR2 sambucus eb
21	334.5	26.0	564	1	AGGL_RICCO	P06750 ricinus com
22	333.5	25.9	527	1	ABRB_ABRPR	Q06077 abrus preca
23	333	25.9	282	1	RIP2_BRVDI	P98184 bryonia dio
24	330.5	25.7	294	1	RIFA_PHYAM	Q03464 phytolacca
25	329	25.6	252	2	Q38760	Q38760 abrus preca
26	327.5	25.4	293	2	Q8VYU0	Q8VYU0 jatrophia cu
27	327.5	25.4	294	2	Q8H1W1	Q8H1W1 phytolacca
28	325.5	25.3	275	2	Q84LJ1	Q84LJ1 gynostemma
29	325	25.3	313	1	RIP1_PHYAM	P10297 phytolacca
30	325	25.3	313	2	Q6PWU4	Q6PWU4 phytolacca
31	324.5	25.2	277	2	Q84JUR1	Q84JUR1 gynostemma

32	324.5	25.2	293	2	Q8S452	Q8S452 jatrophia cu
33	324	25.2	289	2	Q41216	Q41216 trichosanthe
34	323.5	25.1	277	2	Q8GV09	Q8GV09 gynostemma
35	322.5	25.1	275	2	Q8H1Y4	Q8H1Y4 gynostemma
36	321	24.9	289	1	RIP1_TRIKI	P09989 trichosanthe
37	321	24.9	289	2	Q94KE4	Q94KE4 trichosanthe
38	321	24.9	567	2	Q6H267	Q6H267 viscum albu
39	320.5	24.9	277	2	Q8GV11	Q8GV11 gynostemma
40	320.5	24.9	565	2	O04071	O04071 sambucus ni
41	320	24.9	251	2	Q7DM12	Q7DM12 abrus preca
42	320	24.9	252	2	Q38761	Q38761 abrus preca
43	320	24.9	289	2	Q84SV8	Q84SV8 trichosanthe
44	320	24.9	528	1	ABRA_ABRPR	P11140 abrus preca
45	316	24.6	247	2	Q6BBQ4	Q6BBQ4 trichosanthe

ALIGNMENTS

RESULT 1

ID	RIPG_GELMU	STANDARD;	PRT;	316 AA.
AC	P33186;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).			
DE	glycosidase).			
GN	Name=GEL;			
OS	Gelonium multiflorum (Euphorbiaceae himalayal).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid 1; Malpighiales; Euphorbiaceae; Crotonoideae; Gelonioideae;			
OC	Gelonium.			
OX	NCBI_TaxID=3979;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;			
RA	Nolan P.A., Garrison D.A., Better M.;			
RT	"Cloning and expression of a gene encoding gelonin, a ribosome-			
RT	inactivating protein from Gelonium multiflorum.";			
RL	Gene 134:223-227(1993).			
RN	[2]			
RP	SEQUENCE OF 47-93.			
RC	TISSUE=Seed;			
RX	MEDLINE=89326691; PubMed=2753596;			
RA	Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,			
RA	Lappi D.;			
RT	"N-terminal sequence of some ribosome-inactivating proteins.";			
RL	Int. J. Pept. Protein Res. 33:263-267(1989).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).			
RX	MEDLINE=95333189; PubMed=7608981;			
RA	Hosur M.V., Nair B., Sanyamurthy P., Misquith S., Surolia A.,			
RA	Kaman K.K.;			
RT	"X-ray structure of gelonin at 1.8-A resolution.";			
RL	J. Mol. Biol. 250:368-380(1995).			
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			
CC	specific adenosine on the 28S rRNA.			
CC	-!- SUBUNIT: Homodimer.			
CC	-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.			
CC	Type 1 RIP subfamily.			

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CC EMBL; L12243; AAA16312.1; --
DR PIR; JTO753; JTO753.

```

DR HSSP; P09989; lMRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
  Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 26
FT PROPEP 27 46
FT CHAIN 47 297
FT PROPEP 298 316
FT CARBOHYD 90 96
FT ACT SITE 235 235
FT ACT SITE 212 212
FT CONFLICT 90 90
FT CONFLICT 93 93
SQ SEQUENCE 316 AA; 35418 MW; 1252F3E710901B85 CRC64;

Query Match 100.0%; Score 1287; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e-99;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYTYVNFNLRLVKLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 47 GLDTSVSTKGATYTYVNFNLRLVKLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 106
QY 61 GOLAEIAIDVTSVYVGVQVNRNRSYFFKDAADAAAYEGLFKNTIKTRLHFGGS 120
DB 107 GOLAEIAIDVTSVYVGVQVNRNRSYFFKDAADAAAYEGLFKNTIKTRLHFGGS 166
QY 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 167 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 226
QY 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 227 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 286
QY 241 ALLKEVDKDPK 251
DB 287 ALLKEVDKDPK 297

RESULT 2
Q9S9E4 PRELIMINARY; PRT; 258 AA.
ID Q9S9E4
AC Q9S9E4;
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
OS Gelonium multiflorum (Euphorbiaceae himalayana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids I; Malpighiales; Euphorbiaceae; Crotonoideae; Gelonieae;
OC Gelonium.
OX NCBI_TaxID=3979;
RN [1]
RP SEQUENCE.
RX MEDLINE=96006751; PubMed=7553224;
RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
RA Toman P.D., Cheung L.;
RT "Amino acid sequence analysis, gene construction, cloning, and
RT expression of gelonin, a toxin derived from Gelonium multiflorum.";
RL J. Interferon Cytokine Res. 15:547-555(1995).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR HSSP; P09989; lMRJ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017146; P:negative regulation of protein biosynthesis; IEA.

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DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 96.5%; Score 1242.5; DB 2; Length 258;
Best Local Similarity 95.8%; Pred. No. 6.9e-96;
Matches 248; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

QY 1 GLDTSVSTKGATYTYVNFNLRLVKLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYTYVNFNLRLVKLKPEGNHSHGIPLLRKG-DDPGKCFVLVALSNDN 59
QY 61 GOLAEIAIDVTSVYVGVQVNRNRSYFFKDAADAAAYEGLFKNTI-----KTRLHFGGS 112
DB 60 GOLAEIAIDVTSVYVGVQVNRNRSYFFKDAADAAAYEGLFKNTIKNPLLFGGKTRLHFGGS 119
QY 113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTIEASSLLVVIQMVSEAAARFTF 172
DB 120 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTIEASSLLVVIQMVSEAAARFTF 179
QY 173 IENQIRNNFOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTA 232
DB 180 IENQIRNNFOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTA 239
QY 233 VDQVKPKIALLKFDVKDPK 251
DB 240 VDQVKPKIALLKFDVKDPK 258

RESULT 3
Q94BW5 PRELIMINARY; PRT; 581 AA.
ID Q94BW5
AC Q94BW5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
RT from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL; AY039801; AAK82458.1; -.
DR HSSP; P02879; 2AAL.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008597; RicinB_like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR Pfam; PF00652; RicinB_lectin; 5.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 581
  type 2 ribosome-inactivating protein

```

FT SQ SEQUENCE 581 AA; 64215 MW; 6E8F5B8FBA3D196 CRC64; cinnamomin I.

Query Match 30.7%; Score 394.5; DB 2; Length 581;
Best Local Similarity 39.7%; Pred. No. 2.1e-24;
Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;

QY 4 TVSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCCDDP-GKCFVLVALSN--D 59
DB 35 TVTFTTKATKTSYQTFTEALRAQLASGEHPGIPVMERSTVPDSKRFILVELSNWAAD 94

QY 60 NQGLAEIAIDVTSVYVGVQVNRNSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 117
DB 95 SP--VTLAVDVNTAVYVAYRTGSGSFLEDPDAIENLLPDKRYTFPPFGSYTDLER 152

QY 118 --GEKAYRETTDLGIEPLRIGIKKLDENAINDKPTEIASLLVVIQVSEARFTFIEN 175
DB 153 VAGER--REEILLGMDPLENAISALWISNLNQOR--ALARSLIIVVIQVSEARFRFIEY 208

QY 176 QIRNPF--QORIRPANNTISLENKWKLSFOIRTSANGMFSEAELEERANGKYYVTAV 233
DB 209 RVRESITRAEMFRPDPAMLSLENKWSALSNAVQOSQGVFSSPVELRSISNKPVYVGSV 268

QY 234 -DQVKPKIALLKVF 246
DB 269 SDRVISGLAIMLFI 282

RESULT 4

ID Q94BW3 PRELIMINARY; PRT; 580 AA.

AC Q94BW3;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Type 2 ribosome-inactivating protein cinnamomin III precursor.

OS Cinnamomum camphora (Camphor tree).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Cinnamomum.

OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;

OX NCBI_TaxID=13429;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2188636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL; AY039803; AAK82460.1; -.

DR HSP; P02879; 2AAL.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008997; RicinB_like.

DR InterPro; IPR000772; Ricin_B_lectin.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00652; Ricin_B_lectin; 6.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR SMART; SM00458; RICIN; 2.

DR PROSITE; PS50231; RICIN_B_LECTIN; 2.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 32 Potential.

FT CHAIN 33 580 type 2 ribosome-inactivating protein cinnamomin III.

FT SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match 30.6%; Score 393.5; DB 2; Length 580;

Best Local Similarity 39.8%; Pred. No. 2.5e-24;
Matches 101; Conservative 46; Mismatches 90; Indels 17; Gaps 9;

QY 4 TVSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCCDDP-GKCFVLVALSN--D 59
DB 35 TVTFTTKATKTSYQTFTEALRAQLASGEHPGIPVMERSTVPDSKRFILVELSNWAAD 94

QY 60 NQGLAEIAIDVTSVYVGVQVNRNSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 117
DB 95 SP--VTLAVDVNTAVYVAYRTGSGSFLEDPDAIENLLPDKRYTFPPFGSYTDLER 152

QY 118 --GEKAYRETTDLGIEPLRIGIKKLDENAINDKPTEIASLLVVIQVSEARFTFIEN 175
DB 153 VAGER--REEILLGMDPLENAISALWISNLNQOR--ALARSLIIVVIQVSEARFRFIEY 208

QY 176 QIRNPF--QORIRPANNTISLENKWKLSFOIRTSANGMFSEAELEERANGKYYVTAV 233
DB 209 RVRESITRAEMFRPDPAMLSLENKWSALSNAVQOSQGVFSSPVELRSISNKPVYVGSV 268

QY 234 -DQVKPKIALLKVF 246
DB 269 SDRVISGLAIMLFI 282

RESULT 5

ID Q9FV22 PRELIMINARY; PRT; 549 AA.

AC Q9FV22;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Type II ribosome-inactivating protein cinnamomin (Fragment).

OS Cinnamomum camphora (Camphor tree).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Cinnamomum.

OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;

OX NCBI_TaxID=13429;

RN [1]

RP SEQUENCE FROM N.A.

RA Xie L., Liu W.-Y., Wang E.-D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL; AF259548; AAF68978.2; -.

DR HSP; P02879; 2AAL.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008997; RicinB_like.

DR InterPro; IPR000772; Ricin_B_lectin.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00652; Ricin_B_lectin; 5.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR SMART; SM00458; RICIN; 2.

DR PROSITE; PS50231; RICIN_B_LECTIN; 2.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.

FT NON_TER 1

FT SQ SEQUENCE 549 AA; 60648 MW; 02607FE607CA44B0 CRC64;

Query Match 30.5%; Score 392.5; DB 2; Length 549;
Best Local Similarity 39.7%; Pred. No. 2.8e-24;
Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;

QY 4 TVSFSTKGATYTYVNFNLRLVKLPKPGNSHGIPLLRKCCDDP-GKCFVLVALSN--D 59
DB 35 TVTFTTKATKTSYQTFTEALRAQLASGEHPGIPVMERSTVPDSKRFILVELSNWAAD 62

QY 60 NQGLAEIAIDVTSVYVGVQVNRNSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 118
DB 95 SP--VTLAVDVNTAVYVAYRTGSGSFLEDPDAIENLLPDKRYTFPPFGSYTDLER 152

Db 63 SP--VTLAVDTNAYVAYRTGSQSFLLREDNPDPAIENLLPDKTKRYTFFPSGSTDLEG 120
 QY 119 EKA-VRETTDLGIEPLRIGIKKLDENADINRYKPTIEASSLIWVQWSEAAARFTFENQI 177
 Db 121 VAGERREILGMDPLENAISALWTSNLOQR--ALARSLLVVIQWVAEVRFRFIEYRV 178
 QY 178 RNNFO--QRIRPANNTISLENKMGKLSFQIRTSANGMFSEAVELERANGKYYVAV-D 234
 Db 179 RGSISRAEMFRDPAPMLSLNKGWSALSNAVQSQNGGVFSSPVELRSISNKPVYVGSVD 238
 QY 235 QVKPKIALLKVF 246
 Db 239 RVISGLAIMLFI 250

RESULT 6

Q8GZN9 PRELIMINARY; PRT; 299 AA.
 AC Q8GZN9;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Ribosome inactivating protein Euserratin 2 precursor (EC 3.2.2.22).
 GN Name:Eus2;
 OS Euphorbia serrata.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbioidae; Euphorbiae;
 OC Euphorbia.
 OX NCBI_TaxID=196589;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Girbes T., Arias F.J., Benvenuto E.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AF457875; AA015531.1; -;
 DR HSSP; Q9AVR2; 1HNW.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
 KW Signal; Toxin.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 299 ribosome inactivating protein Euserratin
 FT CHAIN 2.
 SQ SEQUENCE 299 AA; 33115 MW; DE791872B9CE2A7D CRC64;

Query Match 30.1%; Score 388; DB 2; Length 299;
 Best Local Similarity 41.3%; Pred. No. 3.1e-24;
 Matches 102; Conservative 36; Mismatches 97; Indels 12; Gaps 5;

QY 4 TVSFSTKGATYITVYNFLNELRVKLKPEGNHGIPLLRKKCD-DPGKCFVLVALNDNGQ 62
 Db 30 SVKFTTHLASVGSYQSFWSLRKLKELDSGESHDIPLLRKPTETNNKYLVLNLYDSQ 89
 QY 63 LA-EIADVTSYVVGQVQRNRSYFFKADPADAAEGLFKNTIKTRLHFGGSYPSLEGEKA 121
 Db 90 LSITLAVTVNYYVIGYKSAGNSFFLKDAPSDAKTLFQGTNKITL---SSVDSNNYNLG 146
 QY 122 YRETTDLGIEPLRIGI---KKLDENADINRYKPTIEASSLIWVQWSEAAARFTFENQIR 178
 Db 147 DRSKVGLGIGLPSRSDITLNFKNFVSNVNNV----FKESLLVVIQWVAEVRFRFIEY 202

QY 179 NNFOQIRPANNTISLENKMGKLSFQIRTSANGMFSEAVELERANGKYYVAVDQVKP 238
 Db 203 NNLLDEYKPKNDTISYENNEKLSQIQLSGTDGKFKKPVLLLYANGTKIVSTVAQVKP 262
 QY 239 KIALKPF 245
 Db 263 DISILLY 269

RESULT 7

Q94BW4 PRELIMINARY; PRT; 580 AA.
 AC Q94BW4;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin II precursor.
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
 RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
 RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated from the seeds of camphor tree and their expression patterns.";
 RL Gene 284:215-223(2002).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AY039802; AAK82459.1; -;
 DR HSSP; P02879; 2AAL.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008997; RicinB-like.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 580 type 2 ribosome-inactivating protein cinnamomin II.
 SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECC0CBFF CRC64;

Query Match 30.0%; Score 386.5; DB 2; Length 580;
 Best Local Similarity 39.8%; Pred. No. 9.7e-24;
 Matches 101; Conservative 43; Mismatches 93; Indels 17; Gaps 9;

QY 4 TVSFSTKGATYITVYNFLNELRVKLKPEGNHGIPLLRKKCD-DP-GKCFVLVALSN---D 59
 Db 35 TVTFTTKNATKTSYQTFIEALRAQLASGEHPHGPVMDRGSTVPDSKRFILVELSNWAAD 94
 QY 60 NGQLAEIADVTSYVVGQVQRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 117
 Db 95 SP--VALADVTVNAYVAYRTGSQSFLLREDNPDPAIENLLPDKTKRYTFFPSGSTDLE 152
 QY 118 --GEKAYRETTDLGIEPLRIGIKKLDENADINRYKPTIEASSLIWVQWSEAAARFTFEN 175
 Db 153 VAGE--LREETLLGMDPLENAISALWTSNLOQR--ALARSLLVVIQWVAEVRFRFIEY 208
 QY 176 QIRNFP--QQRIRPANNTISLENKMGKLSFQIRTSANGMFSEAVELERANGKYYVAV 233
 Db 209 RVRESITRAEMFRDPAPMLSLNKGWSALSNAVQSQNGGVFSSPVELRSISNKPVYVGSV 268

Qy	234	-DQVKPKIALKFV	246	
		: : : : : :		
Db	269	SDRVISGLAIMLF	282	
RESULT 8				
Q8GT32		PRELIMINARY;	PRT;	563 AA.
ID	Q8GT32			
AC	Q8GT32;			
DT	01-MAR-2003	(TrEMBLrel. 23, Created)		
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Type 2 ribosome-inactivating protein Nigrin 1 (EC 3.2.2.22).			
OS	Sambucus nigra (European elder).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	campanulids; Dipsacales; Adoxaceae; Sambucus.			
OX	NCBI_TaxID=4202;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Leaf;			
RA	Girbes T., Arias F.J., Antolin P.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one.			
CC	specific adenosine on the 28S rRNA.			
CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.			
DR	EMBL;	AF249280;	AAN86130.1;	-
DR	HSSP;	Q9AVR2;	1HWV.	
DR	GO;	GO:0016798;	F-hydrolase activity,	acting on glycosyl bonds; IEA.
DR	GO;	GO:0030598;	F-rRNA N-glycosylase activity;	IEA.
DR	GO;	GO:0005975;	P-carbohydrate metabolism;	IEA.
DR	GO;	GO:0006952;	P-defense response;	IEA.
DR	GO;	GO:0017148;	P-negative regulation of protein biosynthesis;	IEA.
DR	GO;	GO:0009405;	P-pathogenesis;	IEA.
DR	InterPro;	IPR008997;	RicinB like.	
DR	InterPro;	IPR000772;	Ricin_B_lectin.	
DR	InterPro;	IPR001574;	RIP.	
DR	Pfam;	PF00652;	Ricin_B_lectin;	6.
DR	Pfam;	PF00161;	RIP;	1.
DR	PRINTS;	PR00396;	SHIGARICIN.	
DR	SMART;	SM00458;	RICIN; 2.	
DR	PROSITE;	PS0231;	RICIN_B_LECTIN;	2.
DR	PROSITE;	PS00275;	SHIGA_RICIN;	1.
KW	Glycosidase;	Hydrolase;	Plant defense;	Protein synthesis inhibitor;
KW	toxin.			
Qy	SEQUENCE	563 AA;	62173 MW;	0EB236421FC5E04F CRC64;
Query Match 28.1%; Score 361.5; DB 2; Length 563;				
Best Local Similarity 41.0%; Pred. No. 1.2e-21;				
Matches 94; Conservative 36; Mismatches 82; Indels 17; Gaps 8				
Qy	1	GLD--TVSFSFKGATYTYVNFLELRVLAKEG--NSHGIPLLRKKDDPKC-FVLVA	55	
Db	25	GIDYPSFNFUDGAKSATYRDFLSNLR-KTVATGTYVNGLPVLRESEVQKSRFVLVP	83	
Qy	56	LSNDNGQLAEIAIDVTSVVVGVGYOVNRNSYFFKQADPAAYEGFLKNTIKTRLHFGGSYPS	115	
Db	84	LTNYNGVTVLADVDTNLVYVAFSGNANSYFFKQATEVQKSNLFVGTQNTLSFTGNDN	143	
Qy	116	LE-GEKAYRETTDIEGIEPLRIGIKKLDENADINYPKPTETIASLLVVIQWSEAAFTTIE	174	
Db	144	LEAANTRRRESIELGPSPLDGAITSL-----YHGDSVARSLLVVIQWSEAAFRVIE	196	
Qy	175	NQIRNNFQQ--RIRPANNITISLENKWLKSLQPIRTSGAN-GMFSEAVEL	220	
Db	197	QEVRSRQQQATSFTPNASHMLSMENNWSMSLEIQAGNNVSPFSGTVQL	245	
RESULT 9				
Q8GZP0		PRELIMINARY;	PRT;	297 AA.
ID	Q8GZP0			
AC	Q8GZP0;			
DT	01-MAR-2003	(TrEMBLrel. 23, Created)		

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Dipsacales; Adoxaceae; Sambucus.
 NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bark;
 RX MEDLINE=96215449; PubMed=8647092;
 RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
 RT "Characterization and molecular cloning of *Sambucus nigra* agglutinin V
 (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
 from the bark of elderberry (*Sambucus nigra*).";
 RL Eur. J. Biochem. 237:505-513(1996).
 RN [2]
 RP SEQUENCE OF 26-49 AND 298-321.
 RC TISSUE=Bark;
 RX MEDLINE=94003077; PubMed=8400135;
 RA Girbes T., Citores L., Ferreres J.M., Rojo M.A., Iglesias R.,
 RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
 RT "Isolation and partial characterization of nigrin b, a non-toxic novel
 type 2 ribosome-inactivating protein from the bark of *Sambucus nigra*
 L.";
 RL Plant Mol. Biol. 22:1181-1186(1993).
 CC -!- FUNCTION: Non-toxic type 2 RIP which strongly inhibits mammalian
 protein synthesis but does not affect plant nor bacterial protein
 synthesis. The A chain is responsible for inhibiting protein
 synthesis through the catalytic inactivation of 60S ribosomal
 subunits by removing adenine from position 4,324 of 28S rRNA.
 CC -!- FUNCTION: The B chain is a galactose-specific lectin that
 facilitates the binding of nigrin b to the cell membrane that
 precedes endocytosis.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -!- SIMILARITY: In the N-terminal section; belongs to the ribosome-
 inactivating protein family. Type 2 RIP subfamily.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 EMBL; U41299; AAB39475.1; -;
 DR PIR; S37382; S37382.
 DR PIR; S37383; S37383.
 DR HSP; Q9AVR2; 1HWM.
 DR InterPro; IPR000772; Ricin B lectin.
 DR InterPro; IPR008997; RicinB_Like.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR Direct protein sequencing; Glycoprotein; Hydrolase; Lectin;
 KW Plant defense; Protein synthesis inhibitor; Repeat; Signal; Toxin.
 FT SIGNAL 1 25
 FT CHAIN 26 297 Nigrin b A chain.
 FT CHAIN 298 563 Nigrin b B chain.
 FT DOMAIN 305 431 Ricin B-type lectin 1.
 FT DOMAIN 434 559 Ricin B-type lectin 2.
 FT REPEAT 316 356 1-alpha.
 FT REPEAT 357 397 1-beta.
 FT REPEAT 400 432 1-gamma.
 FT REPEAT 445 482 2-alpha.
 FT REPEAT 486 524 2-beta.
 FT REPEAT 527 554
 FT ACT SITE 188 188 By similarity.
 FT DISULFID 274 302 Interchain (By similarity).
 FT DISULFID 319 338 By similarity.

FT	DISULFID	360	377	By similarity.
FT	DISULFID	448	463	By similarity.
FT	DISULFID	489	506	By similarity.
FT	CARBOHYD	221	221	N-linked (GLCNAC. . .) (Potential).
FT	CARBOHYD	368	368	N-linked (GLCNAC. . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GLCNAC. . .) (Potential).
FT	CARBOHYD	483	483	N-linked (GLCNAC. . .) (Potential).
FT	CARBOHYD	537	537	N-linked (GLCNAC. . .) (Potential).
FT	CONFLICT	39	39	K -> V (in Ref. 2).
SQ	SEQUENCE	563 AA; 62300 MW; F250CBE24621BF14	CRC64;	

Query Match 27.4%; Score 352; DB 1; Length 563;
 Best Local Similarity 41.1%; Pred. No. 7.3e-21;
 Matches 90; Conservative 34; Mismatches 79; Indels 16; Gaps 7;

QY	1	GLD--TVSFTKGTATYTYNFMELRVKLPKPEG--NSHGPIPLRKKDDPKC-FVLVA	55
Db	25	GIDYPSVFNLDGAKSATYRDLFSLNLR-KTVATGTIEVNGLPVLRRESEVQKSRFLVP	83
QY	56	LSNDNGQLAEIAIDVTSVYVVGQVRNRSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPS	115
Db	84	LITNGNTVTLAVDVTNLYVVAFGNANSYFFKDPATEVQKSNLNFVGTQNTLSFTGNDN	143
QY	116	LE-GEKAYRTTDIGIEPLRIGIKLDENALDNYKPTETIASLLVVIQWSEAAFTFIE	174
Db	144	LETAANTRRRESIELGPSPLDGAITSL-----YHGDSVARSLLVVIQWSEAAFRVIE	196
QY	175	NQIRNNFQQ--RIRPANTTISLENKWKLSQIQTSGAN	211
Db	197	QEVRRSLQQAFTFTPNALMLSMENNWSMSLEIQOAGNN	235

RESULT 11
 Q945S2 PRELIMINARY; PRT; 563 AA.
 AC Q945S2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ribosome-inactivating protein.
 GN Name=AVI;
 OS *Sambucus nigra* (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Dipsacales; Adoxaceae; Sambucus.
 ON NCBI_TaxID=4202;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Van Damme E.J.M.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AF409135; AAL04123.1; -;
 DR HSP; Q9AVR2; 1HWM.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008997; RicinB_Like.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 27.4%; Score 352; DB 2; Length 563;
 Best Local Similarity 41.1%; Pred. No. 7.3e-21;
 Matches 90; Conservative 34; Mismatches 79; Indels 16; Gaps 7;

QY 1 GLD--TVSFTSGATYITVNFNLNLR-VKLKPEGNHSHGIPLLRKKCDPGK-CFVLVAL 56
 DB 25 GIDYPSVFNLDGAKSATYRDLNLR-TKATGTYEVNGLPVLRESEVQVKSRFVLV 84

QY 56 LNDNGQLAIAIDVTSVTVVGVQVNRNSYFFKADPADAAVEGLFKNTIKTRLHFGGSYPSL 115
 DB 84 LTYNGNTVTLAVDVTNLYVAFSGNANSYFFKADATQLOKSNLFGVGTQNTLSFTGNDN 143

QY 116 LE-GEKAYRETTDLGIEPLRIGIKLDENAIIDNYKPTETASSLLVQVMSAAARFTLE 174
 DB 144 LTAANTRESIELGSPDGAITSL-----YHGDSVARSLVQVMSAAARFYIE 196

QY 175 NOIRNFOQ--RIRPANNITISLENKWKLSFOIRTSGAN 211
 DB 197 QEVRESLQOATFTNALMLSMENNWSMSLEIQAGNN 235

RESULT 12
 ID O04367 PRELIMINARY; PRT; 563 AA.
 AC O04367;
 DT 01-JUL-1997 (TREMELrel. 04, Created)
 DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Ribosome inactivating protein precursor.
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98112023; PubMed=9450339;
 RA Van Damme E.J.; Roy S.; Barre A.; Rouge P.; Van Leuven F.;
 RA Peumans W.J.;
 RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
 derived from a truncated type 2 ribosome-inactivating protein.";
 RL Plant J. 12:1251-1260(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; U76524; AAC15886.1; -;
 DR HSP; O9AVR2; 1HW.
 DR GO; GO:0030125; C:clathrin vesicle coat; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:patogenesis; IEA.
 DR InterPro; IPR001473; Clathrin_prop1_N.
 DR InterPro; IPR008997; RicinB_like.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 25
 FT CHAIN 26 297 ribosome inactivating protein, A chain.
 FT CHAIN 298 563 ribosome inactivating protein, B chain.
 SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

Query Match 27.1%; Score 348.5; DB 2; Length 563;
 Best Local Similarity 39.7%; Pred. No. 1.4e-20;
 Matches 91; Conservative 36; Mismatches 87; Indels 15; Gaps 7;

QY 1 GLD--TVSFTSGATYITVNFNLNLR-VKLKPEGNHSHGIPLLRKKCDPGK-CFVLVAL 56
 DB 25 GIDYPSVFNLDGAKSATYRDLNLR-TKATGTYEVNGLPVLRESEVQVKSRFVLV 84

QY 57 SNDNGQLAIAIDVTSVTVVGVQVNRNSYFFKADPADAAVEGLFKNTIKTRLHFGGSYPSL 116
 DB 85 TNYNGNTVTLAVDVTNLYVAFSANANSYFFKADATQLOKSNLFGVGTQHTLPTGNYDNL 144

QY 117 E-GEKAYRETTDLGIEPLRIGIKLDENAIIDNYKPTETASSLLVQVMSAAARFTFIEN 175
 DB 145 ETAAGTRRESIELGSPDGAITSL-----YDESVARSLVQVMSAAARFYIEQ 197

QY 176 QIRNFFQO--RIRPANNITISLENKWKLSFOIRTSGAN-GMFESEAVELE 221
 DB 198 EVRRSLQOATGTPNALMLSMENNWSMSLEVQOQSDNVSPFTGTVLQ 246

RESULT 13
 ID Q684J5 PRELIMINARY; PRT; 264 AA.
 AC Q684J5;
 DT 25-OCT-2004 (TREMELrel. 28, Created)
 DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
 DE Type I ribosome inactivating protein precursor (Fragment).
 OS Momordica charantia (Bitter melon) (Balsam pear).
 GN Momordica charantia (Bitter melon) (Balsam pear).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosida I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nguyen Dinh C.; Nguyen Thuy D.; Le Thi Thu H.; Nguyen Huy H.;
 RA Tran Thi Phuong L.; Nong Van H.;
 RT "Expression of a gene encoding ribosome inactivating protein from
 bitter melon (Momordica charantia).";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nong V.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AJ748278; CAH19208.1; -;
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT NON_TER 1 1 Potential.
 FT SIGNAL <1 1
 FT CHAIN 2 264 type I ribosome inactivating protein.
 SQ SEQUENCE 264 AA; 29775 MW; AD9E1175B70521AD CRC64;

Query Match 26.9%; Score 346; DB 2; Length 264;
 Best Local Similarity 37.4%; Pred. No. 8.8e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

QY 5 VSFSTSGATYITVNFNLNLR-VKLKPEGNHSHGIPLLRKKCDPGKCFVLVALSNDNGQLA 64
 DB 3 VNFDLSTATATYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSAVAYETI 61

QY 65 EIAIDVTSVTVVGVQVNRNSYFFKADPADAAVEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
 DB 62 SVAIDVTNVVAYVTRDVSFFKESPPPEAVNLFKGRKTLPTGTGNYENLQTAHKIR 121

QY 124 ETTDLGIEPLRIGIKLDENAIIDNYKPTETASSLLVQVMSAAARFTFIENQIRNFFQ 183
 DB 122 ENIDLGALPALSAL-----TTLFYNAQSAPALLVLQTTAAARFKYIERHAKYVAT 176

QY 184 RIRPANNITISLENKWKLSFOI-RTSGANGMFESEAVELELANGKKYVYVAVDQ--VKPKI 240

Db 177 NFKENLAIISLENOQSALSQKIFLAQNGGKFRNPVDLIKPTGERFQVNTNDSVVKGNI 236
 QY 241 ALL 243
 Db 237 KLL 239

RESULT 14

RIP2 MOMB
 ID RIP2 MOMB STANDARD; PRT; 286 AA.
 AC P29339;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribosome-inactivating protein momordin II precursor (BC 3.2.2.22)
 DE (rRNA N-glycosidase) (MAP 30) (B-MMC).
 OS Momordica balsamina (Bitter gourd) (Balsam apple).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX Medline=93027170; PubMed=1408771;
 RA Ortigao M., Better M.;
 RT "Momordin II, a ribosome inactivating protein from Momordica
 balsamina, is homologous to other plant proteins.";
 RL Nucleic Acids Res. 20:4662-4662(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.

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DR EMBL; 212175; CAA78166.1; -.
 DR PIR; S25560; S25560.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 286 Ribosome-inactivating protein momordin
 II.
 FT ACT SITE 181 181 By similarity.
 FT SEQUENCE 286 AA; 32031 MW; 3B89FFAE6B25986 CRC64;

Query Match 26.9%; Score 346; DB 1; Length 286;
 Best Local Similarity 37.4%; Pred. No. 9.7e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

QY 5 VSFSTKGATYITVYNFLNELRVKLKPEGNHGIPLLRKKCDPDGKCFVLVALSNDNGQLA 64
 Db 25 VNFDLSTAKYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLDLTSYAYETI 83
 QY 65 ELAIDVTSYVYGVQVRNRSYFKDADPMAYEGLFNKTKLHFGGSGYPSLE-GEKAYR 123
 Db 84 SVAIDVTNYYVAYTRDVSYFKESPPEAYNLFKGRKITLPTGTGNYENLQTAHKIR 143
 QY 124 ETTDGIIEPLRIGIKKIDENADNPKPTETIASLLVLIQWSEAAEFTFIENQIRNFQ 183
 Db 144 ENIDGLPALSSAI-----TTTFYNAQSAPALLVLQTTAAARFKIERHAYVAT 198
 QY 184 RIRPANNTISLKNWGLKLSFQI-RTSGANGMFSEAVELERANGKYYVAVDQ--VKPKI 240

Db 199 NFKENLAIISLENOQSALSQKIFLAQNGGKFRNPVDLIKPTGERFQVNTNDSVVKGNI 258
 QY 241 ALL 243
 Db 259 KLL 261

RESULT 15

RIP3 MOMCH
 ID RIP3 MOMCH STANDARD; PRT; 286 AA.
 AC P24817; Q41257; Q9FSH2; Q9FUV7;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)
 DE (rRNA N-glycosidase) (MAP 30) (B-MMC).
 GN Name=MAP30; Synonym=MAP30;
 OS Momordica charantia (Bitter melon) (Balsam pear).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC TISSUE=Leaf;
 RX Medline=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A;
 RA Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbaier A.,
 Huang H.I., Kung H.-F.;
 RT "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
 melon.";
 RL Gene 161:151-156(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Quanhong Y., Rihe P., Aisheng X.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 23-286 FROM N.A.
 RA Wei Y.-F., Cai L.-B., Zhuang W.;
 RT "Cloning rip gene and identification of its resistance to Aspergillus
 flavus.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 23-286 FROM N.A.
 RA Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;
 RT "Expression of a RIP gene from Momordica charantia in E. coli.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 24-67.
 RC TISSUE=Seed;
 RX Medline=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-O;
 RA Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.,
 Huang H.I., Huang P.L.;
 RT "MAP 30: a new inhibitor of HIV-1 infection and replication.";
 RL FEBS Lett. 272:12-18(1990).
 RN [6]
 RP STRUCTURE BY NMR OF 24-286, AND DNA BINDING.
 RX PubMed=10571185; DOI=10.1016/S0092-8574(00)81529-9;
 RA Wang Y.-X., Neamat N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,
 Huang P.L., Huang P.L., Winslow H.E., Pommer Y., Wingfield P.T.,
 Lee-Huang S., Bax A., Torchia D.A.;
 RT "Solution structure of anti-HIV-1 and anti-tumor protein MAP30:
 structural insights into its multiple functions.";
 RL Cell 99:433-442(1999).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.
 RX PubMed=10329776; DOI=10.1107/S090744499003297;
 RA Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;
 RT "Three-dimensional structure of beta-momorcharin at 2.55 A
 resolution.";
 RL Acta Crystallogr. D 55:1144-1151(1999).
 CC -!- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inhibits
 HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes

```
Qy      241 ALI 243
        ||
Db      259 KLI 261

Search completed: June 20, 2005, 09:20:41
Job time : 117.5 secs
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OM protein - protein search, using sw model

Run on: June 20, 2005, 09:00:05 ; Search time 117 Seconds
(without alignments)
829.717 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGTATITVNF.....AVDQVKPKIALLKFDKDKP 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	251	2	AAR63903 Type I ri
2	1287	100.0	251	8	ADG63044 Gelonium
3	1287	100.0	316	5	ABG71551 G. multilif
4	1287	100.0	507	5	ABG71552 Murine sc
5	1284	99.8	293	2	Aaw29300 BPI pepti
6	1284	99.8	309	2	Aaw29303 BPI pepti
7	1284	99.8	332	2	Aaw29294 BPI pepti
8	1282	99.6	251	2	AAR63923 Type I RI
9	1279	99.4	251	2	AAR63921 Type I RI
10	1279	99.4	251	2	AAR63918 Type I RI
11	1279	99.4	251	2	AAR63920 Type I RI
12	1279	99.4	251	2	AAR63919 Type I RI
13	1279	99.4	251	2	AAR63924 Type I RI
14	1278	99.3	251	2	AAR63922 Type I RI
15	1278	99.3	251	2	AAR63917 Type I RI
16	1278	99.3	251	2	AAR63912 Type I RI
17	1275	99.1	251	2	AAR74177 Type I ri
18	1269	98.6	251	2	AAR37291 Plant typ
19	1269	98.6	251	2	AAR63914 Type I RI
20	1261	98.0	251	2	AAR63915 Type I RI
21	1252	97.3	251	2	AAR63916 Type I RI
22	1242.5	96.5	258	2	AAR22227 Gelonin t
23	1176	91.4	235	2	AAR63913 Type I RI
24	346	26.9	263	2	AAR63905 Type I ri
25	346	26.9	263	2	AAR74179 Type I ri

26	346	26.9	263	8	ADG63043	Adg63043 Momordica
27	344	26.7	565	1	AAP50166	Aap50166 Sequence
28	344	26.7	565	4	AAG78300	Aag78300 Castor be
29	344	26.7	574	1	AAP70325	Aap70325 Sequence
30	343	26.7	267	2	AAR30722	Aar30722 Ricin A f
31	343	26.7	267	2	AAR37290	Aar37290 Ricin A c
32	343	26.7	267	2	AAR63902	Aar63902 Ricin A-C
33	343	26.7	267	3	AAB19265	Aab19265 Amino aci
34	343	26.7	267	7	ADC24288	Adc24288 Ricin tox
35	343	26.7	268	2	AAR39570	Aar39570 Sequence
36	343	26.7	290	2	AAW21699	Aaw21699 Ricin A-C
37	343	26.7	290	2	AAW25136	Aaw25136 Ricin A-C
38	343	26.7	332	1	AAP70097	Aap70097 Ricin A.
39	343	26.7	332	1	AAP70838	Aap70838 Sequence
40	343	26.7	332	1	AAP95639	Aap95639 Ricin A e
41	343	26.7	554	2	AAR70827	Aar70827 Anti-cata
42	343	26.7	562	1	AAP90079	Aap90079 Ricin D.
43	343	26.7	565	4	AAG78304	Aag78304 Modified
44	343	26.7	576	1	AAP70326	Aap70326 Sequence
45	343	26.7	576	2	AAW25787	Aaw25787 Castorbea

ALIGNMENTS

RESULT 1

AAR63903
ID AAR63903 standard; protein; 251 AA.

XX AAR63903;

XX 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I ribosome-inactivating protein gelonin.

XX Type I ribosome-inactivating proteins; RIPS; gelonin;

KW cytotoxic therapeutic agents; autoimmune disease; cancer;

KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

PR 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

PI Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

DR N-PSDB; AAQ75532.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.

XX Example 1; Fig 1; 221pp; English.

XX AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911. RIPS are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targeted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 251 AA;

SQ

Query Match 100.0%; Score 1287; DB 2; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1.6e-125;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYTYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYYTYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
 DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 2
 ADG63044
 ID ADG63044 standard; protein; 251 AA.
 AC ADG63044;
 DT 11-MAR-2004 (first entry)
 DE Gelonium anti-HIV protein 31kDa (GAP31).
 KW anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
 KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
 OS Gelonium multiflorum.
 XX US6652861-B1.
 PN 25-NOV-2003.
 PD 25-AUG-2000; 2000US-00645603.
 PF 26-AUG-1999; 99US-0150885P.
 PR (UYNV) UNIV NEW YORK STATE.
 PA Lee-Huang S;
 PI WPI; 2004-050519/05.
 DR New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
 PT antiviral activity, useful for treating human immunodeficiency virus
 PT infection or tumor.
 XX Example 1; SEQ ID NO 2; 22pp; English.
 PS The invention describes an isolated peptide or polypeptide having an anti-
 CC tumour and antiviral activity. Also described is a composition
 CC comprising the isolated peptide or polypeptide, and a carrier, excipient
 CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
 CC polypeptides. The peptide or polypeptide is useful for treating HIV
 CC infection, and tumour. This is the amino acid sequence of Gelonium anti-
 CC HIV protein 30kDa (MAP30).
 XX Sequence 251 AA;

Query Match 100.0%; Score 1287; DB 8; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1.6e-125;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYTYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYYTYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
 DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 3
 ABG71551
 ID ABG71551 standard; protein; 316 AA.
 AC ABG71551;
 XX 08-JAN-2003 (first entry)
 DT G. multiflorum recombinant gelonin (rGel) toxin.
 DE Modified protein; reduced antigenicity; modified toxin; gelonin;
 KW designer toxin; immunotoxin; proteinaceous compound; cancer;
 KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
 KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
 KW inflammatory disease; cardiovascular disease; diabetes;
 KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
 KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
 KW recombinant gelonin; rGel.
 XX Gelonium multiflorum.
 OS WO200269886-A2.
 PN 12-SEP-2002.
 PD 12-FEB-2002; 2002WO-US004195.
 PF 12-FEB-2001; 2001US-0268402P.
 PR (RERE-) RES DEV FOUND.
 PA Rosenblum MG, Cheung L;
 PI WPI; 2002-750431/81.
 DR N-PSDB; ABS56021.
 DR Generating a modified protein with reduced antigenicity for treating
 PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
 PT antigenic in the first subject using antiserum from either the first or a
 PT second subject.
 XX Claim 63; Page 169-170; 176pp; English.
 PS The present invention relates to a method of generating a modified
 CC protein with reduced antigenicity while maintaining its biological
 CC activity. The method comprises identifying a region of the protein that
 CC is antigenic in a first subject using antiserum from either the first
 CC subject or a second subject of the same species as the first subject. In
 CC particular the invention discloses modified toxin compounds, for example
 CC gelonin toxin derived from Gelonium multiflorum, that are truncated

CC and/or possess reduced antigenicity. Such designer toxins have
 CC therapeutic, diagnostic, and preventative benefits, particularly as
 CC immunotoxins. The method of the invention is useful for generating
 CC proteinaceous compounds with less antigenicity. The immunotoxin and
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
 CC compositions of the invention are also useful for treating microbial
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
 CC diseases, hyperproliferative disorders including cancer, leukaemias,
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
 CC diseases, and diabetes. The method provides less antigenic proteins,
 CC peptides and polypeptides, which are more effective than prior art. The
 CC present sequence represents G. multiflorum recombinant gelonin (rGel).
 XX
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1287; DB 5; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.2e-125; Indels 0; Gaps 0;
 Matches 251; Conservative 0; Mismatches 0;
 QY 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 47 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 106
 QY 61 GOLABIAIDVTSVYVGVQVRNRSYFFKADPAAYEGGLPKNTIKRLHFGGSPSLEGEK 120
 DB 107 GOLABIAIDVTSVYVGVQVRNRSYFFKADPAAYEGGLPKNTIKRLHFGGSPSLEGEK 166
 QY 121 AYRETTDGLIEPLRIGIKKLDENAIDNYKPTIASSLVVIQVSEAAFTFIENQIRN 180
 DB 167 AYRETTDGLIEPLRIGIKKLDENAIDNYKPTIASSLVVIQVSEAAFTFIENQIRN 226
 QY 181 FQORIRPANNITISLENKWKLSFQIRTSANGMWFSEAVELEERANGKYYVTVAVDQVKPKI 240
 DB 227 FQORIRPANNITISLENKWKLSFQIRTSANGMWFSEAVELEERANGKYYVTVAVDQVKPKI 286
 QY 241 ALLKFVDKDPK 251
 DB 287 ALLKFVDKDPK 297

RESULT 4
 ABG71552
 ID ABG71552 standard; protein; 507 AA.

AC ABG71552;

DT 08-JAN-2003 (first entry)

DE Murine scfWEL/G. multiflorum rGel fusion protein.

KW Modified protein; reduced antigenicity; modified toxin; gelonin;
 KW designer toxin; immunotoxin; proteinaceous compound; cancer;
 KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
 KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
 KW inflammatory disease; cardiovascular disease; diabetes;
 KW pathogenic disease; cytotoxic; antiarthritic; antiinflammatory;
 KW cardiant; antidiabetic; virucide; antiprotocacid; fungicide; antibacterial;
 KW murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;
 KW scfWEL/rGel; mutant; mutein.

OS Mus sp.
 OS Gelonium multiflorum.
 OS Synthetic.
 OS Chimeric.

PN WO200269886-A2.

PD 12-SEP-2002.

XX 12-FEB-2002; 2002WO-US004195.

PF

XX 12-FEB-2001; 2001US-0268402P.
 PR (RERE-) RES DEV FOUND.
 XX Rosenblum MG, Cheung L;
 XX WPI: 2002-750431/81.
 DR N-PSDB; ABS56029.

XX Generating a modified protein with reduced antigenicity for treating
 PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
 PT antigenic in the first subject using antiserum from either the first or a
 PT second subject.
 XX

PS Disclosure; Page 174-176; 176pp; English.

XX The present invention relates to a method of generating a modified
 CC protein with reduced antigenicity while maintaining its biological
 CC activity. The method comprises identifying a region of the protein that
 CC is antigenic in a first subject using antiserum from either the first
 CC subject or a second subject of the same species as the first subject. In
 CC particular the invention discloses modified toxin compounds, for example
 CC gelonin toxin derived from Gelonium multiflorum, that are truncated
 CC and/or possess reduced antigenicity. Such designer toxins have
 CC therapeutic, diagnostic, and preventative benefits, particularly as
 CC immunotoxins. The method of the invention is useful for generating
 CC proteinaceous compounds with less antigenicity. The immunotoxin and
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
 CC compositions of the invention are also useful for treating microbial
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
 CC diseases, hyperproliferative disorders including cancer, leukaemias,
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
 CC diseases, and diabetes. The method provides less antigenic proteins,
 CC peptides and polypeptides, which are more effective than prior art. The
 CC present sequence represents murine single-chain ZME-018 antibody/G.
 CC multiflorum recombinant gelonin (rGel) (scfWEL/rGel) fusion protein
 XX

SQ Sequence 507 AA;

Query Match 100.0%; Score 1287; DB 5; Length 507;
 Best Local Similarity 100.0%; Pred. No. 4.4e-125;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 257 GLDTSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 316
 QY 61 GOLABIAIDVTSVYVGVQVRNRSYFFKADPAAYEGGLPKNTIKRLHFGGSPSLEGEK 120
 DB 317 GOLABIAIDVTSVYVGVQVRNRSYFFKADPAAYEGGLPKNTIKRLHFGGSPSLEGEK 376
 QY 121 AYRETTDGLIEPLRIGIKKLDENAIDNYKPTIASSLVVIQVSEAAFTFIENQIRN 180
 DB 377 AYRETTDGLIEPLRIGIKKLDENAIDNYKPTIASSLVVIQVSEAAFTFIENQIRN 436
 QY 181 FQORIRPANNITISLENKWKLSFQIRTSANGMWFSEAVELEERANGKYYVTVAVDQVKPKI 240
 DB 437 FQORIRPANNITISLENKWKLSFQIRTSANGMWFSEAVELEERANGKYYVTVAVDQVKPKI 496
 QY 241 ALLKFVDKDPK 251
 DB 497 ALLKFVDKDPK 507

RESULT 5
 AAW29300
 ID AAW29300 standard; protein; 293 AA.
 XX
 AC AAW29300;

XX 20-APR-1998 (first entry)
 DT BPI peptide fusion protein PING3797 vector construct protein.
 DE Bactericidal/permeability increasing peptide; BPI; fusion protein;
 XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector.
 XX Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.
 XX WO9735009-A1.
 XX 25-SEP-1997.
 XX 18-MAR-1997; 97WO-US005287.
 XX 22-MAR-1996; 96US-00621803.
 XX (XOMA) XOMA CORP.
 XX Better MD;
 XX WPI; 1997-480215/44.
 DR N-PSDB; AAT86336.
 XX Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX Example 1; Page 160-161; 186pp; English.
 XX A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the PING3797 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts
 XX Sequence 293 AA;
 Query Match 99.8%; Score 1284; DB 2; Length 293;
 Best Local Similarity 99.6%; Pred. No. 4.1e-125;
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLDTSVSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 23 GLDTSVSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 82
 QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPAAAYEGLFKNTIKTRLHFGGSYPSLEGK 120
 DB 83 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPAAAYEGLFKNTIKTRLHFGGSYPSLEGK 142
 QY 121 AYRETTDLGIEPLRIGIKKLDENADINRYKPTBIASLLVVIQWSEAAARFTFIENQIRN 180
 DB 143 AYRETTDLGIEPLRIGIKKLDENADINRYKPTBIASLLVVIQWSEAAARFTFIENQIRN 202
 QY 181 FOORTIRPANNTISLENKWKLSFQIRTSANGMPSEAVELEERANGKKYVTVAVDQVKPKI 240
 DB 203 FOORTIRPANNTISLENKWKLSFQIRTSANGMPSEAVELEERANGKKYVTVAVDQVKPKI 262

QY 241 ALLKFVDKDPK 251
 DB 263 ALLKFVDKDPK 273

RESULT 6
 ID AAW29303 standard; protein; 309 AA.
 XX AAW29303;
 AC AAW29303;
 XX 20-APR-1998 (first entry)
 XX BPI peptide fusion protein PING3795 vector construct protein.
 XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector.
 XX Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.
 XX WO9735009-A1.
 XX 25-SEP-1997.
 XX 18-MAR-1997; 97WO-US005287.
 XX 22-MAR-1996; 96US-00621803.
 XX (XOMA) XOMA CORP.
 XX Better MD;
 XX WPI; 1997-480215/44.
 DR N-PSDB; AAT86341.
 XX Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX Example 1; Page 152-153; 186pp; English.
 XX A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the PING3795 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts
 XX Sequence 309 AA;
 Query Match 99.8%; Score 1284; DB 2; Length 309;
 Best Local Similarity 99.6%; Pred. No. 4.4e-125;
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLDTSVSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 23 GLDTSVSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 82
 QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDAPAAAYEGLFKNTIKTRLHFGGSYPSLEGK 120

Db 83 GQLAIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 142
 QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAFTFTIENQIRNN 180
 Db 143 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAFTFTIENQIRNN 202
 QY 181 FQORIRPANNTISLENKWKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 Db 203 FQORIRPANNTISLENKWKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 262
 QY 241 ALLKFVDKDPK 251
 Db 263 ALLKFVDKDPK 273

RESULT 7
 AAW29294
 ID AAW29294 standard; protein; 332 AA.
 AC AAW29294;
 XX
 DT 20-APR-1998 (first entry)
 DE BPI peptide fusion protein pING3793 vector construct protein.
 XX
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector.
 OS Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO9735009-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US005287.
 XX
 PR 22-MAR-1996; 96US-00621803.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD;
 XX
 DR WPI; 1997-480215/44.
 DR N-PSDB; AAT86332.
 XX
 PT Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX
 PS Example 1; Page 148-150; 186pp; English.
 XX
 CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the pING3793 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts
 XX
 SQ Sequence 332 AA;

Query Match 99.8%; Score 1284; DB 2; Length 332;
 Best Local Similarity 99.6%; Pred. No. 4.9e-125;
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSFTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKCDPDKCFVLVSLNDN 60
 Db 23 GLDTSVSFTKGATYITYVNFNLNLRVKKLPEGNHSHGIPLLRKKCDPDKCFVLVSLNDN 82
 QY 61 GOLABIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 120
 Db 83 GOLABIAIDVTSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 142
 QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAFTFTIENQIRNN 180
 Db 143 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAFTFTIENQIRNN 202
 QY 181 FQORIRPANNTISLENKWKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 Db 203 FQORIRPANNTISLENKWKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 262
 QY 241 ALLKFVDKDPK 251
 Db 263 ALLKFVDKDPK 273

RESULT 8
 AAR63923
 ID AAR63923 standard; protein; 251 AA.
 XX
 AC AAR63923;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX
 DE Type I RIP gelonin analog Gel(C103).
 XX
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 OS Gelonium multiflorum.
 XX
 PN WO9426910-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US005348.
 XX
 PR 12-MAY-1993; 93US-00064691.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD; Carroll SF, Studnicka GM;
 XX
 DR WPI; 1995-006804/01.
 XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.
 XX
 PS Example 3; Page 187-188; 221pp; English.
 XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 99.6%; Score 1282; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 5.3e-125;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVVVGVQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVVVGVQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDGIPLRIGIKKLDENADNYKPTFIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDGIPLRIGIKKLDENADNYKPTFIASSLLVVIQWSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 9
AAR63921
ID AAR63921 standard; protein; 251 AA.
AC AAR63921;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C10).
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 186; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

SQ Sequence 251 AA;
Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVVVGVQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVVVGVQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDGIPLRIGIKKLDENADNYKPTFIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDGIPLRIGIKKLDENADNYKPTFIASSLLVVIQWSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 10
AAR63918
ID AAR63918 standard; protein; 251 AA.
XX
AC AAR63918;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (C248).
KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 183-184; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

XX Sequence 251 AA;
SQ Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFLELRYKLPKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRYKLPKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSVPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSVPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 11
AAR63920
ID AAR63920 standard; protein; 251 AA.
XX AC AAR63920;
XX DT 25-MAR-2003 (revised)
XX DT 27-JUL-1995 (first entry)
XX DE Type I RIP gelonin analog Gel (C244).
XX KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX OS Gelonium multiflorum.
XX PN WO9426910-A1.
XX PD 24-NOV-1994.
XX PF 12-MAY-1994; 94WO-US005348.
XX PR 12-MAY-1993; 93US-00064691.
XX PA (XOMA) XOMA CORP.
XX PI Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX PS Example 3; Page 185; 221pp; English.
XX CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

CC correct PN field.)
XX Sequence 251 AA;
SQ Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFLELRYKLPKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFLELRYKLPKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSVPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKDPADAAAYEGLEFKNTIKTRLHFGGSVPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 12
AAR63919
ID AAR63919 standard; protein; 251 AA.
XX AC AAR63919;
XX DT 25-MAR-2003 (revised)
XX DT 27-JUL-1995 (first entry)
XX DE Type I RIP gelonin analog Gel (C239).
XX KW Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX OS Gelonium multiflorum.
XX PN WO9426910-A1.
XX PD 24-NOV-1994.
XX PF 12-MAY-1994; 94WO-US005348.
XX PR 12-MAY-1993; 93US-00064691.
XX PA (XOMA) XOMA CORP.
XX PI Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX PS Example 3; Page 184; 221pp; English.
XX CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSELEGEK 120
DB 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSELEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
AAR63924
ID AAR63924 standard; protein; 251 AA.
AC AAR63924;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX Type I RIP gelonin analog Gel (C184).
XX Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
XX PD 24-NOV-1994.
XX
XX PF 12-MAY-1994; 94WO-US005348.
XX
XX PR 12-MAY-1993; 93US-00064691.
XX
XX PA (XOMA) XOMA CORP.
XX
XX PI Better MD, Carroll SF, Studnicka GM;
XX
XX DR WPI; 1995-006804/01.
XX
XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX PS Example 3; Page 188-189; 221pp; English.
XX
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the

CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKCDPDKCFVLVALSNDN 60
QY 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSELEGEK 120
DB 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSELEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
AAR63922
ID AAR63922 standard; protein; 251 AA.
XX
AC AAR63922;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
XX Type I RIP gelonin analog Gel (C60).
XX Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
XX PD 24-NOV-1994.
XX
XX PF 12-MAY-1994; 94WO-US005348.
XX
XX PR 12-MAY-1993; 93US-00064691.
XX
XX PA (XOMA) XOMA CORP.
XX
XX PI Better MD, Carroll SF, Studnicka GM;
XX
XX DR WPI; 1995-006804/01.
XX
XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX PS Example 3; Page 187; 221pp; English.
XX
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of

CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX correct PN field.)
SQ Sequence 251 AA;

Query Match 99.3%; Score 1278; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 15

AAR63917
ID AAR63917 standard; protein; 251 AA.

XX AAR63917;

XX 25-MAR-2003 (revised)

XX 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel (C247).

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.

XX Example 3; Page 182-183; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunocjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is

CC targetted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX correct PN field.)
SQ Sequence 251 AA;

Query Match 99.3%; Score 1278; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYVNFNLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYITYVNFNLVRLKPEGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:16:44

Job time : 119 secs

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